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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

#### NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

#### 1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

#### 2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, ferexample, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

#### 3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

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The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, \* corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like:

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

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The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

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effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

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#### 4. DETAILED DESCRIPTION OF THE INVENTION

#### 4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

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nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4<sup>20</sup> possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match  $(1 \div 4^{25})$  times the increased probability for mismatch at each nucleotide position  $(3 \times 25)$ . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

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The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

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The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polypucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

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can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

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in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO<sub>4</sub>, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

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In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

5 As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a 10 substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, 15 by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed 20 amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

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term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

#### 4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEO ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEO ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

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The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

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the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

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hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

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vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacl, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for

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transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

#### **4.3 ANTISENSE**

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

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In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-

- 25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,
- 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a
- nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the

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inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

## 4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

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constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

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portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

#### **4.5 HOSTS**

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

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the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, ct al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

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HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

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protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No.

25 PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

## 4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

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set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polypucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

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retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

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methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat<sup>TM</sup> kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl<sup>TM</sup> or Cibacrom blue 3GA Sepharose<sup>TM</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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# 4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP 20 (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-25 Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST 30 Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

## 4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

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example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

#### 4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of 10 the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of 15 gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of 20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively 25 regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

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added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial 10 xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

#### 4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

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promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

### 4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

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polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

## 4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

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The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

#### 4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

# 4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

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confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,

Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 20 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology, J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 25 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. 30 J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

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Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

## 4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

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layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

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sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

#### 4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

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Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in:

Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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## 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

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endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

## 4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

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rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

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composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β₂ microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and

Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;
Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### 4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

## 4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

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Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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## 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

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Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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## 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

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Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate. 10

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

#### RECEPTOR/LIGAND ACTIVITY 4.10.12

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

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recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

#### 4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

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transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

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molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

#### 4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

#### 4.10.15 ANTI-INFLAMMATORY ACTIVITY

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Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

## 4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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## 4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
  - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
  - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
  - (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

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differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
  - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

## 4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

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elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### 4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

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nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

## 4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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### 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

#### 4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

# 15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered 20 to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the 25 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined 30 with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

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The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

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factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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#### 4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

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Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

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The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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#### 4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

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enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

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an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

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known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

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lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

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may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

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modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

#### 4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC<sub>50</sub> as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the

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population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD<sub>50</sub> and ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01  $\mu$ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1  $\mu$ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

# **4.12.4 PACKAGING**

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

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invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

# 4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$ ,  $F_{ab}$ , and  $F_{(ab)}$  fragments, and an  $F_{ab}$  expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as  $IgG_1$ ,  $IgG_2$ , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

# 15 5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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#### 5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol., 133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

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polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

# 5 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, 10 immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the 15 corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the 20 humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human 25 immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

# 5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

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antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse<sup>TM</sup> as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

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An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

# 20 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of  $F_{ab}$  expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.

# 5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

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binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

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stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRII (CD16) so as to focus cellular

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defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

# 5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

### 5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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# 5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>I, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

# 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

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a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

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software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

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# 4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

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# 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

#### 4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
  - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

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from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

# 10 4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

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chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

# 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

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The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm<sub>7</sub>), is then added to a final concentration of 10 mM 1-MeIm<sub>7</sub>. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm<sub>7</sub>, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

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To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

#### 4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *CviII*, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

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of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviII normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviII\*\*), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviII\*\* digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviII\*\* restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

# 4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

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Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm<sup>2</sup> and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

#### 5.0 EXAMPLES

#### **5.1.1 EXAMPLE 1**

#### Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

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#### 5.1.2 EXAMPLE 2

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# Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from <a href="http://fasta.bioch.virginia.edu">http://fasta.bioch.virginia.edu</a>) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

#### 5.2.2 EXAMPLE 3

### **Novel Nucleic Acids**

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1-327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

#### **5.3.2 EXAMPLE 4**

#### 20 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

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the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

# 25 **5.3.2 EXAMPLE 5**

### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

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Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

# 5.4.2 EXAMPLE 6

#### Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

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UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119,

UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

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# **5.6.2 EXAMPLE 8**

# Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

-	IABLEI			
	Tissue Origin	RNA Source	Hyseq Library Name	. SEQ ID NOS:
·	adult brain	GIBCO	AB3001	9 19-21 50-51 65-66 72 78 80 82
- [			120002	85 87 107-108 113 116 123 138
- 1		}		140 150-152 159 169 177 192-193
- }				202-203 212-214 225-226 235-236
		<b>f</b>		251 258 268-269 272 280-281 295
				298 301 321 326 331-332 334 356-
		· .		357 362 369 379 382-383 416 423
		1		443 459-460 473 475 477 488 496
- [		!		500 503 519 526 547 574 582 587
- 1		1 1		608-609 613 618 633-634 645-646
		}		652 657-658 660 669-671 678 687
- 1				695 697 710 715 724 731 775-777
1		ì		796 804 811 857-859 862 869 899- 900 912 919 922 924-929 933 936
				962 979 988-989 996 1001 1004-
				1008 1018 1039 1047 1059 1064
- 1				1067 1070 1078 1082 1107 1113
				1116-1117 1131 1134-1137 1140
-				1149 1151 1157 1180 1206 1229
				1234 1241 1243 1258 1272-1273
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		İ		1400 1417 1446 1468 1482 1493-
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l	}	İ	ł	941-942 945 955-958 963 966-969
Į	į.	[	1	977 979~980 985-986 990 992-993
ļ		1	1	997-1001 1005-1007 1012 1017- 1020 1023-1024 1029-1031 1034
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Tissue Origin	RNA Source	Нузед	SEQ ID NOS:
1	.0, 00000	Library Name	
			1097 1103 1107 1109 1112 1116- 1117 1119 1121 1124 1127 1130
			1134 1144-1145 1149 1151 1157-
		!	1158 1167 1170 1178 1184 1188
,			1190 1193-1194 1200 1202 1215-
			1217 1220 1226-1227 1229 1231 1241 1243 1247 1252 1258 1263
			1267 1269 1279 1281 1284 1286-
			1289 1293-1294 1306-1307 1312
	}		1316-1320 1326 1333 1338 1341 1344 1348 1351 1355-1357 1368
			1374 1377 1380 1386 1389-1390
			1394 1400 1409 1414 1422-1423
			1425-1427 1437 1443 1446 1454 1456 1458-1459 1468 1470-1472
	ĺ		1478 1482-1483 1487-1488 1493
	1		1497 1499 1506 1508-1511 1517
			1522-1524 1530-1533 1545-1546 1548-1550 1552 1557-1559:1563
			1565 1567 1569 1571 1586 1588
		1	1591 1593 1595 1598-1601 1608
		1	1611 1620-1621 1624-1626 1628 1630-1632 1636 1640-1641 1644-
	j		1645 1647 1649 1653-1655 1657
			1664 1667 1669 1673 1678-1681
		[	1686 1690 1694-1696 1701 1709 1711 1719 1722-1723 1726-1727
		į	1731-1733 1738 1740 1743-1744
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adult brain	Clontech	ABROOL	1761 1765 1771 1785 9 29 68-69 113 115 146 152 206
addic brain	Croncech	ABRUUL	223 245 277 307 320 324 330-331
			344 348 352 362 379 384 393 404
1			408 414 441-442 454 469 481 490
			715 799 803 833 865 871 875 880
			882 908 920 937 1000 1005-1006
			1027 1036 1041 1043 1075 1107 1112 1121 1127 1136-1137 1144-
}			1147 1231 1238-1239 1280 1293
			1320 1345 1355 1361 1383-1384
}			1400 1417 1448 1456 1476 1507 1570 1572 1609-1610 1614 1620
	1		1626 1645 1653 1754 1759 1770
3.32	ļ		1786
adult brain	Clontech	ABR006	5-8 15-16 168 212-213 271 278 280-281 291-292 300-301 310 314
	1		321 326 336-338 341 352 357 359-
			360 362 369 374 379 384 393 396- 397 414 419-420 426-428 430 441-
			442 453 506 616-617 661 689 785
			798 845 1018 1109 1113 1124 1148
	1		1167 1187 1207 1227 1252 1265 1285 1312 1317-1319 1324-1327
			1344 1369 1381 1400 1416 1421
			1427 1430-1431 1436 1471 1501
			1557-1559 1586 1588 1651 1653 1664-1665 1671 1673 1690 1697-
		1	1698 1700 1711 1717 1719-1720
			1728 1736 1740 1743-1744 1757 1760-1761
adult brain	Clontech	ABR008	5-10 13-19 22-23 25 29 33 37-39 43-45 50-51 54-55 57-58 60-66
1			68-70 72 75 77-80 83 85 89-92 94
		1	99-105 108-110 112-113 116-117
		1	123 128 133 135-137 139 143 145- 146 148 152 154-155 157 166 168-
		1	172 174-175 181-184 188-190 193-
1			194 196 198-200 202 204-205 207-

	Tissue Origin	RNA Source	- Turan	
		RNA SOUICE	Hyseq Library Name	SEQ ID NOS:
	,			208 210 214-215 218 221-226 229
				231-232 234-241 245-247 251-253 255 257-259 268-269 271 276-281
				285-286 288 290-292 300-302 304
				307 309-311 313 315 317-318 320-
				322 325-326 328 330-331 333-338
Į				341 344-347 349 352 354 356-357 362 369-373 376 379-380 382 384
				387 390-391 393-394 397 399-403
				405-411 414-415 417-420 426-428
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- [				784-785 787-789 794 796 799 802-
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1	1	į		883-884 887 889-892 894-895 897-
1		j		898 901 904 908 916 912 914 917
1	ļ			919 921-924 926-927 930-932 935-
	!		[	941 943 945 949 953-954 958 961- 963 967 969 971 975 977 981-983
				986 988-990 992 997 999-1002
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adult spleen	GIBCO	ASP001	106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446
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adult spleen	GIBCO	ASP001	106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684
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adult spleen	GIBCO	ASPOO1	106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794
adult spleen	GIBCO	ASP001	106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744

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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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bone marrow	Clontech	EMD007	17 56-58 103 110 117 144 150 171
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 156 271
l		1	218-221 225-226 231 237 251 277
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M	ixture of 16	Various	CTL016	401 1490 1686
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М-	mRNAS ixture of 16	- Va-/		
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- 1	mRNAs*	Vendors		
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- 1	Lanc Colvin	BIOCHAIN	CAYOOT	1 4-8 11 13 18-21 25-26 30-31 33
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<sup>\*</sup>The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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908 910-911 913-914 922-92 927 929 932-934 937 939 94 948 953 957 961 963-964 96 979 981-982 987 990 992 10 1004-1006 1010 1014 1020 1	/8 88C- 95 898
948 953 957 961 963-964 96 979 981-982 987 990 992 10 1004-1006 1010 1014 1020 1	23 926-
979 981-982 987 990 992 10 1004-1006 1010 1014 1020 1	1-942
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1105-1106 1112-1113 1116-1	117
1124 1126 1128-1129 1131 1	134
1136-1137 1142-1143 1146-1 1149-1150 1156 1161-1164 1	
1170-1173 1177-1181 1190 1	192
1197 1200 1204 1208-1209 1	214
1217 1219 1222 1230 1232-1 1235 1241 1245 1247 1254 1	233 257
1258 1260 1262 1271-1273 1	283
1286-1289 1299 1306 1314 1	320
1330-1332 1334-1335 1342 1 1349 1365-1367 1370-1372 1	345 374
1381 1394 1407 1419 1428 1	436-
1437 1440-1441 1443 1446-1	449
1454 1459 1461-1462 1468 1411 1471 1475 1477 1479 1482 1411 1475 1477 1479 1482 1411 1411 1411 1411 1411 1411 1411	470-
1497-1498 1504-1505 1507 1	513
1522 1524-1526 1528 1531 19	534
1536-1537 1548 1550 1553 15 1559 1563 1563 1573 1570 1570 1570	555-
1559 1562 1567 1578 1590-15 1597 1599-1601 1612 1614 16	516
1619-1620 1622 1624-1626 16	528
1631-1632 1634 1636 1639 16	544-
1645 1648 1651 1653-1656 16 1660 1662-1663 1667 1669 16	558
1675 1678-1681 1683-1686 16	
1691-1692 1703 1709-1711 17	717
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158 222 262 266 286 301 318	0 135

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	j		593 597 607 612 626 681 702 719
			810 859 866 878 894-895 912 916
	}	ł	922 932 935 1046 1075 1080 1099-
	1	1	1102 1113 1208 1215 1232-1233
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	ł	į	1414 1424 1430 1437 1447 1505
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		}	1667 1671 1676-1677 1683 1691-
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			1626-1627 1649 1652 1661 1670
		ł	1719 1722-1723

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SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T
NO:	NUMBER			WATERMAN SCORE	IDENTITY
1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectir precursor	10535	98
6	X02761	Homo sapiens		8990	89
В	X02761	Homo sapiens	fibronectin precursor	12564	99
9	AJ011679	Homo sapiens	Rab6 GTPase activating	5251	99
10	W88501	Homo sapiens	protein, GAPCenA Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex	11336	98
12	297630	Homo sapiens	component TRAP240  dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein RIP60	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyce s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate	1485	99
22	AF140507	Homo sapiens	reductase isolog Ca2+/calmodulin-dependent	3083	99
23	AF140507	Homo sapiens	protein kinase kinase beta Ca2+/calmodulin-dependent	2300	99
24	AJ289131	Homo sapiens	protein kinase kinase beta chondroitin 4-0-	2211	99
25	U33460 ·	Homo	sulfotransferase DNA-directed RNA polymerase	8777	
26	Y44488	sapiens	I, largest subunit	8777	98
27	U43701	Homo sapiens	ACRP30R2 variant protein.	1387	100
28	U02032	Homo sapiens	ribosomal protein L23a	791	100
29	Y41324	Homo sapiens	ribosomal protein L23a Human secreted protein	767	97
		Monto Baptens	encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens		715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	229481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34	1667	99
36	Y00644	Homo sapiens	to 287) precursor polypeptide (AA -34	1104	98
37	¥78795	Homo sapiens	to 287)  Human antizuai-2 (AZ-2) amino	3586	78
38	Y78795	Homo sapiens	acid sequence.  Human antizuai-2 (AZ-2) amino		
	l	- Lapiens	acid sequence.	4726	99

39 40 41 42	¥78795	Homo sapiens		SCORE	1
41		TOWN DAPTONS	Human antizuai-2 (AZ-2) amino acid sequence.	3556	77
42	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
	¥42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1)	795	100
	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus norvegicus	rab-related GTP-binding protein	1089	96
53	L31783	Mus musculus	uridine kinase	917	71
54	X83973	Homo sapiens	transcription factor	4486	98
55	AF224741	Homo sapiens	chloride channel protein 7	4128	99
56	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	1491	100
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	¥66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	282059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPA1 protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	¥41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccha romyces pombe	similarity to S. cerevisiae ktil2 protein	210	31
79	AF129756	Homo sapiens	G4	1554	99

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER		DESCRIPTION	SMITH-	\$ ************************************
NO:	1			WATERMAN	IDENTITY
80	AL096768	Homo sapiens	dJ858B16.2	2033	100
1	1	-	(phosphatidylserine	2033	100
	•		decarboxylase (PSSC, EC	1	{
L		}	4.1.1.65))	}	j
81	AL096768	Homo sapiens	dJ858B16.2	1220	96
ļ	1	1	[phosphatidylserine	1	1 -0
1	ĺ		decarboxylase (PSSC, EC	(	İ
			4.1.1.65))		
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984 1	2700	98
84	X73113	Homo sapiens		5959	199
85	AF097330	Homo sapiens	H1 chloride channel; p64H1;	1305	99
			CLIC4	1	1 33
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo	triggering receptor expressed	1214	100
L		sapiens	on monocytes 1	1223	100
89	AB016879	Arabidopsis	contains similarity to pre-	634	36
l	-{	thaliana	mRNA splicing	1034	1 36
L			factor-gene_id:MRB17.2	ľ	ì
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino	3890	100
<u> </u>	ł	1	acid sequence SEQ ID NO:86.	3030	100
94	Y87231	Homo sapiens	Human signal peptide	1031	100
1	1	1	containing protein HSPP-8	1001	100
		•	SEQ ID NO:8.	Ť	
95	AF227741	Rattus	protein kinase WNK1	2428	95
		norvegicus		1	1 22
96	AF227741	Rattus	protein kinase WNK1	1961	94
		norvegicus			
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related	3423	100
			protein)	]	} ~~~
99	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like	4092	99
	I		kinase substrate sGNK.	1	{ ``
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1509	100
	1		(translation of the cDNA		
100	+		DKFZp566A0946, Em:AL050069))		
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa	.2042	96
104	1		protein AUP1	1	
105	AB015982	Homo sapiens	serine/threonine kinase	4718	100
	AF151074	Homo sapiens	HSPC240	831	64
106	M35522	Canis	GTP-binding protein (rab7)	354	50
107		familiaris		1 1	
107	R99800	Homo sapiens	NTII-1 nerve protein,	2337	93
	1		facilitates regeneration of	}	
108	2022555		nerve cells.	)	
100	AF125533	Homo sapiens	NADH-cytochrome b5 reductase	1290	93
109	20005614		isoform		
110	AC005614	Homo sapiens	F23269_2	3369	99
111	AF064729	Homo sapiens	RAN binding protein 16	3285	100
	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo	Human PRO274 protein	2285	100
115	W15505	sapiens	sequence.	]	1
113	W15506	Homo sapiens	Mitogen activating protein	1991	100
			kinase ERK1.	1	J
	l-1222		Unimon materials and the second secon		99
114	Y71071	Homo sapiens	Human membrane transport	1190	<i>99</i> 1
			protein, MTRP-16.	1190	"
114	Y71071 AL049548	Homo sapiens	protein, MTRP-16. dJ398G3.1 (ortholog of rat	3497	99
115	AL049548	Homo sapiens	protein, MTRP-16. dJ398G3.1 (ortholog of rat CPG2)		
			protein, MTRP-16. dJ398G3.1 (ortholog of rat		

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	identity
	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	sapiens	PRO1038	1469	100
118	AF116618	Homo sapiens	alpha 4 protein	1748	100
119 120	Y08915 AF098070	Homo sapiens Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabdit is elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu s sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
14).	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	Z68493	Caenorhabdit is elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A.human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	Human secreted protein encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue	785	99
151	010397	Saccharomyce s cerevisiae	Yhrl46wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T - %
ID	NUMBER	1	i i	WATERMAN	IDENTIT
NO:				SCORE	1
			similar to arginyl-tRNA)	<del> </del>	
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein	1471	100
			encoded from gene 6.	1	1
158	W77404	Homo sapiens	Secreted salivary polypeptide zsig32.	937	100
159	Y17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible	484	98
		F	protein, HIFI.		1 30
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster	1357	100
	Į.	1	Androgen-dependent Expressed	1337	100
	l		Protein LIKE PUTATIVE	į.	i
	1	j	protein) (isoform 1)	1	1
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ	463	97
		1	ID NO: 7713.	1.00	1 - 1
165	AJ250839	Homo sapiens	serine/threonine protein	1442	71
		1	kinase		1 '-
166	L09649	Zymomonas	zm2	173	37
		mobilis			1 "
167	¥73337	Homo sapiens	HTRM clone 1944530 protein	1204	100
		1	sequence.	, 2001	100
168	W88645	Homo sapiens	Secreted protein encoded by	1084	100
			gene 112 clone HUKFC71.	2001	] 100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacte	conserved protein	166	27
	}	rium	,	100	~ ′
		thermoautotr		ſ	ĺ
		ophicum	ļ	j	j
171	¥27684	Homo sapiens	Human secreted protein	821	100
			encoded by gene No. 118.	)	}
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	¥07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo	Human DP1 homologue proteir.	966	100
		sapiens		ļ	
177	Y41675	Homo sapiens	Human channel-related	1122	100
		L	molecule HCRM-3.		
178	Y41674	Homo sapiens	Human channel-related	936	99
			molecule HCRM-2.		
179	AF220492	Homo sapiens	krueppel-like zinc finger	4100	99
		<u></u> j	protein HZF2		
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear	1389	58
1			protein		
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein	1188	99
}	1	1	encoded by gene 2 clone		
			HLDBG33.		
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
.90	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
91	Y22203	Homo sapiens	Human calcium-binding	1083	99
J	į	J	phosphoprotein, CBPP-1,		
		(	protein sequence.		
.92	W63692	Ното	Human secreted protein 12.	1975	100
		sapiens	• • • • • • • • • • • • • • • • • • • •		
193	W87772	Homo sapiens	Human serum glucocorticoid-	2605	99
	1	7 1	regulated kinase (H-SGK2)	· · · · · · · · · · · · · · · · ·	- <del>-</del>
1	i	1	regulated killase (n-SGK2)	1	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61.
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase- 2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	¥87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	X05860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chair.	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	229328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe	-	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens		5199	98
225	AB032401	Mus musculus		1761	92
226	AB032401	Mus musculus		1988	92
227	X83502	Saccharomyce s cerevisiae		112	
228	X83502	Saccharomyce s cerevisiae	: - }	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	¥66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens		1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	_ 1 <del>-</del>	2218	99
234	Y53762	Homo sapiens		1017	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
235	250749	<del> </del>	designated RAQ.		†
236	250749	Homo sapiens		1800	100
237	AB026491	Homo sapiens		1754	98
238	AJ270205	Homo sapiens		2137	100
230	AD270205	caudatum	putative	114	37
ì	1	Caudacum	phosphatidylinositol-4-		1
239	AB030189	Mus musculus	phosphate 5-kinase		1
-02	1.2030103	Mus musculus	contains transmembrane (TM)	710	93
240	W56538	Homo sapiens	region and ATP binding region		1
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	10000 Baptens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	protein (HIP). Human hedgehog interacting		1
		nome adpicina	protein (HIP).	3436	99
242	AF155107	Homo sapiens	Protein (HIP). NY-REN-37 antigen		<u> </u>
243	AF155107	Homo sapiens	NI-REN-37 antigen	996	99
244	AL031320	Homo sapiens		1005	100
	123332520	nomo saptens	dJ20N2.1 (novel protein	763	99
}	}		similar to yeast and	!	1
	1	[	bacterial cytosine deaminase)	1	ſ
245	U37026	Rattus	dealithase)		<u> </u>
1	1	norvegicus	sodium channel beta 2 subunit	162	30
246	AL078599	Homo sapiens			
		nomo sapiens	dJ991C6.1 (novel protein	2391	98
		1	similar to C. elegans	İ	
247	U32274	Saccharomyce	F55A12.9 (Tr:P91086))		<u> </u>
	000271	s cerevisiae	Ydr386wp; CAI: 0.12	191	37
248	Y41719	Homo	The proof		L
	1 2 2 7 2 3	sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor		
250	X97831	Rattus	carnitine/acylcarnitine	611	100
	}	norvegicus	carrier protein	246	38
251	W80993	Homo	Human RIP-interacting factor	<u> </u>	
		sapiens	RIF.	1724	100
252	¥94873	Homo	Human protein clone HP02632.		
	ļ	sapiens	didness process crosse Apo2632.	1876	100
253	W59878	Homo sapiens	Amino acid sequence of the	765	
	į	]	CDNA clone AIF-2 (HEBGM49).	765	100
254	AL354533	Leishmania	possible adenylate kinase	265	34
	<b>!</b>	major	F-10-220 adenytate kinase	205	34
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal	2247	99
	j .	-	regulator CKSR-1 SEQ ID	2247	99
			NO:1.	i i	
257	AL035539	Arabidopsis	putative amino acid transport	390	27
	L	thaliana	protein	1 3 50	21
258	W74787	Homo sapiens	Human secreted protein	1171	100
1	i i		encoded by gene 58 clone	/-	100
	L		HHFHN61.		l
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein	974	100
	!		similar to protein kinase C	1	100
			inhibitors)		l
260	AE000909	Methanobacte	serine/threonine protein	363	30
		rium	kinase related protein	1	30
		thermoautotr			1
		ophicum			
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel	1072	100
			protein similar to APOBEC1)		-50
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein	1888	99
- 1		-	kinase domains containing	-300	7.7
l	1	ſ	protein similar to	í	ſ
			phosphoprotein C8FW)	Į.	

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	CMTTH	· · · · · · · · · · · · · · · · · · ·
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	NOMBER	Į.		SCORE	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Homo saprens	HHa5 hair keratin type I	2190	99
270	V20107	sapiens	intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1.050	<u> </u>
272		1		1952	100
272	M32334	Homo sapiens	intercellular adhesion	1436	100
	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	<del></del>	molecule 2		
273	AF161483	Homo sapiens	HSPC134	663	61
274	Y53052	Homo sapiens	Human secreted protein clone	587	100
	<b>!</b>		df202_3 protein sequence SEQ	ļ	
		<u> </u>	ID NO:110.		<u> </u>
276	¥77576	Homo sapiens	Human cytoskeletal protein	762	100
	\		(HCYT) (clone 2195418).	L	<u> </u>
277	AF077042	Homo sapiens	30S ribosomal protein S7	1269	100
			homolog		1
278	Y94907	Homo sapiens	Human secreted protein clone	1619	98
			ca106_19x protein sequence	1	1
			SEQ ID NO:20.		1
279	Y68788	Homo sapiens	Amino acid sequence of a	2801	.99
	1		human phosphorylation	[	1
	1		effector PHSP-20.	ŀ	1
280	275134	Canis	rod transducin	1816	100
	1	familiaris	1	1	1
281	Z75134	Canis	rod transducin	1718	96
	1	familiaris	İ		1
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	Y35897	Homo sapiens	Extended human secreted	1250	99
		· -	protein sequence, SEQ ID NO.		1
	i	İ	146.		ì
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y66724	Homo	Membrane-bound protein	2321	100
		sapiens	PRO836.		1
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein	1738	100
·			(isoform 1))	1 -/	1 -00
294	Y73348	Homo sapiens	HTRM clone 839651 protein	1245	99
	1	F-0.10	sequence.	1 2223	1
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ20[3.1 (brain mitochondrial	1024	79
	1	July Suprems	carrier protein-1 (BMCP1))	1024	( "
297	AF198532	Homo sapiens	lymphoid enhancer binding	2173	100
	220052	nome suprems	factor-1	21/3	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	breast cancer metastasis-	1236	
~~~	1 2 2 3 2 3 2	aapre:is	suppressor 1	1230	99
300	U26397	Rattus	inositol polyphosphate 4-	160	30
100	) "2033"	norvegicus	phosphatase	160	30
301	AF036145	Homo sapiens	1	3450	1100
301	VE 020T#2	nomo sapiens	meningioma-expressed antigen	3458	100
302	Z82022	Nomo en el en el	<u> </u>	1	100
303	AF269232	Homo sapiens	GlcNac-1-P transferase	2067	99
203	AE 403434	was musculus	butyrophilin-like protein	271	50
300	77777644	+ Name 2	BUTR-1	1	<del> </del>
304	AJ222644	Arabidopsis	asparaginyl-tRNA synthetase	659	50
	<del> </del>	thaliana		<u> </u>	
305	AF054180	Homo	hematopoietic cell derived	351	79
		sapiens	zinc finger protein	<u> </u>	1
306	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	3056	100
308	¥44486	Homo	Human GPRW receptor	1721	100
		sapiens	polypeptide.	I	L
309	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

SEQ	ACCESSION	SPECIES	DEGOD-PMTON		
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	8
NO:	HOLDER			WATERMAN	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	SCORE	
311	AF176525	Mus musculus	F-box protein FBL12	1248	92
312	X57802	Homo sapiens	immunoglobulin lambda light	1501	93
1 322	1.57002	nomo paprens	chain tambda light	959 .	81
313	236715	Homo sapiens	Net		<u> </u>
314	AF161532	Homo sapiens	HSPC047	2048	98
315	AF208068			727	100
316	Y66666	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	100000		Membrane-bound protein	1166	100
317	¥29666	sapiens Homo sapiens	PRO1013.	<u> </u>	J.,
318			Human Ras protein RAPR-1.	1253	98
319	AJ387747	Homo sapiens	sialín	2614	99
1	AF161362	Homo sapiens	HSPC099	224.	40
320	Y68773	Homo sapiens	Amino acid sequence of a	2243	99
			human phosphorylation		ł
			effector PHSP-5.		
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein	913	100
			vc48_1, SEQ ID NO:66.		i
324	Y13381	Homo sapiens	Amino acid sequence of	1976	100
	ļ <u>.</u>	<u>}</u>	protein PRO271.	j	
325	Y94944	Homo sapiens	Human secreted protein clone	2305	98
		1	bf157 16 protein sequence		1
	_		SEQ ID NO:94.		
326	Y76884	Homo sapiens	Retinoblastoma binding	6728	99
		,	protein-7sequence.		
327	AF198532	Homo sapiens	lymphoid enhancer binding	2173	100
J	j	,	factor-1	]	]
328	278013	Caenorhabdit	Similarity to Drosophila	569	33
1		is elegans	Cadherin-related tumor	1	l
	•		suppressor		1
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	275330	Homo	nuclear protein SA-1	6492	99
[		sapiens]	-		
! !		>R65207			
1		R65207 02-			
1 1		MAR-1995 27-		ł	
†		AUG-1993			
í		Human	<del>}</del>	ľ	
		stromalin-1.		1	
1		[Homo			
		sapiens		ļ	
331	AL008583	Homo sapiens	dJ327J16.3 (supported by	2133	99
			GENSCAN, FGENES and GENEWISE)		
332	Y36104	Homo sapiens	Extended human secreted	310	41
			protein sequence, SEQ ID NO.		
			489.		
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria	em100 gene is homologous the	154	26
		maxima	Eimeria tenella gene et100	)	-
336	Y85564	Homo sapiens	Human homologue of UNC-53	3386	97
			(Hs-UNC-53/1) sequence.		- 1
337	Y85564	Homo sapiens	Human homologue of UNC-53	2602	94
		-	(Hs-UNC-53/1) sequence.		
338	Y85564	Homo sapiens	Human homologue of UNC-53	3447	98
		-	(Hs-UNC-53/1) sequence.		
339	266561	Caenorhabdit	Similarity to Human rab13	716	34
ŀ	1	is elegans	protein (PIR Acc. No.		
ĺ	į		A49647).		ľ
340	AB021643	Homo	gonadotropin inducible	2761	99
ı	ļ	sapiens	transcription repressor-3	~ ′ ′ * †	<i></i>
341	G01946	Homo sapiens	Human secreted protein, SEO	465	98
1	l		ID NO: 6027.	703	50
342	AF020591	Homo sapiens	zinc finger protein	1091	48
343	L29154	Homo sapiens	immunoglobulin heavy chain	439 .	84
				-22	04

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			VDJ region	-	
344	U10281	Sus scrofa	gastric mucin	279	99
345 346	L22557	Homo sapiens Rattus norvegicus	unnamed protein product calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSB196.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	¥53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	pl16Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	¥73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PR00518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
	1 175 4 5 6 6	Caenorhabdit	coded for by C. elegans cDNA	246	36
383	U64608	is elegans	yk173cl2.5		<u> </u>
383 384 385	U50133 AJ238520		yk173cl2.5 ankyrin putative transcription	502 4123	33

SEO	ACCESSION	SPECIES	DECORTOR		
ID NO:	NUMBER	J. D. L.	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	, wambaa 11911c	797	76
390	AF182404	Homo sapiens		1670	99
391	Y85564	Homo sapiens	1	3386	97
393	AF178432	Homo sapiens	(Hs-UNC-53/1) sequence.	3700	100
394	AF229928	Drosophila	cytoplasmic protein 89BC	1616	62
395	AF181721	melanogaster Homo sapiens			
396	Y69197	Homo sapiens		2254	100
			human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha	WD repeat protein	447	27
		romyces pombe		1 3 7	27
401	AC004859	Homo sapiens	similar to 2-oxoglutarate	4176	78
L			dehydrogenase; similar to Q02218 (PID:g1352618)	117.0	/*
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to	761	100
			D.melanogaster CG5986 protein)	, 01	100
404	Z68753	Caenorhabdit	ZC518.3b	888	48
405	-	is elegans		***	30
	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing	2961 .	99
416	U43503	Saccharomyce	Subunit Lph1p	115	42
417	AL160493	s cerevisiae Leishmania	possible t26f17.21	239	35
430	V00100	major		]	· ·
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
423	AL137530	Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	son-a	7269	100
425	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7	1084	55
			precursor		

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1 - 2
ID NO:	NUMBER	_		WATERMAN SCORE	IDENTITY
427	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1259	56
428	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin .	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	piL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	Z68753 W39160	Caenorhabdit is elegans	ZC518.3b	951	49
452	W85727	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	Y53629	Homo sapiens Homo sapiens	Novel protein (Clone BM46_10).	2799	99
454	D87438	Homo sapiens	A bone marrow secreted protein designated BMS115. Similar to a C.elegans	2810	100
455	AF240468	sapiens Homo sapiens	protein in cosmid C14H10	4069	100
456	Z15005	Homo sapiens	CENP-E	3687 13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	¥73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	F25965_1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	- Guyeny	
ID NO:	NUMBER	0.2022	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
466	AF22340B	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus	Jun dimerization protein 1	196	49
L		norvegicus	JDP-1	1 - 3 - 3	133
469	AL031297	Homo sapiens	dJ97P20.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation	1274	95
			initiation factor EIF2B subunit 3		
471	L28125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease	838	100
			related polypeptide IMX39.		,
475	¥95006	Homo sapiens	Human secreted protein vel3_1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccha romyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38961	Saccharomyce s cerevisiae	mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST F08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportinl	2929	100
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	X16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2056	
503	AJ249732	Homo sapiens	G8 protein	2856	99
504	AF208861	Homo sapiens	BM-019	669	100
505	L09708	Homo sapiens	complement component C2	1629	100
507	X66285	Mus musculus	HC1 ORF	4022	100
508	D00189	Rattus	Na+,K+-ATPase alpha-subunit	115 5227	43
		norvegicus	are aspiration of the second	2421	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
509	Y94971	Homo sapiens	Human secreted protein clone fa171_1 protein sequence SEQ ID NO:148.	2176	100
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513	X84908	Homo sapiens	phosphorylase kinase	5729	99
514	X52851	Homo sapiens	peptidylprolyl isomerase	650	76
515	AF186084	Homo sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	¥99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu s fulgidus	chromosome segregation protein (smc1)	153	20
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	93
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	35
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	1616	100
529	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBBI88) similar to mouse IFN-gamma induce MG11.)	1059	95
531	¥91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit	carrier protein (c2)	576	50
533	X76116	is elegans Caenorhabdit	carrier protein (c2)	506	50
534	X12966	is elegans Homo sapiens	3-oxoacyl-CoA thiolase	1972	100
		-	propeptide (424 AA)	1	
535	Y09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
540 541	D84224 J03244	Homo sapiens Bos taurus	methionyl tRNA synthetase H+ ATPase 31kDa subunit (EC	4529 848	99
543	1,0055	<del> </del>	3.6.1.3)	1	1
542	Y92514	Homo sapiens	Human OXRE-11.	2301	99
543	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacte rium thermoautotr ophicum	conserved protein	207	38
545	A06669	synthetic construct	preTGF-betal	2070	99

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Section				encoded by gene 49 clone	854	9B
A60271					2275	100
Acolisary				c-rel	2264	
Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapiens   Sapi			thaliana	putative GTPase		
SS2			sapiens	protein-2.	429	68
1553   NF119855   Homo sapiens   Human transembrane protein   1112   95				NEDD4-like ubicuitin ligase 1	8290	99
Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile   Mile			Homo sapiens	Human transmembrane protein	1112	
					265	67
AC006963   Homo sapiens   Similar to Kelch proteins;   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar to Bah77027   Similar t				MHC HLA-DQ alpha precursor		
Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sect		AL078468		putative protein		
1623   98   1623   98   1625   98   1625   98   1626   98   1627   1627   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   1628   162				similar to BAA77027	515	44
Mile					1623	98
Secreted protein   225   56   56   56   56   56   56   5		.1			_1 .	1
AF003136   Caenorhabdit   Sontains weak similarity to   2926   54				encoded by gene 97 clone HAQBF73.	225	
AF003136   Caenorhabdit   contains weak similarity to   selegams   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity to   selegams   contains weak similarity   contains   contains weak similarity   contains   contains weak similarity   contains   contains weak similarity   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   contains   conta		1		junD protein	373	88
AF181640   Drosophila   BcDNA.GH09817   289   42			is elegans	an AMP-binding motif	2926	_
School				(poly(A)-binding protein)	877	100
Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   Second   S	_		melanogaster	BcDNA.GH09817	289	42
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100			leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100					439	44
Mono sapiens   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April   April				pt326_4 secreted protein.	3338	
AF155113				zinc finger protein	-1	
AL032821   Homo sapiens   MT-REN-55 antigen   3951   99					3603	
AL032821   Homo sapiens   dJ55C23.1 (vanin 1)   1821   98					3951	99
M69181   Homo sapiens   non-muscle myosin B   7350   99				dJ55C23.1 (vanin 1)		
Homo sapiens   Homo sapiens   Homo sapiens   Homo sapiens   Secreted protein   108-008-5-0-   772   100				non-muscle myosin B	1	
Y59678			Homo sapiens	non-muscle myosin B	4.	
thaliana Arabidopsis thaliana  576 AL365234 Arabidopsis putative protein  577 X06745 Homo sapiens DNA polymerase alpha-subunit  578 AB041642 Homo sapiens PAR-6  579 D86984 Homo sapiens similar to yeast adenylate cyclase (S56776)  580 AF165124 Homo sapiens gamma-aminobutyric acid A cyclase (S56776)  581 W88812 Homo sapiens Polypeptide fragment encoded by gene 58.  582 U82319 Homo sapiens novel ORF  583 P92219 Homo sapiens CRI protein.  584 AJ223948 Homo sapiens RNA helicase  585 Y08612 Homo sapiens RNA helicase  586 Y42384 Homo Amino acid sequence of sapiens sapiens lv310 7.			•	Secreted protein 108-008-5-0-		
Thaliana			thaliana	putative protein	788	40
No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.			thaliana	•	788	40
D86984			·		7619	99
D86984			Homo sapiens		1342	100
Second Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Septem   Sep			j	cyclase (S56776)		
W88812			1	receptor gamma 2	2499	99
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100			Homo sapiens	Polypeptide fragment encoded	2339	99
P92219			Homo sapiens		342	100
1007   37   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   1007   10		ľ	Homo sapiens			
Y08612   Homo sapiens   88kDa nuclear pore complex   99	84	AJ223948		RNA helicase	6600	
586 Y42384 Homo Amino acid sequence of 1007 37 sapiens 1v310 7.	85	Y08612		88kDa nuclear pore complex		
587 AF129756 Homo sanione Barrier	86	Y42384	Homo sapiens	Amino acid sequence of	1007	37
1873 98	87	AF129756	Homo sapiens	BAT4	1873	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
588	AF131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TESS 2	2348	100
591	298885	Homo sapiens	dJ522J7.2 (bromodomain- containing 1 (similar to peregrin, BR140))	4167	100
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GF003	2009	99
598	AJ278112	Homo sapiens] >Y49635 Y49635 21- OCT-1999 15- APR-1998 Human sdp3.5 protein. (Homo	putative cell cycle control protein	335	23
		sapiens		1	
599	Y59741	Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens	GGA1	3265	100
603	¥13115	Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralari	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 ElA protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Bnsis minor	nuclear protein	345	30
613	Y91954	Homo sapiens	Human cytoskeleton associated protein 9 (CYSKP-9).	3668	100
614	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
615	X85786	Homo sapiens	binding regulatory factor	3203	100
616	Y08319	Homo sapiens	kinesin-2	3487	99
617 618	D12644 U28789	Mus musculus	KIF2 protein PACT	3609 5936	97 89
619	¥35914	Mus musculus Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 163.	1684	99
620	AB046382	Mus musculus	testis-abundant finger protein	199	23
621	Y00062	Homo sapiens	precursor polypeptide (AA -23 to 1120)	3440	99
622	AF068286	Homo sapiens	HDCMD38P	861	100
623	X98248	Homo sapiens	sortilin	4436	99
624	X61100	Homo sapiens	75 kDa subunit NADH dehydrogenase precursor	3734	99
625	S58544	Homo sapiens	75 kda infertility-related sperm protein	2125	99
626	AF151027	Homo sapiens		582	93
627	X14968	Homo sapiens	RII-alpha subunit (AA 1-404)	2079	100
628	Y50911	Homo sapiens		1983	100

NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW   NOW	SEQ	ACCESSION	SPECIES	DESCRIPTION	ON YOUR	
No.	J		0.20120	DESCRIPTION	SMITH- WATERMAN	F DENIE Tour
Section	I-					TDENTITY
100   175   16   175   16   175   16   175   16   16   175   16   16   175   16   16   175   16   16   175   16   16   175   16   16   175   16   16   175   16   16   175   16   175   16   175   175   16   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   175   17	629	Y50911	Homo sapiens	Human fetal brain cDNA clone	•	100
Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Saplens   Sapl	(22	100000	<u> </u>	vb7 1 derived protein.		
Sal	630	AF098786		17 beta-hydroxysteroid	1754	100
Sapiens	631	AT-034555		denydrogenase type VII		
632   W74826   Homo sapiens   Human secreted protein   794   96	1 031	1 40034333			4273	100
encoded by gene 98 clone	632	W74826		Human secreted protein		
AP289288	j	]		encoded by gene 98 clone	794	96
APO41429   Home sapiens   PROM   PROM   2236   100	I			HAOBT94.		i
		AF288288	Homo sapiens	HPT protein	2236	1200
Section   New   Septemble   Sering   Sering   Chreenine   Protein   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninase   Ninas	L					
Ninase	635	X66357	Homo sapiens	serine/threonine protein		
ABOOLSB8		ļ				200
A					2571	98
100		<u> </u>		*	3718	99
100					1020	100
D87682   Homo Sapiens   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synaphropy   Synap				synaptogyrin 1b	1002	100
### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  #### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cosmid T26AS.  ### Protein Encoded in Cashida Incoming T26AS.  ### Protein Encoded in Cashida Incoming T26AS.  ### Protein Encoded in Cashida Incoming T26AS.  ### Protein Encoded in Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Protein Cashida Incoming T26AS.  ### Prote		_1		synaptogyrin 1c	933	94
T26A5.	041	D07002	Homo sapiens		2676	100
642   M14660   Homo sapiens   ISC-K54   2473   99			ł		1	1
643   X06661   Homo sapiens   Calbindin (AA 1-261)   1358   100	642	M14660	Homo saniene			
AF11990	643					
AB031048	644					
melanogaster	645	AB031048		·		1
AF250842   Drosophila   melanogaster   melanogaster   melanogaster   melanogaster   Mi-2 protein   10110   99					/38	27
Memo sapiens   Mi-2 protein   10110   99	646	AF250842			834	20
		<u></u>	melanogaster	•	554	23
AF236061   Oryctolagus cuniculus   RING-finger binding protein   3930   91					10110	99
AF236061   Oryctolagus cuniculus cuniculus cuniculus cuniculus cuniculus cuniculus cuniculus similar to Mus musculus activity-dependent neuroprotective protein (Admp)   2388   99   99   99   99   99   99   99	648	U67934	Homo sapiens		827	
Cuniculus   GJ914P20.2 (KIAA0784 protein   S708   S708   Similar to Mus musculus activity-dependent neuroprotective protein (Adnp))   GABA-A receptor alpha 1   S388   99   Similar to f-spondin proteins   S3026   99   Similar to f-spondin proteins   S3026   S708   Similar to f-spondin proteins   S1026   S108   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109   S109	<u> </u>	37036061		<del></del>		
AL034553   Homo sapiens   GJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))   GABA-A receptor alpha 1 subunit   Similar to f-spondin proteins   3026   99   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026   3026	649	AF236061		RING-finger binding protein	3930	91
Similar to Mus musculus activity-dependent neuroprotective protein (Adnp)   CABA-A receptor alpha   2388   99	650	AT-034553		470.470		<u></u>
activity-dependent   neuroprotective protein (Adnp)		12001333	LIOUIO SAPTEIIS	Gimilar to Mus musellus	5708	100
neuroprotective protein (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adnp)   (Adn		].				
AC004614   Homo sapiens   GABA-A receptor alpha 1   2388   99		1		neuroprotective protein	1	
Subunit   Similar to f-spondin proteins   3026   99				(Adnp))		
AC004614   Homo sapiens   Similar to f-spondin proteins   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   AB006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (PID:g2529225)   Ab006086 (	653	X14766	Homo sapiens	GABA-A receptor alpha 1	2388	99
AB006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g2529225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g25292225)  4B006086 (PID:g252922225)  4B006086 (PID:g252922225)  4B006086 (PID:g252922225)  4B006086 (PID:g252922225)  4B006086 (PID:g252922225)  4B00608	664	3 00 3 4 4 4		subunit		
Homo sapiens	654	AC004614	Homo sapiens	similar to f-spondin proteins	3026	99
State	ZEE	VE7000	· · · · · · · · · · · · · · · · · · ·			
According to the complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex   Complex	055	15/906	Homo sapiens		608	99
ALOS0306	656	234975	Homo sanione			
W76734						
Sapiens   Protein.   34			Homo	Human mDia Pho targetina	1 1	
660         AF202724         Homo sapiens         Sadl unc-84 domain protein 1         2172         100           661         Z21966         Homo sapiens         mPOU homeobox protein         1529         100           662         AJ242954         Mus musculus         dysferlin         4752         59           663         AF182316         Homo sapiens         myoferlin         6232         99           665         AL161516         Arabidopsis thaliana         hypothetical protein         209         30           667         X59303         Homo sapiens         valyl-tRNA synthetase         3393         99           668         Y13355         Homo sapiens         Amino acid sequence of protein PRO220.         3692         100           669         AB010692         Arabidopsis contains similarity to endobeta-N-acetylglucosaminidase gene         611         52           671         X56123         Mus musculus talin         4474         76           672         AB039371         Homo sapiens         mitochondrial ABC transporter         2902         99           673         AF269223         Homo sapiens         TCP11         806         42           674         AF229633         Mus musculus         groucho-related prot			sapiens	protein.	'81 ·	34
661         Z21966         Homo sapiens         mPOU homeobox protein         1529         100           662         AJ242954         Mus musculus         dysferlin         4752         59           663         AF182316         Homo sapiens         myoferlin         6232         99           665         AL161516         Arabidopsis thaliana         hypothetical protein         209         30           667         X59303         Homo sapiens         valyl-tRNA synthetase         3393         99           668         Y13355         Homo sapiens         Amino acid sequence of protein PRO220.         3692         100           669         AB010692         Arabidopsis contains similarity to endobeta-N-acetylglucosaminidase gene         611         52           671         X56123         Mus musculus talin         4474         76           672         AB039371         Homo sapiens         mitochondrial ABC transporter         2902         99           673         AF269223         Homo sapiens         TCP11         806         42           674         AF229633         Mus musculus         groucho-related protein 4         4053         99		AF202724			2172	100
AJ242954   Mus musculus   dysferlin   4752   59			Homo sapiens	mPOU homeobox protein		
663         AF182316         Homo sapiens         myoferlin         6232         99           665         AL161516         Arabidopsis thaliana         hypothetical protein         209         30           667         X59303         Homo sapiens         valyl-tRNA synthetase         3393         99           668         Y13355         Homo sapiens         Amino acid sequence of protein PRO220.         3692         100           669         AB010692         Arabidopsis tontains similarity to endobeta-N-acetylglucosaminidase gene         52           671         X56123         Mus musculus         talin         4474         76           672         AB039371         Homo sapiens         mitochondrial ABC transporter         2902         99           673         AF269223         Homo sapiens         TCP11         806         42           674         AF29633         Mus musculus         groucho-related protein 4         4053         99						
AL161516 Arabidopsis thaliana hypothetical protein 209 30  667 X59303 Homo sapiens valyl-tRNA synthetase 3393 99  668 Y13355 Homo sapiens Amino acid sequence of protein PRO220.  669 AB010692 Arabidopsis contains similarity to endobeta-N-acetylglucosaminidase gene  671 X56123 Mus musculus talin 4474 76  672 AB039371 Homo sapiens mitochondrial ABC transporter 2902 99  673 AF269223 Homo sapiens TCP11 806 42  674 AF29633 Mus musculus groucho-related protein 4 4053 99					l I	
thaliana	665	AL161516		hypothetical protein		
Homo sapiens	567	VERNO				l
AB010692   Arabidopsis   contains similarity to endobeta-N-acetylglucosaminidase   gene						
AB010692 Arabidopsis contains similarity to endobeta-N-acetylglucosaminidase gene  671 X56123 Mus musculus talin 4474 76 672 AB039371 Homo sapiens mitochondrial ABC transporter 2902 99 673 AF269223 Homo sapiens TCP11 806 42 674 AF29633 Mus musculus groucho-related protein 4 4053 99	-55	******	nomo sapiens		3692	100
thaliana beta-N-acetylglucosaminidase gene 671 X56123 Mus musculus talin 4474 76 672 AB039371 Homo sapiens mitochondrial ABC transporter 2902 99 673 AF269223 Homo sapiens TCP11 806 42 674 AF229633 Mus musculus groucho-related protein 4 4053 99	669 +	AB010692	Arabidonaia			
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671 X56123 Mus musculus talin 4474 76 672 AB039371 Homo sapiens mitochondrial ABC transporter 2902 99 673 AF269223 Homo sapiens TCP11 806 42 674 AF229633 Mus musculus groucho-related protein 4 4053 99		ļ				1
672 AB039371 Homo sapiens mitochondrial ABC transporter 2902 99 673 AF269223 Homo sapiens TCP11 806 42 674 AF29633 Mus musculus groucho-related protein 4 4053 99	671	X56123	Mus musculne	<del></del>	4474	
673 AF269223 Homo sapiens TCP11 806 42 674 AF229633 Mus musculus groucho-related protein 4 4053 99						
673 AF269223 Homo sapiens TCP11 806 42 674 AF229633 Mus musculus groucho-related protein 4 4053 99		Į.			2902	99
674 AF229633 Mus musculus groucho-related protein 4 4053 99		AF269223	Homo sapiens		806	42
675 114463 Pattus			Mus musculus			
	675	L14463				

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		norvegicus			
	AC005757		R32611 1	2779	100
76		Homo sapiens	reverse transcriptase	252	65
77	\$61069		homolog=pol (retroviral element)		
78	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
79	X79066		ERF-1	1783	100
80	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	sapiens	Human wild type pKe83 . protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99 .
684	Y94952	Homo sapiens	Human secreted protein clone fh116_11 protein sequence SEO ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
	AF039697	Homo sapiens	antigen NY-CO-31	508	98
688 689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PR01327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703	AJ243274	Homo sapiens	AP-2rep protein	2078	
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1697	94
705	Y71262	Homo sapiens	protein, Zchml.	1736	99
706	¥41257	Homo sapiens	human FAIM.	1060	100
707	AL022237	Homo sapiens	Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))		
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	170	777	99
710	Y08698	Homo sapiens	ranbo3	2849	98
711	Y68770	Homo sapiens		754	99

SEO	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	8
NO:				WATERMAN	IDENTITY
712	U93574	Homo sapiens	putative pl50	SCORE 799	<u> </u>
713	AC004531	Homo sapiens	Gene with similarity to DEAD	2715	59
1		I some suprems	box helicases	2/15	99
714	D89016	Homo sapiens	Neuroblastoma		<del> </del> _
715	Y92175	Homo sapiens	Human cardiovascular system	538	48
'	13273	nono saprens	associated protein tyrosine	734	98
	1		phosphatase 2.		
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil	-	
'		" Bupicins	phosphoribosyltranferase)	862	100
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b	<del> </del>	
'-'	12000225	"" " " " " " " " " " " " " " " " " " "	alpha synthase	1696	93
718	Y96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	<del> </del>	
1 -20	130030	P40254 25-	Admen 16FAN-2 Immunoglobulin.	2345	85
· ·		OCT-1984 09-	·	1	(
]		APR-1983		I	1
1		Human IqD.		1	
ł		[Homo		1	
1		sapiens		1	
719	X07979	1 7			
'-'	10,313	Homo sapiens	integrin beta 1 subunit	4347	99
720	77274010	77.	precursor		
	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	¥07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo	Human calpain.	1591	99
		sapiens]			
1	i	>W41564	,		Į.
l	1	W41564 08-	ł	}	1
		OCT-1997 05-		i	]
ŀ		APR-1996		1	
j	1	Human	•		t
i		calpain.	1	1	t
l		[Homo		1	
					l .
		sapiens		1	
723	AF161341	Homo sapiens	HSPC078	1097	98
724	AF187318	Homo sapiens	F-box protein Fbx2	1097 1607	98
	1	Homo sapiens Homo sapiens Caenorhabdit	F-box protein Fbx2 contains simlarity to	. 4	
724	AF187318	Homo sapiens	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre-	1607	100
724	AF187318	Homo sapiens Homo sapiens Caenorhabdit	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	1607	100
724 725	AF187318 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans	F-box protein Fbx2 contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)	1607	100
724	AF187318	Homo sapiens Homo sapiens Caenorhabdit is elegans Caenorhabdit	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to	1607	100
724 725	AF187318 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre-	1607	100
724 725	AF187318 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans Caenorhabdit	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	1607	100
724 725 726	AF187318 AC006708 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2  contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)	1607	100
724 725	AF187318 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2  contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam	1607	100
724 725 726	AF187318 AC006708 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain,	1607 1143 988	100 46 46
724 725 726	AF187318 AC006708 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8,	1607 1143 988	100 46 46
724 725 726	AF187318 AC006708 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	988 950	100 46 46
724 725 726 727	AC006708  AC006708  AC006708  AC024818	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS	988 950	100 46 46 44
724 725 726	AF187318 AC006708 AC006708	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS  Human secreted protein	988 950	46
724 725 726 727	AC006708  AC006708  AC006708  AC024818	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene	988 950	100 46 46 44
724 725 726 727 728 729	AC006708  AC006708  AC006708  AC024818  AJ005897  Y45377	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.	988 950	100 46 46 44
724 725 726 727	AC006708  AC006708  AC006708  AC024818	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene	988 950	100 46 46 44
724 725 726 727 728 729	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.	988 950 831 908	100 46 46 44 47 97
724 725 726 727 728 729	AC006708  AC006708  AC006708  AC024818  AJ005897  Y45377	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ	988 950 831 908	100 46 46 44 47 97
724 725 726 727 728 729 730	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.	988 950 831 908	100 46 46 44 47 97
724 725 726 727 728 729	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377	Homo sapiens Homo sapiens Caenorhabdit is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.	988 950 831 908	100 46 46 44 47 97 100
724 725 726 727 728 729 730 731	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens  Oncorhynchus masou	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.  GTF-binding protein	988 950 950 831 908 578	100 46 46 44 47 97
724 725 726 727 728 729 730	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens  Oncorhynchus masou	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012. GTP-binding protein  Human secreted protein encoded by Gene No. 8.	988 950 831 908 578 3865	100 46 46 44 47 97 100 76
724 725 726 727 728 729 730 731	AF187318 AC006708 AC006708 AC004818 AJ005897 Y45377 G03931 AB012720	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Abomo sapiens Homo sapiens Abomo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012. GTP-binding protein  Human secreted protein	988 950 950 831 908 578	100 46 46 44 47 97 100
724 725 726 727 728 729 730 731	AF187318 AC006708 AC006708 AC004818 AJ005897 Y45377 G03931 AB012720	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Abomo sapiens Homo sapiens Abomo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.  GTP-binding protein  Human secreted protein encoded by Gene No. 8.  Human secreted protein, SEQ ID NO: 6731.	988 950 950 831 908 578 3865 862	100 46 46 44 47 97 100 76 97
724 725 726 727 728 729 730 731 732 733	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	Homo sapiens Homo sapiens Caenorhabdit is elegans Caenorhabdit is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: 272876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: 272876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.  GTF-binding protein  Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein	988 950 831 908 578 3865	100 46 46 44 47 97 100 76
724 725 726 727 728 729 730 731 732 733	AF187318 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens  Homo sapiens  Caenorhynchus masou Homo sapiens  Caenorhabdit is elegans	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: Z72876)  contains simlarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012. GTP-binding protein  Human secreted protein encoded by Gene No. 8.  Human secreted protein, SEQ ID NO: 6731.  Hypothetical protein Y54F10AL.a	988 950 950 831 908 578 3865 862 644	100 46 46 44 47 97 100 76 97 97
724 725 726 727 728 729 730 731 732 733	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens  Oncorhynchus masou Homo sapiens  Homo sapiens  Caenorhabdit	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: Z72876) contains simlarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	988 950 950 831 908 578 3865 862	100 46 46 44 47 97 100 76 97
724 725 726 727 728 729 730 731 732 733	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens Homo sapiens  Homo sapiens  Homo sapiens  Caenorhynchus masou Homo sapiens  Caenorhabdit is elegans	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	988 950 950 831 908 578 3865 862 644	100 46 46 44 47 97 100 76 97 97
724 725 726 727 728 729 730 731 732 733	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elecans  Homo sapiens Homo sapiens  Homo sapiens  Homo sapiens  Caenorhabdit is elegans  Homo sapiens  Homo sapiens  Homo sapiens	F-box protein Fbx2 contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	988 950 831 908 578 3865 862 644 152	100 46 46 44 47 97 100 76 97 97 24
724 725 726 727 728 729 730 731 732 733 734 735	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens  Homo sapiens  Oncorhynchus masou Homo sapiens  Homo sapiens  Caenorhabdit is elegans  Homo sapiens  Caenorhabdit Caenorhabdit Caenorhabdit Caenorhabdit	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012. GTP-binding protein  Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	988 950 950 831 908 578 3865 862 644	100 46 46 44 47 97 100 76 97 97
724 725 726 727 728 729 730 731 732 733 734 735	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens  Homo sapiens  Oncorhynchus masou Homo sapiens  Caenorhabdit is elegans  Homo sapiens  Caenorhabdit is elegans  Caenorhabdit is elegans	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3  JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012.  GTP-binding protein  Human secreted protein, SEQ ID NO: 6731.  Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2 protein	988  950  831  908  578  3865  862  644  152  1562	100 46 46 44 47 97 100 76 97 97 24 98
724 725 726 727 728 729 730 731 732 733 734 735	AF187318 AC006708 AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	Homo sapiens Homo sapiens Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Caenorhabdit is elegans  Homo sapiens  Homo sapiens  Oncorhynchus masou Homo sapiens  Homo sapiens  Caenorhabdit is elegans  Homo sapiens  Caenorhabdit Caenorhabdit Caenorhabdit Caenorhabdit	F-box protein Fbx2  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)  contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS  Human secreted protein fragment encoded from gene 27.  Human secreted protein, SEQ ID NO: 8012. GTP-binding protein  Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	988 950 831 908 578 3865 862 644 152	100 46 46 44 47 97 100 76 97 97 24

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
		Homo sapiens	M-phase phosphoprotein 9	564	74
741	X98258		strong similarity to the YPT1	960	85
742	U97191	Caenorhabdit	sub-family of RAS proteins	500	""
		is elegans	sub-family of RAS process	2191	100
743	X76057	Homo sapiens	phosphomannose isomerase		98
744	G03209	Homo sapiens	Human secreted protein, SEQ	496	30
		1	ID NO: 7290.		
745	X97064	Homo sapiens	Sec23 protein	4034	99
746	W93946	Homo sapiens	Human regulatory molecule	994	100
			HRM-2 protein.		
747	Y73388	Homo sapiens	HTRM clone 3376404 protein	1565	99
			sequence.	1906	98
748	M19529	Sus scrofa	follistatin A		J
749	AJ249457	Trichomonas	centrin, putative	183	28
		vaginalis			
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity	4005	100
, 56	DI 232204		factor Spl	1	
<del></del>	AB049629	Homo sapiens	phospholysine	1375	99
753	AB049629	HOMO Sapiens	phospholistidine inorganic		
	1		pyrophosphate phosphatase	ļ	}
		<u> </u>		160	77
754	D79205	Homo sapiens	ribosomal protein L39	142	29
755	AB008430	Homo sapiens	CDEP	1	
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo	Human cell signalling	625	100
, , ,		sapiens	protein-13.	1	1
761	AF218586	Homo sapiens	Cide-b	1136	100
	U38934	Gallus	histone H2A	625	97
762	038934	gallus	Histone		ł
		Homo sapiens	HSKM-B	606	32
763	AF226053		Oct-1 protein (AA 1 - 743)	3626	100
764	X13403	Homo sapiens	Oct-1 protein (AA 1 = 7437	568	38
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)		
766	AL023828	Caenorhabdit is elegans	Y17G7B.14	200	27
767	Y82777	Homo sapiens	Human chordin related protein	2551	99
		1	(Clone dw665_4).	1429	100
76B	X92475	Homo sapiens	ITBA1		100
769	¥42752	Homo sapiens	3 (CaBP-3).	·	
770	X51416	Homo sapiens	521)	2641	97
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	1.00
772	A08695	Homo sapiens	rap2	935	100
773	Z12173	Homo sapiens		2970	100
774	Y91950	Homo sapiens		565	43
776	AL023799	Homo sapiens		855	56
776				855	56
777 778	AL023799 G01880	Homo sapiens		849	98
L		100000000000000000000000000000000000000		4155	99
779	AJ012590	Homo sapiens	grucose 1-dellydrogenase	1321	68
780	AL078582	Homo sapiens			1
781	Z75955	Caenorhabdit		384	34
1	l l	is elegans	carrier protein		
782	AL109965	Homo	dJ1121G12.2 (SCAN domain-	900	100
1	1	sapiens	containing 1 protein)		
783	AF061262	Mus	semaF cytoplasmic domain	1316	83
				1	ı
1,03	l	musculus	associated protein 2  Human secreted protein, SEQ	1	1

SEO	ACCESSION	SPECIES	DESCRIPTION		· · · · · · · · · · · · · · · · · · ·
ID	NUMBER	3130123	DESCRIPTION	SMITH- WATERMAN	\$ TDD1:======
NO:	}	ŀ		SCORE	IDENTITY
		<del> </del>	ID NO: 7954.	DCORE	<del> </del>
785	Y84441	Homo sapiens	Amino acid sequence of a	2074	100
	İ		human RNA-associated		1 -00
<u></u>	<u> </u>		protein.		
786	Y00918	Homo sapiens	Human Rab protein, RABP-1,	1048	99
787	Z97029		protein sequence.		
78B	AB035384	Homo sapiens	ribonuclease HI large subunit	1548	99 ·
789	AF024631	Homo sapiens	SRp25 nuclear protein	962	94
790	AJ006710	Homo sapiens		2644	100
,,,,	70000710	norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophag	reading frame eal0	600	
		e lambda	reading frame eart	600	100
793	AF049103	Homo sapiens	Huntingtin interacting	819	100
		1	protein	013	100
795	226317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding	5080	99
		<u> </u>	protein-7sequence.		55
797	U15155	Gallus	trypsinogen	372	37
798		gallus		1	
798	U97189	Caenorhabdit	strong similarity to thw	227	28
799	AF112201	is elegans	P13/P14 family of kinases	1	1
800	AF112201	Homo sapiens	neuronal protein NP25	1053	100
500	AE 234 /65	norvegicus	serine-arginine-rich splicing	958	63
801	AF267852	Homo sapiens	regulatory protein SRRP86 placental protein 13-like	1	
	1-20,052	nomo sapteme	protein	743	99
802	AF208851	Homo sapiens	BM-009	766	80
803	281097	Caenorhabdit	Similarity to Human	152	27
		is elegans	retinoblastoma-binding	132	4 ′
	}	}	protein RBAP46 yk662d12.5		
	<u> </u>		comes from this gene		
804	G02113	Homo sapiens	Human secreted protein, SEQ	496	98
805	AL121673	ļ. <u></u>	ID NO: 6194.		
806	AC013483	Homo sapiens Arabidopsis	bA305P22.1 (novel protein)	1160	100
500	ACUISABS	thaliana	putative GTPase activator protein	264	30
807	AC013483	Arabidopsis	putative GTPase activator	264	
		thaliana	protein	264	3C
808	AB013885	Homo sapiens	beta-ureidopropionase	1494	100
809	AF078842	Homo sapiens	HOTTL protein	1581	99
810	AF161421	Homo sapiens	HSPC303	2134	96
811	AF261689	Homo sapiens	DNA polymerase epsilon p17	734	100
		·_	subunit	1	
812	Z74029	Caenorhabdit	Similarity to C.elegans	610	71
		is elegans	alcohol dehydrogenase comes		
813	273497	Homo sapiens	from this gene cU240C2.2 (Core histone		· · · · · · · · · · · · · · · · · · ·
		nomo sapiens	H2A/H2B/H3/H4)	324	100
814	W87689	Homo		1400	
		sapiens	Human HTXFT19 polypeptide.	1484	99
815	X16282	Homo	zinc finger protein (217 AA)	1109	99
		sapiens	(1 is 2nd base in codon)	12203	33
816	Z92539	Mycobacteriu	pth	300	36
		m ·	_	]	
	2000	tuberculosis		j	I
818	AB030483	Mus musculus	В9	197	27
819 820	λL117555	Homo sapiens	hypothetical protein	321	94
820 .	AC005328	Homo sapiens	R26660_2, partial CDS	865	97
<b>4</b> 21	G03951	Homo sapiens	Human secreted protein, SEQ	700	99
822	L34807	Musca	ID NO: 8032.	1	
	23300/	domestica	transposase	174	20
823	G02928	Homo sapiens	Human cograted section and		
		oubtens	Human secreted protein, SEQ ID NO: 7009.	558	78
824	Z99531	Schizosaccha	caffeine-induced death	184	29
			Induced death	¥04	43

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
	<del></del>	romyces combe	protein 1		
325	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
326	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30327	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	<b>Y3</b> 2199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted . protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKI-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98.
843	AE003615	Drosophila melanogaster	ade3 gene product	113	100
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	3305	96
845	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog		
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen M130 antigen extracellular	6205 6380	100
853	Z22971	Homo sapiens	variant Human secreted protein, SEQ	330	96
854	G03362		ID NO: 7443.  Human secreted protein, SEQ	203	100
855	G03362	Homo sapiens	ID NO: 7443.	452	100
856 857	AF285118 AC006069	Homo sapiens Arabidopsis	putative cleavage and	1383	55
857	ACOUGUES	thaliana	polyadenylation specifity factor	1355	
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus		1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit is elegans	mitochondrial carrier protein		43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
865	AE001530	Helicopacter	receptor associated protein		
866	X57807	pylori J99	[	230	32
867		Homo sapiens	chain	699	91
	AL031673	Homo sapiens	KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
868	Y11652	Homo sapiens	phosphate cyclase	238	3.00
869	AF192968	Homo sapiens	high-glucose-regulated protein 8	3041	99
870	AB020648	Homo sapiens	KIAA0841 protein	3237	59
871	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
872	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
873	AL021331 X14608	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	100
875	AL117334	Homo sapiens	propionyl-CoA carboxylase	3579	100
			dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
876	X79489	Saccharomyce s cerevisiae	E-925 protein	446	35
877	Y53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
878	AF231064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyce s cerevisiae	Soilp	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885 886	Y10936	Homo sapiens	hypothetical protein	1104	99
887	AF073997	Mus musculus	myotubularin related protein	866	36
	Y57893	Homo sapiens	Human transmembrane protein HTMPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	¥36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	192	57
892	AF237631	Homo sapiens	ubiquitous tropomodulin U-	1798	100
393	AF090929	Homo sapiens	PRO0477p		
394	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	3196	100
		Homo sapiens	MNG10 and C. elegans F28D1.1) dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta	2825	96
	AF171102	Homo sapiens	retinal degeneration B beta	1302	
97	AE003551		CG18176 gene product		95

TABLE 2

AU237946   Romo sapiens   DEAD Box Protein 5   2443   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100		CCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100					SCORE	100
1970   277184						
100	1	·	TOTAL DEFE			
1002   APC191034   Homo sapiens   TOP-Dinding protein RAB22A   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL   TOTAL			1.0			
100	1			Kruppel-type zinc linger	ł =	
104   104733   Homo sapiens   Kimesin light chain   1936   72   72   72   72   72   72   72   7				GTP-binding protein RABZZA		
100	R9	95953	Homo sapiens	inhibiting factor.		
M55542   Homo sapiens   Suanylate binding protein   2993   98	LO	04733	Homo sapiens			1
M55542   Homo sapiens   guanylate binding protein   2993   98   98   997   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   1	AE	E003540		CG10984 gene product	446	33
MS5542   Homo sapiens   Suganylate binding protein   2901   96	М5	55542			2993	98
W84085   Homo sapiens   Human membrane fusion protein   1889   100   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO1.   WDPO	NE	55542	Homo sapiens	guanylate binding protein	2901	96
API68676   Homo   Sapiens   NPF intracellular domain-	WE	84085	Homo sapiens	Human membrane fusion protein	1889	100
100   AB029150   Homo sapiens   KRAB zinc finger protein   HFB101L   Homo sapiens   Human secreted protein   SEQ   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100	A	F168676		TNF intracellular domain-	647	100
10   10   10   10   10   10   10   10		B. 0.0.			2196	100
ID NO: 6952.	Ā	B029150		HFB101L		
ID NO: 7243.	G	02871	Homo sapiens	ID NO: 6952.		
AJ243721   Homo   Sapiens   AJ243721   Homo   Sapiens   Sy92508   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   4-reductase   5-reductase   5-reductase   5-reductase   5-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-reductase   6-re	G	303162	Homo sapiens	ID NO: 7243.		
14	A	M243721 ~~	sapiens) >Y92508 Y92508 13- APR-2000 06- OCT-1998 Human OXRE- 5. [Homo		1710	
1915   Y02591   Homo sapiens   A human progesterone receptor   S43   99	<del>    0</del>	J24189	Caenorhabdit	hypothetical protein 1207-1;	244	41
915   Y02591   Homo sapiens   A human progesterone receptor complex p23-like protein.   999			is elegans	translation supplied by		
AE000984   Archaeoglobu   S fulgidus   Archaeoglobu   S fulgidus   Archaeoglobu   S fulgidus   Archaeoglobu   S fulgidus   Archaeoglobu   S fulgidus   Archaeoglobu   S fulgidus   Archaeoglobu   Archaeoglobu   Archaeoglobu   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coamplified protein   AFFR-coampl	Y	Y02591	Homo sapiens	A human progesterone receptor	843	99
S Fulgidus   activating glycohydrolase (draG)				complex p23-11ke process.	1777	126
M23159	A	AE000984		activating glycohydrolase	1/1	
1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232   1232	-+	W03150	Codection		163	30
12018   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemormatic   caemor	·   M	M23159	ľ	DAFK-COAMPITITED PROCESS		
920         AF102177         Homo sapiens         tumor antigen SLP-8p         1260         97           921         AL096712         Homo sapiens         dJ744124.2 (similar to a novel human gene mapping to Activator)         1017         78           922         AL161495         Arabidopsis thaliana         putative WD-repeat protein         866         42           923         AL161495         Arabidopsis thaliana         putative WD-repeat protein         442         36           924         U97001         Caenorhabdit similar to is elegans         Schizosaccharomyces pombe         605         51           925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         beta-spectrin         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100	I	L12018		1	1232	
921         AL096712         Homo sapiens         dJ744124.2 (similar to a novel human gene mapping to Activator)         1017         78           922         AL161495         Arabidopsis thaliana         putative WD-repeat protein         866         42           923         AL161495         Arabidopsis thaliana         putative WD-repeat protein         442         36           924         U97001         Caenorhabdit is elegans         Schizosaccharomyces pombe         605         51           925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         beta-spectrin         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100	)   F	AF102177		tumor antigen SLP-8p		
922         AL161495         Arabidopsis thaliana         putative WD-repeat protein         866         42           923         AL161495         Arabidopsis thaliana         putative WD-repeat protein         442         36           924         U97001         Caenorhabdit is elegans         Schizosaccharomyces pombe         605         51           925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         beta-spectrin         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9.         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100				dJ744124.2 (similar to a novel human gene mapping to Activator)	1017	78
923         AL161495         Arabidopsis thaliana         putative WD-repeat protein         442         36           924         U97001         Caenorhabdit is elegans         similar to Schizosaccharomyces pombe         605         51           925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         beta-spectrin         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100	2 7	AL161495		putative WD-repeat protein	866	42
924         U97001         Caenorhabdit is elegans         similar to Schizosaccharomyces pombe         605         51           925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         Drosophila melanogaster         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9.         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100	3 1	AL161495	Arabidopsis	putative WD-repeat protein	442	36
925         X71978         Mus musculus         Fif         1503         95           926         M92288         Drosophila melanogaster         beta-spectrin         290         51           927         Y27575         Homo sapiens         Human secreted protein encoded by gene No. 9.         1392         100           928         Y22499         Homo sapiens         Human secreted protein         2249         100	1 1	U97001	Caenorhabdit		605	51
926 M92288 Drosophila beta-spectrin 290 51  927 Y27575 Homo sapiens Human secreted protein encoded by gene No. 9.  928 Y22499 Homo sapiens Human secreted protein 2249 100	<sub>-</sub>	V71079			1503	95
927 Y27575 Homo sapiens Human secreted protein encoded by gene No. 9.  928 Y22499 Homo sapiens Human secreted protein 2249 100			Drosophila	beta-spectrin		
928 Y22499 Homo sapiens Human secreted protein 2249 100	7   3	Y27575		Human secreted protein	1392	100
acquience alone mb703 1	<sub>B</sub> -  -,	Y22499	Homo sapiens	Human secreted protein	2249	100
930 AJ224326 Homo sapiens ribulose-5-phosphate- 912 100				sequence clone mh703_1.	912	100
930 AD224326 Homo Sapiens Indusers sphosphate epimerase 931 U28991 Caenorhabdit coded for by C. elegans cDNA 660 . 55			<u> </u>	epimerase		

SEQ ID NO:	ACCESSION NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
932	AL080065	is elegans	cm21c7		
933	G01884	Homo sapiens		767	25 98
934	AJ276485	Homo sapiens	integral membrane transporter	1200	100
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila	1142	80
936	AB026808		transcriptional repressor)		
937	AB026808 AB015345	Mus musculus	1 2	2142	95
938	X65724	Homo sapiens		2601	99
939	W89024	Homo sapiens		498	100
940	G04047	Homo sapiens	by gene 156.	1487	100
941		Homo sapiens	ID NO: 8128.	117	100
942	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	100
342	AC024200	Caenorhabdit is elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	GSc		<u> </u>
944	M23765	Rattus norvegicus	alpha-tropomyosin	273 133	100 96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	\- <u></u>	
947	AF055473	Homo sapiens	GAGE-8	551	44
948	X75756	Homo sapiens	protein kinase C mu	273	51
949	AF143956	Mus musculus	corcnin-2	2300	68
950	Y36729	Homo sapiens	Human PG1 protein sequence.	1861	93 99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXCl7.7~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BCDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus norvegicus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel putative Ca2+ channel protein	317	30
		Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
			interferon-induced protein	202	46
966	D38169	Homo	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
1					

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo	quanine nucleotide exchange	2752	99
		sapiens	factor (long isoform)		İ
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	U53336	Caenorhabdit	weak similarity over a short	536	23
		is elegans	region to myosin heavy chain	i	İ
972	AC018749	Leishmania major	L8840.12	589	53
973	AP188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Taxl binding protein	852	98
975	AF049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ	626	100
311	309020	nomo saptens	ID NO: 8101.	023	1 200
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
		sapiens			
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH:	964	85
<b>30</b> 3.		Job Guazas	ubiquinone oxidoreductase		
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445 1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A .	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930 1.	1340	99
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens		428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
	I WINGSTAST			L	
1005	S45367	Canis	centractin	1949	100

SEO	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	3120120	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	S45367	Canis	centractin	SCORE	
		familiaris	Centractin	1315	98
1007	AB022158	Mus	chaperonin containing TCP-1	2649	96
1008	Y76332	musculus Homo sapiens	epsilon subunit Fragment of human secreted		
2000	170332	nomo saprens	protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger	1671	58
1010	Z68218	Caenorhabdit	protein		1
1010	200210	is elegans	K01H12.1	269	67
1011	AB011414	Homo sapiens		1671	58
1012	Z14000	<u> </u>	protein		
1012	G02841	Homo sapiens	RINGI	2017	100
1013	002041	nomo saptens	Human secreted protein, SEQ ID No: 6922.	332	93
1014	AF145659	Drosophila	BcDNA.GH10333	1244	52
1015	Y02860	melanogaster			
1015	102860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor	772	97
			complex p23-like protein.	' ' "	] ,
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino	2323	100
1018	X67250	Rattus	acid sequence SEQ ID NO:374.	1710	97
		norvegicus		1 1/10	97
1019	AF183417	Homo	microtubule-associated	631	100
1020	AF164795	sapiens Homo sapiens	proteins 1A/1B light chain 3 sex-regulated protein janus-a		
1021	AF190625	Coturnix	qdgl-1	674	100 96
		coturnix		030	36
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens	2243	100
	·	•	mammalian inositol		
			hexakisphosphate kinase 2 (IP6K2) mRNA with Ge		
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736 AB029333	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme	1045	100
1029			isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ	749	98
1030	G01797	Homo sapiens	ID NO: 5878. Human secreted protein, SEO	749	98 -
		-	ID NO: 5878.	/43	
1031	AF193795	Homo sapiens	vacuolar sorting protein	960	100
1032	AJ222968	Mus musculus	VPS29/PEP11		
1033	281317	Schizosaccha	DNA2-NAM7 helicase family	120 685	30
		romyces	protein	000	31
1034	¥41519	pombe Homo sapiens			
		nomo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit	H14A12.3 gene product	190	30
1037	U37251	is elegans Homo sapiens	Decorintion, VDNR -1 E		
		sabtens	Description: KRAB zinc finger protein; this is a splicing	196	43
1000			supplied by author	1	ì
103B	W74580	Homo	Human membrane protein	1921	97
1039	U88173	sapiens Caenorhabdit	BA0306. weak similarity to		
		is elegans	Arabidopsis thaliana	331	80
1					

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1040	AF290204	Homo sapiens	blood group carrier molecule DOK1	1637	99
1041	Y96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
LO43	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BCDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1.047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdgl-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gere product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona s reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1050	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	(HYDRL-10).	2547	100
1064	AF263614	Homo sapiens		3493	99
1065	Y13356	Homo sapiens	protein PROZZ1.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens		3109	99
1072	U92794	Mus musculus		147	36
1073	G03889	Homo sapiens		698	98
1074	U15779	Homo sapiens		380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	* TDENIMY MY
NO:				SCORE	IDENTITY
1076	AF161457	Homo sapiens	protein PRO328.		
1077	¥79509	Homo sapiens		571	100
1		nome suprem	protein CRBAP-5.	2151	98
1078	AF223466	Homo sapiens		831	<u> </u>
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
		thaliana	ļ	200	29
1080	AB024937	Homo sapiens		1284	100
1081	Y14768	Homo sapiens		579	100
			protein	1	1
1082	AF016416	Caenorhabdit	F29A7.4 gene product	141	31
1083	L13291	is elegans		_l_	1
1084	AB041541	Homo sapiens Mus musculus		802	45
1085	G01922	Homo sapiens		151	44
1000	001922	nomo sapiens	Human secreted protein, SEQ ID No: 6003.	202	97
1086	AB030814	Homo sapiens			L
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	833	100
1		Jupacing	protein	1142	100
1088	Y84432	Homo sapiens		2783	100
1	<b>!</b>	•	human RNA-associated	2763	100
			protein.		ļ
1089	Y94867	Ното	Human protein clone HP10563.	613	100
1090	124000000000000000000000000000000000000	sapiens	<u>. i</u>		
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586 Y71277	Mus musculus		1103	81
1093	U34973	Homo sapiens Mus musculus		606	100
2000	054973	Mus muscutus	protein tyrosine phosphatase-	1131	95
1094	Y66677	Ното	Membrane-bound protein	600	
		sapiens	PRO828.	522	56
1095	Y87276	Homo sapiens	Human signal peptide	1029	99
		Ī	containing protein HSPP-53	1025	"
7005			SEQ ID NO:53.		
1096	Y87276	Homo sapiens	Human signal peptide	863	98
	•		containing protein HSPP-53		
1097	AF161455	Homo sapiens	SEQ ID NO:53.		
1098	U80029	Caenorhabdit	similar to thioredoxin	742	98
		is elegans	similar to thioredoxin	242	39
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005865	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244	Homo sapiens	hypothetical protein	299	31
1104	AF242194	Drosophila	brakeless-B	147	52
1105	AL031010	melanogaster Homo sapiens			
	12031010	romo sapiens	dJ422F24.1 (PUTATIVE novel protein similar to C. elegans	968	100
			C02C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	1634	
			(phosphotriesterase) -related	1624	87
			protein		
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
1100	X 112 2 12 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		ID NO: 7814.	l l	ļ
1109	AF217287	Drosophila	G protein RhoBTB	834	54
1110	Y28921	melanogaster			
	120321	Homo sapiens	Human regulatory protein	941	48
1111	Y28921	Homo	HRGP-7.		
		sapiens	Human regulatory protein HRGP-7.	1331	51
1112	AF176704	Homo sapiens	F-box protein FBX9		
1113	AF182076	Homo	glioma tumor suppressor	2027	99
		sapiens	candidate region protein 2	C410	100
1114	G04039	Homo sapiens	Human secreted protein, SEQ	475	96
					[

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	% IDENTITY
ID NO:	Machon			SCORE	
			ID NO: 8120.		91
1115	AF229439	Mus musculus	zinc finger protein 289	1697 509	100
1116	L40357	Homo sapiens	thyroid receptor interactor	404	85
1117	L40357	Homo sapiens	thyroid receptor interactor	1673	100
1118	A12155	Homo sapiens	Human X5L cDNA.	607	53
1119	AL161542	Arabidopsis thaliana	isomerase like protein		
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1125	AJ000217	Homo sapiens	CLIC2	1286	99
1126	AB030505	Mus musculus	UBE-1c2	1069	79
1127	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces	putative nuclear pore protein	596	39
1133	Z68197	pombe Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange	3597	100
1135	AF079765	Mus misculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	¥76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein-	3309	100
1142	¥13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens		750	98
1145	Y12917	Homo sapiens		1096	100
1146	AL022157	Homo sapiens		1233	100
1147	AL022157	Homo sapiens		1233	100
1148	G02548	Homo sapiens		370	98
1149	¥73338	Homo sapiens	HTRM clone 2019742 protein sequence.	1492	100
1150	W74841	Homo sapiens		228	55

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION		·,
ID	NUMBER	SFECTES	DESCRIPTION	SMITH- WATERMAN	700000000
NO:	1	Ì		SCORE	IDENTITY
	<b>†</b>	<del> </del>	HEAAR60.	SCORE	<del></del>
1151	AF044201	Rattus	neural membrane protein 35;	1570	92
İ		norvegicus	NMP35	13.0	1
1152	AF156774	Homo	lysophosphatidic acid	1855	99
		sapiens	acyltransferase-gammal		
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	872	64
			(translation of the cDNA		1
	1	ł	DKFZp566A0946, Em:AL050069))		1
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo	Human PRO352 protein	1381	97
		sapiens	sequence.		ļ
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
			ID NO: B117.		1
1157	AF112444	Lupinus	L-asparaginase	287	43
L	ļ	luteus			
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Ciona	PEM-6	196	33
1161	V02220	savignyi			
1161	¥87330	Homo sapiens	Human signal peptide	746	83
			containing protein HSPP-107	1	{
1162	Y87330	Homo sapiens	SEQ ID NO:107.		
1102	187330	nomo sapiens	Human signal peptide	746	83
ı			containing protein HSPP-107 SEQ ID NO:107.		
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
	12220		(translation of the cDNA	1051	'1
			DKFZp566A0946, Em:AL050069))		
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	76
			(translation of the cDNA		'
			DKFZp566A0946, Em:AL050069))		
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	1191	100
			by gene 6.		
1171	L03188	Saccharomyce	putative ·	180	22
		s cerevisiae	<u> </u>	•	ļ
1172	AF113751	Mus musculus	nuclear pore membrane	3941	81
	7.70		glycoprotein POM210	ļ	1
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
1176	M35617	is elegans Homo sapiens		1	
1710	M2201/	nomo sapiens	T-cell receptor V-alpha-J-	284	83
1177	AC012680	Arabidopsis	alpha region	1	
/	130012000	thaliana	putative protein phosphatase 2C; 55455-56414	209	37
1178	G01345	Homo sapiens		1 603	
		Sabrenz	Human secreted protein, SEQ ID NO: 5426.	692	99
1179	AL096767	Homo sapiens	dJ579N16.3 (novel protein	1342	100
		ovb + evre	similar to worm, Arabidopsis	1374	100
			and pine proteins)		
1180	AF039716	Caenorhabdit	similar to ATP synthase B	496	55
		is elegans	chain	100	33
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo	T cell leukemia/lymphoma 1	617	100
1	A02240			1 444	
- 1	X62240	sapiens]		ł I	
	X02240	sapiens] >R94974			
}	X62240				
	X62240	>R94974			
	X62240	>R94974 R94974 09-			
	X82240	>R94974 R94974 09- MAY-1996 27-			·

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	* IDENTITY
		[Homo			
		sapiens	short region of weak	161	33 .
183	U42841	Caenorhabdit is elegans	similarity to collagen		1
185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHFF03.	636	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182	. 33
1190	X89602	Homo sapiens	rTSbeta	197	100
1190_	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	¥50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	¥70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	39
1198	AF125443	Caenorhabdit is elegans	contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	460	
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	285986	Homo sapiens	dJ108kll.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	56
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	¥27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus			66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	structural protein 1	1950	77
1215	G03022	Homo sapiens	ID NO: 7103.	590	100
1216	Z72510	Caenorhabdit	similarity to yeast UTR3	634	49

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		is elegans	protein (Swiss Prot accession yk677h11.5 comes from this gene		
1217	Z49703	Saccharomyce s cerevisiae		134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit is elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L08239	Homo sapiens	located at OATL1	2274	100
1232	AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AF121863 AC024805	Homo sapiens	sorting nexin 14	1203	84
		Caenorhabdit is elegans	contains similarity to TR:004595	744	31
1235	AC006634 Y18101	Caenorhabdit is elegans Mus musculus	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162) macrophage actin-associated-	357	33
			tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:q1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	98
1251	M24852	Rattus	neuron-specific protein PEP-	124	46

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
L253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	Z35094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming protein; similar to P14373 (PID:g132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rapl	433	97
1265	¥70473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP- 1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	Cl3F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle 68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis thaliana	putative protein	348	49
1275	AC004449	Homo sapiens	R33683_3	556	100
1276	Y86295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210	1920	99
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).		
1278	S94421	Homo sapiens		1909	100
1279	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1303	100
1280	AF161380	Homo sapiens	l	772	100
1281	Y48610	Homo sapiens		779	100
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	405	35
1283	AK024432	Homo sapiens		403	35
1284	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1825	81
1285	AJ001019	Homo sapiens		1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)		100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to 138027 (PID:g2135214)		93
1290	AB023811	Homo sapiens		351	54

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
NO:	NUMBER			WATERMAN	IDENTITY
1291	Z73424	Caenorhabdit is elegans		235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF190425	Homo sapiens	protein RAP140	489	29
1294	G03856	Homo sapiens	ID NO: 7937.	538	99
1295	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens		1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	Ú58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF0447.74	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	282263	Caenorhabdit is elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	¥41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	F-box protein Fbx25	467	70
	M61732 Y17013	Trypanosoma cruzi	neuraminidase	214	24
	1	porcine endogenous	pol	304	64

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	\$ IDENTITY
		retrovirus			<u> </u>
1324	AL138655	thaliana	putative protein	1174	37
1325	AL138655	thaliana	putative protein	946	35
1326	AL133215	-	bA108L7.2 (novel protein similar to rat tricarboxylate carrier)	1322	99 1
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	¥73346	Homo sapiens	HTRM clone 619699 protein sequence.	785	96
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2) polypeptide.	232	39
1332	Y41741	Homo sapiens	Human PRO704 protein sequence.	1860	100
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabdit is elegans	Similarity to Mouse kinensin- like protein KIF4 comes from this gene	578	44
1335	AE000810	Methanobacte rium thermoautotr ophicum	conserved protein	290	43
1336	Y68779	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-11.	1019	91
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit is elegans	weak similarity to TPR domains	215	40
1339	AE001394	Plasmodium falciparum	protein of the YMR7 family	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis thaliana	putative mutT protein; 68398-67881	289	45
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain interacting protein MIR	2303	99
1344	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:q4650844)	894	35
1345	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
1346	¥25896	Homo sapiens	Human secreted protein fragment encoded from gene	1148	100
1347	AJ272073	Torpedo marmorata	male sterility protein 2-like protein		58
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
1351	G02144	Homo sapiens	Human secreted protein, SEQ ID NO: 6225.	418	100
1352	D90869	Escherichia coli	similar to	2047	100
1353	A12029	Homo sapiens	MRP-14	613	100
1353	AC005328	Homo sapiens		870	74
1355	AC024876	Caenorhabdit is elegans		829	61
1356	AF077226	Homo sapiens		1876	64
1359		Mus musculus		801	63
1360		Homo sapiens	ZNF234	3869	100
1361		Homo sapiens		5035	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			element binding and beta	BCORB	<del> </del> -
1250			transducin family proteins		1
1362	Z48475	Homo sapiens	1 0 00000	3160	99
1363	Z48475	Homo sapiens		2682	97
1364	AF195764	Homo sapiens		2055	99 .
			transcript 1 protein; MEGT1		
1365	AF116609	Homo sapiens	protein PR00915	.,	
1366	AF116609	Homo sapiens		581	100
1367	AL117352	Homo sapiens		581	100
			similar to C. elegans	2581	99
1	1		T19B10.6 (Tr:022557))	1	
1368	Y34124	Homo	Human potassium channel	1342	100
	†	sapiens	K+Hnov15.	1372	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus	YtaG	429	45
		subtilis		1	33
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens		1296	-
ł	1.		protein)	1290	99
1373	AF154415	Homo sapiens		10253	100
1374	U20286	Rattus	lamina associated polypeptide	1567	69
		norvegicus	10	1	""
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Ното	bA393J16.1 (zinc finger	250	60
		sapiens	protein 33a (KOX 31))	ł	
1377	AC005328	Homo sapiens	R26660_1, partial CDS	1126	100
1378 1379	U35113 L15313	Homo sapiens	metastasis-associated gene	1823	69
13/3	112313	Caenorhabdit is elegans	putative	856	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus		1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386 1387	AF212162	Homo sapiens	ninein	10369	99
1388	AL031685 AC004890	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1300	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659_5	280	54
1402	X91489	Saccharomyce	putative HMG box	164	27
		s cerevisiae		1	

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	- 8
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
1403	Y79222	Homo sapiens	Human transferasc TRNSPS-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus rattus	PTB-like protein	2684	99
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887 1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	Organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo sapiens	L-kynurenine/alpha- aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus auratus	guanine nucleotide-binding protein beta 5	2179	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	100
			protein, presumed ortholog of mouse K-Cl cotransporter KCC2))		
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ	4039	99
1423	AF177388	Homo	ID NO:52.		
1423	AF1//388	sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour- associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	¥66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99900	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of	707	51
1435	AF220530	Homo sapiens	nerve cells. myo-inositol 1-phosphate synthase Al	2904	100
1436	X70944	Homo sapiens	PTB-associated splicing factor	1261	72
1437	AF271732	Homo sapiens	bridging integrator-3	1282	100
1438	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	595	98
1439	AJ293659	Homo sapiens	mucolipidin	628	97
1440	AF219138	Homo sapiens	GGA3 long isoform	3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	100

SEQ	ACCESSION	SPECIES	DECORTOR	T	··
ID	NUMBER	SFECIES	DESCRIPTION	SMITH-	e
NO:		1		WATERMAN SCORE	IDENTITY
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila	Diablo	191	27
1		melanogaster		131	1 2 '.
1444	AJ011896	Homo sapiens	Naf1 beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated	3999	99
			antigen BCAA		1
1447	λF003924	Homo sapiens		2645	99
1448	AF003136	Caenorhabdit	" Ozmazuzzcy CO	2843	52
L		is elegans	an AMP-binding motif	1	
1449	AF155112 Y95004	Homo sapiens	NY-REN-50 antigen	1184	89
1450	195004	Homo sapiens	Human secreted protein	985	100
1451	AF107203	<del>  ,,</del>	vc54_1, SEQ ID NO:48.		}
1452	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1453	Z38011	Homo sapiens Mus musculus	ataxin 2-binding protein	456	78
1454	X90568	Homo sapiens		882	56
1 -131	A 90368	nomo sapiens	Protein sequence and	510	28
1	1		annotation available soon via LABEIT@EMBL-Heidelberg.DE	İ	
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to	1356	
}		nome saptems	sialyltranferase)	1356	100
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase HDB/DTCE1	478	45
1459	AF242552	Gallus	retinovin	945	34
1		gallus		733	34
1460	U11036	Homo sapiens	Ibd1	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	99
			phosphodiesterase		
1463	AC004997	Homo sapiens	match to ESTs Z43979	869	98
}	J		(NID:g573097), R19699		}
1464	AC004997	Homo sapiens	(NID:g774333)	<u> </u>	
1404	ACOU4997	nomo sapiens	match to ESTB 243979	869	98
i			(NID:g573097), R19699 (NID:g774333)		] ]
1465	U32743	Haemophilus	fucose operon protein (fucU)	315	<u> </u>
1		influenzae	racosc operon procesh (tuco)	312	50
l	ļ	Rd		Ì	] [
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney-	1072	99
			specific (KS) gene		
1468	AF071544	Spinacia	ribulose-1,5-bisphosphate	333	26
		oleracea	carboxylase/oxygenase small		
1469	Y57930	1	subunit N-methyltransferase I		
1409	15/930	Homo sapiens	Human transmembrane protein	1053	100
1470	AF032666	Rattus	HTMPN-54.		
	AF 032000	norvegicus	rsec5	4504	93
1471	Y70467	Homo sapiens	Human membrane charnel		
		nomo saprens	protein-17 (MECHP-17).	452	74
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large	1694	- 3 00
1			Subunit Pseudouridine	1034	100
			Synthase protein)	1	
1473	AF177292	Homo sapiens	genethonin 3	4026	98
1474	S45936	Homo sapiens	HTS1	1101	50
1475	Y86241	Homo sapiens	Human secreted protein	1879	98
		<u> </u>	HOABR60, SEQ ID NO:156.		
1476	AJ010317	Fugu	Sand	1278	68
3.477	114 20 2 2	rubripes			ŀ
1477	U42831	Caenorhabdit	coded for by C. elegans cDNA	846	44
		is elegans	yk99b4.3; similar to human	i	ł
	]		transforming protein		]
1478	X62447	Homo sapiens	(PIR:S22157)		
1479	X82209	Homo sapiens	PR 264 MN1	543	61
1480	U10536	Pan paniscus	MHC class I A	7116	100
		Pastacus	MIC CLOBB I M	675	84

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<del></del>
ID NO:	NUMBER	SPECIES	DESCRIPTION	WATERMAN SCORE	IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein	1274	65
			similar to C. elegans F55Al2.9 (Tr:P91086))		
1482	Z98977	Schizosaccha	putative vacuolar protein	256	29
		romyces pombe			
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyce s cerevisiae	ATHL	341	29
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabdit	coded for by C. elegans cDNA	620	42
		is elegans	yk30b3.5; coded for by C. elegans cDNA yk30b3.3		
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	452	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo	Human protein clone HP10574.	1371	100
1496	AL049699	sapiens			
1496	AF037447	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1498	AL445067		ribosomal S6 protein kinase	2427	100
1430	ALIGATION	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1502	AF179896	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2a	1177	100
1504	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ	1442	99
2505	W02404		ID NO:16.		
1505 1506	X82494 X98296	Homo sapiens	fibulin-2	3580	99
1505	AL034548	Homo sapiens	ubiquitin hydrolase	783	42
1508	Y76144	Homo sapiens	dJ1103G7.6 (novel protein) Human secreted protein	1098	100
1509	AF220182	·	encoded by gene 21.	1736	100
1510		Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
	U64601	Caenorhabdit is elegans	Gene probably begins in the next cosmid	415	58
1511	AL356192	Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514	AJ243531	Homo sapiens	nM15 protein	735	100
1515	AC003672	Arabidopsis thaliana	putative C3HC4-type RING zinc finger protein	407	30
1516	AF115435	Rattus norvegicus	syntaxin 17	1374	90
1517	AF003140	Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
1519	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30
				1	1

SEQ ID NO:	ACCESSION NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		romyces	homolog		
1520	AF255910	Homo	vascular endothelial	547	<u> </u>
	j	sapiens	junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo	Membrane-bound protein	985	100
1523	X94450	sapiens	PRO190.		
1323	194450	Homo sapiens	Human inflammation associated protein	250	43
1524	AC000107	Arabidopsis	F17F8.22	277	L
L		thaliana		2//	37
1525	AF109377	Mus musculus		1277	83
1526	AL031427	Homo sapiens		1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like	1496	79
1528	AK024423		phosphodiesterase		1
1529	AF154502	Homo sapiens Homo sapiens		611	100
1323	AL 134302	Homo sapiens	quiescent cell proline dipeptidase	679	100
1530	AF205598	Homo sapiens	transposase-like protein	1368	<u> </u>
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	100 50
1532	W74805	Homo sapiens	Human secreted protein	493	57
1533	2 7 7 7 7 7 7		encoded by gene 77 clone HOEAS24.		
1534	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1536	AB027564 Y36178	Homo sapiens	DINB1	4482	100
1537	Y50507	Homo sapiens Homo sapiens	Human secreted protein	377	87
1538	AF017368	Mus musculus	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99 .
1539	AF266756		faciogenital dysplasia protein 2	177	47
1540	Z48804	Homo sapiens Homo sapiens	sphingosine kinasc .	2011	99
1541	AF000195	Caenorhabdit	Contains similarity to Pfam	2238 379	100
1542		is elegans	domain: PF30169 (PH),   Score=20.6, E-value=1.9e-05,   N=1	379	42
1542	Y71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545 1546	AF198487 AF016417	Homo sapiens	transcription factor LBP-1b	2822	100
_		Caenorhabdit is elegans	Similar to BZIP transcription factor	518	42
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme E1	836	42
1549	AL021707	Homo sapiens	dJ508115.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus subtilis	YvqK protein	292	42
1551	AF145615	Drosophila melanogaster	BcDNA.GH03377	822	44
1552	AL157734	Schizosaccha romyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
1553	AF079527	Mus musculus	IERS	691	63
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
1556	AF116553	Drosophila melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens			

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	3
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	İ
			protein, MTRP-1.		
1.558	Y71056	Homo sapiens	Human membrane transport	1975	99
		- I	protein, MTRP-1.		
1559	Y71056	Homo sapiens	Human membrane transport	1894	97
	Ī		protein, MTRP-1.		
1560	AF092050	Mus musculus	beta-1,3-N-	262	44
	l		acetylglucosaminyltransferase		1
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
		· ·	ACRSS (similar to rat sperm		1
			antigen 4 (SPAG4)))		
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein	3015	100
		1	similar to Drosophila Kelch	Ì	1
			proteins)	<u> </u>	
1564	AC002400	Homo sapiens	Gene product with similarity	2790	100
	1		to Ubiquitin binding enzyme		ł
1565	AC005306	Homo sapiens	R27216 1	919	82
1566	AF000195	Caenorhabdit	Contains similarity to Pfam	550	45
	1	is elegans	domain: PF00169 (PH),		
	1		Score=20.6, E-value=1.9e-05,	į.	I
			N=1	1	
1567	AB033281	Homo	F-box and WD-repeats protein	2879	100
,	1	sapiens	beta-TRCP2 isoform C		
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388 .	100
1572	AE003831	Drosophila	CG18445 gene product	180	31
15/2	AEOO3631	melanogaster	Corosas gene product	1 200	1
1573	AF074603	Streptomyces	NonF	205	38
15/3	AF0/4603	griseus	NOME	203	1 30
		subsp.		1	
		griseus		i .	1
1574	U28993	Caenorhabdit	F22D3.3 gene product	144	27
7214	020993	is elegans	F22D3.5 gene produce	1	1
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila	Diablo	421	54
12//	AF 23 / /11	melanogaster	Diabio	124	37
1578	G00975	Homo sapiens	Human secreted protein, SEQ	480	100
15/8	G00975	HORO Bapiens	ID NO: 5056.	1400	1 -00
1576	N F24 2744	Crackernerid	thrombospondin-related	123	33
1579	AF248744	Cryptosporid	adhesive protein	123	1 33
1000		ium parvum	dJ585I14.2 (novel protein	663	100
1580	AL121782	Homo sapiens	(translation of cDNA	963	100
	1	<b> </b>	Em:AK000219))		1
	120110	<del> </del>		345	33
1581	AF041853	Homo sapiens	kinesin family member protein	345	33
	1 2005455		KIF3A	1198	100
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5		34
1583	AE001803	Thermotoga	glycerate kinase, putative	349	34
		maritima	<u> </u>	<u> </u>	1.00
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo	leucine-rich repeat	3494	99
		sapiens	transmembrane protein FLRT1		
1586	AF118274	Homo sapiens		2628	97
1587	X79440	Homo sapiens		3167	99
1588	X99802	Homo sapiens		3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone	181	47
		1	cb98_4.	L	_L
1591	225535	Homo sapiens	nuclear pore complex protein	7567	99
		-	hnup153	J	1
1592	X13293	Homo sapiens		3678	99
1593	M74027	Homo sapiens		242	27
1594	AL139314	Schizosaccha		235	54
		romyces	1	1	i

SEQ	ACCESSION	SPECIES	DESCRIPTION	CHICAGO	
ID	NUMBER		DESCRIPTION	SMITH- WATERMAN	*
NO:				SCORE	IDENTITY
		pombe		3CORE	<del>-</del>
1595	W78324	Homo sapiens		1318	98
			protein encoded by gene 81	12020	1 -0
1596	Y94906	Homo sapiens	Human secreted protein clone	2236	98
ļ	1		rb649_3 protein sequence SEQ		"
			ID NO:18.		
1597	AF174605	Homo sapiens		1408	99
1598	AB032254	Homo	bromodomain adjacent to zinc	9676	98
		sapiens	finger domain 2A	1	
1599	X73114	Homo sapiens		5568	95
1600	X82200	Homo sapiens	JE	2305	100
1601	Y00876	Homo	Human LAPH-1 protein	1149	98
1.500	2 7000	sapiens	sequence.	İ	
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	99
1603	AJ222801	Homo sapiens		2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription	3435	97
1505	3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		factor ODA-8		1
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic	IFN-pseudo-omega 2	800	98
1500	VERA 18	construct		1	
1608	Y57949	Homo sapiens	Human transmembrane protein	1868	100
1.500			HTMPN-73.	1	
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl	2976	100
			transferase		1
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis	nodulin-like protein	371	26
		thaliana	<u>}</u>		
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus	Castration induced prostatic	890	62
	1	norvegicus	apoptosis related protein-1,		
1617	X58079	ļ <u></u>	(CIPAR-1)		
1618	Y66678	Homo sapiens	S100 alpha protein	481	100
1010	1000/8	Homo	Membrane-bound protein	967	100
1619	AJ242973	sapiens	PRO1009.		}
1019	AU2429/3	Homo sapiens	peptide methionine sulfoxide	929	100
1620	AF150733	Homo sapiens	reductase		
1621	AJ007509	I	AD-014 protein	288	100
1622	X64177	Homo sapiens	E1B-55kDa-associated protein	4646	98
1623	AE001045		metallothionein	380	100
1025	72501043	Archaeoglobu s fulgidus	A. fulgidus predicted coding	240	36
1624	AL355013	Schizosaccha	region AF0859		
		romyces	mitochondrial carrier protein	403	34
		pombe			
1625	¥66746	Homo	Membrane-bound protein		
		sapiens	PRO1198.	1184	100
1626	D90053	Sus scrofa	destrin		
1627	Y35954	Homo sapiens	Extended human secreted	863	100
		nomo supreme	protein someone and to we	756	100
			protein sequence, SEQ ID NO. 203.	j	
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	I	
1629	AF132484	Mus musculus	unknown	470	100
1630	AF017096	Drosophila	similar to C. elegans	286	68
		melanogaster	PinHin 6 and 6 and a	493	61
			R10H10.6 and S. cerevisiae YD8419.03c	] [	· ]
1631	X03077	Homo sapiens	lactate dehydrogenase-A	1500	
1632	AF151084	Homo sapiens	HSPC250	1704	100
1633	AJ001874	Homo sapiens	orf	763	100
1634	AC012187	Arabidopsis		255	97
-		thaliana	Contains weak similarity to	143	38
	ĺ		GATA-6 DNA-binding protein		ł
l	1	j	gb H36135, gb Z26200 come from this gene.	l l	
<del></del>			Trom cura dene.	[	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone ve8 1 derived protein.	1126	95
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	М19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-1	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	туом	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	Z48613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle Bl/91, horse brain, field isolate,	p40	397	43

SEO	ACCESSION	SPECIES			
ID NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1669	Z99753	aa			
1670	G03130	Schizosaccha romyces pombe	nucleolar protein	569	47
1671		Homo sapiens	ID NO: 7211.	427	97
	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1672	AF174482	Homo sapiens		2005	199
1673	Y51846 .	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1674	AF255334	Homo sapiens		152	29
1675	Y94867	Homo sapiens	Human protein clone HP10563.	109	30
1676	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	Y25712	Homo sapiens	Human secreted protein	1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein	170	<b> </b>
1679	AF163151	Homo sapiens	precursor		17
1680	AK024453		dentin sialophosphoprotein precursor	170	17
1681	AF019236	Homo sapiens Dictyosteliu	FLJ00045 protein	1349	100
1682	AJ243459	m discoideum		613	34
		Leishmania major	proteophosphoglycan	153	26
1683	269369	Schizosaccha romyces pombe	putative GTP-binding protein	560	46
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	196	100
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila melanogaster	heat shock protein	138	43
1690	AF240463	Rattus norvegicus	LIS1-interacting protein	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus laevis	katanin p60	1664	66
1694	AP263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo sapiens	protein arginine N- methyltransferase 1-variant 2	1182	81
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
170:	AK022407	Homo sapiens	unnamed protein product	315	98
1701	AD02455		GTP-binding like protein 2		100
1702	AB024574	Homo sapiens		1172	100
1702 1703	AF055078	Homo sapiens	zinc finger protein 42	421	52
1702		Homo sapiens Mus musculus Drosophila		<del></del>	52 77
1702 1703 1704 1705	AF055078 AF198092	Homo sapiens Mus musculus Drosophila melanogaster Drosophila	zinc finger protein 42 RP42	421 1057 161	52 77 33
1702 1703 1704 1705 1706	AF055078 AF198092 AE003573	Homo sapiens Mus musculus Drosophila melanogaster	zinc finger protein 42 RP42 CG12474 gene product aquaporin	1057 161 164	52 77 33
1702 1703 1704 1705 1706 1707	AF055078 AF198092 AE003573 AB036345	Homo sapiens Mus musculus Drosophila melanogaster Drosophila melanogaster	zinc finger protein 42 RP42 CG12474 gene product	1421 1057 161 164 2146	52 77 33

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID	NUMBER			WATERMAN	IDENTITY
NO:	L	·		SCORE	
		thaliana			
1710	B01311 U40750	Homo sapiens	Human PRO241 polypeptide.	1649	97
1711 1712	1	Mus musculus	formin binding protein 30	4561	85
	AJ011118	Mus musculus	skeletal muscle and cardiac protein	1490	89
1713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	Rattus norvegicus	Ras-related protein	511	51
1716	AF168795	Rattus norvegicus	schlafen-4	1129	44
1717	AF196304	Homo sapiens	SUMO-1-specific protease	5804	99
1718	AL355737	Homo sapiens	HMG20A	1782	100
1719	AB029333	Halocynthia	HrPET-1	1069	46
		roretzi		}	10
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	Caenorhabdit is elegans	similar to Uncharacterized protein family UPF0034,	825	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ ID NO: 6053.	586	92
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	1231	100
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus gallus	tensin	1411	84
1730	273423	Caenorhabdit is elegans	cDNA EST EMBL:214908 comes from this gene-cDNA EST this gene	233	41
1732	AF090891	Homo sapiens	PRO0105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ	503	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila virilis	failed axon connections protein	276	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit is elegans	contains similarity to Pfam family PF01772 N=1	206	37
1739	X54618	Listeria monocytogene s	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	dJ319013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens	Extended human sccreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	Homo sapiens	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1748	AK024436	17000 0007	enzyme CoAEN-2.		<del></del>
1749	AE000877	Homo sapiens Methanobacte		1619	100
		rium thermoautotr	process.	231	36
1750	AF101361 Y15067	Drosophila melanogaster	Abnormal X segregation	193	33
1752	AF251038	Homo sapiens		889	100
1753	AC003093	Homo sapiens		822	100
1754			45% similarity to P22059 (PID:g129308)	352	57
1755	X69089 AL049795	Homo sapiens		5703	99
1756	AL031393	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1757	AB040672	Homo sapiens	dJ733D15.1 (Zinc-finger protein)	2765	100
1758	AL022238	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	2020	99
1759	AF117653	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1760	Y12065	Homo sapiens	double homeobox protein	375	54
1761	AL049712	Homo sapiens		2959	99
1762	AC002394	Homo	dJ686C3.2 (nucleolar protein hNop56) Gene product with similarity	2595	99
1763	AF169017	sapiens Homo sapiens	to dynein beta subunit formiminotransferase	1542	51
1764	U91541	Homo sapiens	cyclodeaminase	877	100
		Homo sapiens	human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end	596	100
1765	AB013365	Bacillus halodurans	YlqF	350	34
1766	Y38421	Homo sapiens	Human secreted protein encoded by gene No. 36.	145	71
1767	AC009176	Arabidopsis thaliana	putative ribulose-1,5- bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	216	27
1768 1769	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1771	U73522 U89435	Homo sapiens	AMSH	1214	56
1772	S70011	Mus musculus	unknown	829	86
1773	AL035086	Rattus sp. Homo sapiens	tricarboxylate carrier	1604	95
1774	Y99426	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1775	AF110330	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	1057	99
1776	AJ269529	Homo sapiens	glutaminase	3146	100
1777	Z81579	Caenorhabdit is elegans	glycerol 3-phosphate permease cDNA EST yk76f1.5 comes from this gene	2787	31
1778	AY007239	Homo sapiens	monooxygenase X		
1779	AL109608	Schizosaccha romyces	oxysterol-binding protein family	1875	38
1780	NR254252	pombe	·		i
1781	AF254260	Homo sapiens	tuftelin 1	1729	100
1782	L07924		guanine nucleotide dissociation stimulator	247	50
		Homo sapiens	ral guanine nucleotide dissociation stimulator	142	49.
1783 1784	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1785	AK024475 G03933	Homo sapiens	FLJ00068 protein		93
1786			Human secreted protein, SEQ ID NO: 8014.		100
(		aprens	Ig lambda-like gene/beta-	247	100

WO 01/53312 PCT/US00/34263

# TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	identity
			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
2	NO.		
3	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e- 12 157-181
	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e- 13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353-
6	BL00023	Type II fibronectin collagen-binding domain proteins.	390 BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353-
7	BL00023	Type II fibronectin collagen-binding domain proteins.	390 BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 89-99 PF00023B
14	DM00031	IMMUNOGLOBULIN V REGION.	14.20 2.636e-09 56-66 DM00031B 15.41 3.848e-
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	09 79-113 PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
	PD00066	PROTEIN ZINC-FINGER METAL-BINDI	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	PL00845 16.43 2.200e- 25 55-80
	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 348-390
2	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
23	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333
25	BL00115	Eukaryotic RNA	BL00115T 8.45 7.273e-
		polymerase II	29 1208-1242 BL00115Q
		heptapeptide repeat	18.08 2.776e-21 953-
		proteins.	983 BL00115Y 11.86
			8.000e-17 1604-1650
			BL00115M 19.19 8.130e- 16 731-774 BL00115H
			14.34 9.392e-16 463-
			496 BL00115A 15.44
			7.414e-15 43-82
			BL00115R 6.50 6.128e-
	<u> </u>		14 983-1010 BL00115J
		· ·	16.71 9.289e-14 591- 617 BL00115I 8.33
			4.336e-13 535-590
			BL00115L 12.25 5.939e-
			13 662-694 BL00115G
		1	11.65 6.011e-13 435-
			463 BL00115K 15.03
			3.417e-10 617-659 BL001150 16.76 5.805e-
	!	1	10 863-913 BL00115P
	İ		11.54 7.538e-10 913-
			953 BL00115S 18.24
			7.968e-10 1010-1052
	1	1	BL00115U 10.34 4.475e-
26	BL00420	Speract receptor repeat	09 1242-1265 BL00420A 20.42 4.109e-
**	2500420	proteins domain	11 81-110 BL00420A
		proteins.	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
	1	proteins.	27 94-127 BL00050B
	ì		14.81 8.125e-12 133-
28	PR00925	NONHISTONE CHROMOSOMAL	PR00925B 3.73 3.089e-
}		PROTEIN HMG17 FAMILY	10 41-54
		SIGNATURE	
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e- 09 486-516
32	BL00557	FMN-dependent alpha-	BL00557D 17.76 5.065e-
	1	hydroxy acid	37 274-316 BL00557A
1		dehydrogenases proteins.	35.08 8.909e-29 24-73
ĺ		i	BL00557C 15.59 1.000e-
	1		28 227-257 BL00557B 21.27 8.898e-22 130-
1			169
34	PR00629	SHC PHOSPHOTYROSINE	PR00629E 9.90 5.886e-
		INTERACTION DOMAIN	35 299-328 PR00629F
		SIGNATURE	10.95 8.364ė-32 334-
1			361 PR00629B 13.66 3.786e-27 224-247
[		Į.	PR00629A 13.45 8.364e-
		]	21 206-222 PR00629C
ļ		1	3.80 4.000e-12 249-261
<b>{</b>			PR00629D 12.45 3.739e-
35	PD01270	PECEDTOR EC	11 276-286
, ,	ED012/0	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B
(			22.18 2.875e-38 94-131
	1		PD01270D 24.66 3.700e-
			34 171-207 PD01270C
			19.54 3.455e-30 137-
36	PD01270	RECEPTOR FC	PD012708 17 22 1 000g-
1 - 0	2501270	IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B
İ			22.18 2.875e-38 94-131
	<del></del>		

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			PD01270D 24.66 3.700e-
			34 171-207 PD01270C 19.54 3.455e-30 137-
			166
37	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
38	BL00412	Neuromodulin (GAP-43)	10 264-298
	5255.12	proteins.	BL00412C 10.28 9.241e- 10 264-298
39	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
40	PR00380	proteins.	10 264-298
] ] "	PROUSEU	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e- 14 342-360 PR00380C
			13.18 6.927e-13 375-
			394 PR00380D 9.93
			2.180e-12 429-451
			PR00380A 14.18 5.154e- 12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
			40 239-290 BL00345A
			13.96 2.452e-14 204- 223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
		-	40 215-266 BL00345A
	İ		13.96 2.452e-14 180-
46	DM01551	kw OSTEOINDUCTIVE YOPM	199 DM01551A 15.63 3.538e-
		MEMBRANE OUTER.	26 172-202 DM01551C
			14.62 3.571e-17 232-
	ľ		252 DM01551B 8.84
47	PR00876	NEMATODE METALLOTHIONEIN	4.750e-11 214-226 PR00876B 7.66 9.328e-
		SIGNATURE	11 246-260
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.231e-
	1	BINDING NU.	33 6-45
50	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
		terminal hydrolases	19 994-1019 BL00972A
		family 2 proteins.	11.93 7.120e-18 216- 234 BL00972E 20.72
		1	9.471e-14 1020-1042
			BL00972C 16.48 7.000e-
		·	13 360-375 BL00972B
51	BL00972	Ubiquitin carboxyl-	9.45 8.269e-10 302-312 BL00972D 22.55 7.750e-
		terminal hydrolases	19 990-1015 BL00972A
		family 2 proteins.	11.93 7.120e-18 216-
			234 BL00972E 20.72 9.471e-14 1016-1038
			BL00972C 16.48 7.000e-
	1		13 360-375 BL00972B
52	BL01115	GTP-binding nuclear	9.45 8.269e-10 302-312
		protein ran proteins.	BL01115A 10.22 3.063e- 14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-
			17 20-38 PR00988F
•			12.23 7.828e-15 196- 210 PR00988C 13.64
			6.108e-14 104-120
			PR00988E 8.27 3.872e-
			11 174-186 PR00988D
	l		5.95 6.878e-10 160-171 PR00988B 11.60 2.915e-
			09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e-
		STGIVEOKE	21 294-314 PR00762D 11.29 4.103e-19 509-
			530 PR00762A 14.22
		<u> </u>	9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	<del> </del>		PR00762F 15.12 3.100e-
			16 563-583 PR00762B
	j		12.12 6.063e-16 230-
		1	250 PR00762E 12.07
	l .	ļ	2.286e-15 545-562
	1		PR00762G 14.13 6.276e-
	1	<b>\</b>	13 601-616
56	BL00216	Sugar transport	BL00216B 27.64 8.800e-
		proteins.	10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
30		and Unc5-like netrin	10 1080-1135
		receptors.	}
59	PF00791	Domain present in ZO-1	PFC0791B 28.49 2.049e-
<b>3</b> 3		and Unc5-like netrin	10 1062-1117
		receptors.	
61	PD01929	KINASE TYPE RESISTANCE	PD01929E 10.76 9.018e-
P.T	PD01925	ANTIBIOTIC TRANSFERASE	09 206-221
	1	AM.	1 53 200 222
	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
68	PR00360	C2 DOMAIN SIGNALURE	09 680-693
	1 500 000 C	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
69	PR00360	CZ DOMAIN SIGNATURE	09 670-683
			PF00651 15.00 8.714e-
70	PF00651	BTB (also known as BR-	10 51-64
	<u> </u>	C/Ttk) domain proteins.	DM00179 13.97 5.304e-
72	DM00179	w KINASE ALPHA ADHESION	09 108-118
		T-CELL.	
73	BL00239	Receptor tyrosine kinase	Вь00239В 25.15 7.075е-
		class II proteins.	12 118-166
74	BL00790	Receptor tyrosine kinase	BL00790N 13.25 6.116e-
		class V proteins.	10 93-120
76	DM00471	0 PROKARYOTIC DNA	DM00471A 11.73 9.357e-
	1	TOPOISOMERASE I.	13 53-66 DM00471B
	1		8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
	1	PHOSPHATIDYLSERINE.	13 223-236 PD02876D
			12.13 2.588e-12 334-
			351
81	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
		PHOSPHATIDYLSERINE.	13 282-295 PD02876D
			12.13 2.588e-12 393-
		1	410
83	BL00708	Prolyl endopeptidase	BL00708B 24.91 7.197e-
		family serine proteins.	12 570-601
84	PR00014	FIBRONECTIN TYPE III	PR00014C 15.44 8.043e-
-		REPEAT SIGNATURE	09 985-1004
86	PR00678	PI3 KINASE P85	PR00678H 9.13 1.379e-
00	TROUGHT.	REGULATORY SUBUNIT	09 246-269
	1	SIGNATURE	
89	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.200e-
0.7	FR00320	REPEAT SIGNATURE	09 264-279 PR00320B
		KEI DAI DIGITIONS	12.19 8.650e-09 264-
		<b>!</b>	279
		2	BL00455 13.31 2.588e-
93	BL00455	Putative AMP-binding	
		domain proteins.	BL00107A 18.39 4.000e-
95	BL00107	Protein kinases ATP-	
		binding region proteins.	10 123-154
96	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
	_	binding region proteins.	10 212-243
97	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.318e-
		DEHYDROGENASE FAMILY	13 134-146 PR00081A
	1	SIGNATURE	10.53 2.500e-12 54-72
98	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
ا آ	1.2.2.2.2.2	SIGNATURE	24 401-423 PR00380D
	ı		9.93 7.188e-20 613-635
			PR00380B 12.64 7.517e-
İ			16 529-547 PR00380C
	(	1 .	1 -0 -223 -11, 2.00-300
	1	ł –	13.18 2.756e-13 560-

SEO ID NO	: ACCESSION	DESCRIPTION	
_	NO.		RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e- 14 289-308
104	BL00479	Phorbol esters/ diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e- 18 298-314 BL00479A 19.86 4.913e-16 155- 178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e- 12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.013e- 12 43-83
107	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III	DM01970B 8.60 5.000e-
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	3L00191K 17.38 4.951e- 27 238-282 BL00191J 11.37 6.447e-17 182- 204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.938e- 37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e- 10 38-50
113	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 5.800e- 23 156-187 BL00107B 13.31 9.100e-14 225- 241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e- 17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 8.560e- 13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e- 10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e- 09 80-95
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e- 13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e- 12 147-157 BL01032H 11.25 5.680e-11 318- 331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e- 09 379-389
129	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 6.694e- 26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e- 09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.575e- 26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e- 14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e- 10 475-496
136	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e- 29 71-107
140	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e- 14 214-231 BL00028 16.07 9.471e-14 102- 119 BL00028 16.07 2.800e-13 18-35

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
CDQ ID NO.	NO.	2255KII IIGN	1.2002.0
			BL00028 16.07 5.500e-
			13 74-91 BL00028
		4	16.07 9.100e-13 186-
	i		203 BL00028 16.07
		į.	8.043e-12 46-63
			BL00028 16.07 8.435e-
		1	12 130-147 BL00028
	1		16.07 9.217e-12 270-
	ļ		287 BL00028 16.07
		Į.	6.192e-11 242-259
			BL00028 16.07 4.000e-
			10 158-175
141	BL00501	Signal peptidases I	BL00501D 16.69 9.538e-
		serine proteins.	14 113-133 BL00501C
			9.61 8.688e-10 89-101
143	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e-
			20 79-130
146	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.400e-
		ZINC-FINGER METAL-	25 335-374
		BINDING NU.	DI 001260 22 07 1 450
149	BF00156	3'5'-cyclic nucleotide	BL00126C 22.07 1.450e-
	}	phosphodiesterases	25 509-550 BL00126E
		proteins.	35.22 3.951e-16 654- 709 BL00126D 25.50
			1.360e-15 565-604
			BL00126B 15.20 8.200e-
			11 483-495 BL00126A
1		<b>!</b>	27.56 8.269e-11 442-
			479
151	BL00632	Ribosomal protein S4	BL00632 23.79 5.271e-
		proteins.	20 106-149
154	BL00559	Eukaryotic molybdopterin	BL005591 13.63 5.304e-
		oxidoreductases	19 29-58 BL00559K
	}	proteins.	13.17 2.957e-18 172-
		] -	199 BL00559J 19.63
		1	8.385e-13 99-151
		1	BL00559L 13.60 5.814e-
			12 241-259
155	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.692e-
157	- DT 00406	RAS SIGNATURE	13 13-35   BL00406D 12.58 2.547e-
137	BL00406	Actins proteins.	18 275-330 BL00406A
	1	1	9.95 5.776e-16 15-50
	į	1	BL00406B 5.47 7.429e-
	1	1	12 69-124 BL00406C
	· ·	1	6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
		zinc-binding region 1	14 22-63 BL00132C
		proteins.	21.35 3.466e-12 104-
		\	145
165	PR00109	TYROSINE KINASE	PR00109B 12.27 9.043e-
ł	1 .	CATALYTIC DOMAIN	13 139-158
}		SIGNATURE	
168	BL00362	Ribosomal protein S15	BL00362 24.67 9.700e-
ľ		proteins.	15 129-172
169	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.000e-
1		dependent helicases	35 640-686 BL00039A
		proteins.	18.44 1.964e-13 212-
l			251 BL00039B 19.19
1	1		4.553e-13 378-404
			BL00039C 15.63 8.773e-
		·	12 465-489
175	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.721e-
330		RAS SIGNATURE	12 14-36
178	BL01310	ATPIGI / PLM / MAT8	BL01310 14.74 2.432e-
170	Photoss	family proteins.	29 133-169
179	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.455e-
1	1	ZINC-FINGER METAL-	36 6-45

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		ABODIS
		BINDING NU.	
180	PR00007	COMPLEMENT CIQ DOMAIN SIGNATURE	PR00007B 14.16 7.429e- 20 160-180 PR00007A 19.33 4.938e-19 133- 160 PR00007C 15.60 1.225e-15 206-228
	<u>L</u>		PR00007D 9.64 6.885e- 11 238-249
1.81	BL00027	'Homeobox' domain	BL00027 25.43 9.526e-
182	BL00027	'Homeobox' domain	24 280-323 BL00027 26.43 9.526e-
183	BL00027	'Homeobox' domain	24 263-306 BL00027 26.43 9.526e-
184	BL00027	proteins. 'Homeobox' domain	24 280-323 BL00027 26.43 9.526e-
188	PR00929	proteins. AT-HOOK-LIKE DOMAIN	24 263-306
		SIGNATURE	PR00929C 5.26 3.328e- 09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e- 09 440-451
190 191 193 194	PR00450 PF00564 PR00503 BL00901	RECOVERIN FAMILY SIGNATURE  Octicosapeptide repeat proteins.  BROMODOMAIN SIGNATURE  Cysteine synthase/cystathionine	BL00383F 15.51 7.188e- 17 666-682 BL00383A 13.34 8.714e-17 162- 177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e- 14 628-639 BL00383F 15.51 1.720e-13 371- 387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e- 13 295-308 BL00383F 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e- 09 509-520 BL00383D 11.92 4.000e-09 589- 602 BL00383B 7.61 8.000e-09 479-488 PR00450C 12.22 7.911e- 15 83-105 PR00450C 12.22 6.286e-13 47-69 PF00564B 24.74 6.164e- 16 227-278 PR00503D 20.81 9.156e- 15 204-224 PR00503B 9.96 9.571e-13 170-187 BL00901C 20.63 3.429e- 18 67-117
197	BL00636	beta-synthase P- phosphate att. Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e-
198	DU00600	2000	17 40-57 BL00636B 15.11 2.000e-13 67-88
	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e- 09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e- 12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e- 12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	10 39-72 PR00261A 11.02 4.462e- 19 65-87 PR00251C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e- 18 65-87 PR00261B 14.12 4.000e-18 143- 165 PR00261A 11.02

SEQ ID NO:	ACCESSION	DESCRIPTION	DRetti ne+
	NO.	DESCRIPTION	RESULTS*
			4.833e-18 143-165
		į	PR00261D 12.47 7.500e-
			18 143-165 PR00261B
	İ		14.12 5.065e-16 65-87 PR00261C 11.37 8.967e-
			16 143-165 PR00261F
			11.57 4.938e-13 143-
		•	165 PR00261E 11.08
			7.188e-13 65-87
			PR00261F 11.57 7.188e-
			11.08 1.643e-11 143-
			165
209	PF00791	Domain present in ZO-1	PF00791B 28.49 6.143e-
		and Unc5-like netrin receptors.	13 118-173 PF00791C
		receptors.	20.98 7.680e-10 132-
211	PR00007	COMPLEMENT CIQ DOMAIN	PR00007A 19.33 5.781e-
		SIGNATURE	19 131-158 PR00007B
	]		14.16 4.115e-18 158-
			178 PR00007C 15.60
			1.675e-15 201-223 PR00007D 9.64 7.231e-
			11 233-244
212	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.545e-
213	BL00183	enzymes proteins.	30 43-91
213	BE00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e- 30 43-91
215	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.900e-
		dependent helicases	29 568-614 BL00039A
		proteins.	18.44 1.871e-23 21-60
		·	BL00039C 15.63 1.720e-
			11 364-388 BL00039B 19.19 4.064e-11 277-
	ĺ		303
217	BF00100	Chloramphenicol	BL00100D 17.22 8.484e-
		acetyltransferase	09 68-106
219	PR00213	proteins. MYELIN PO PROTEIN	PD002175 15 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
		SIGNATURE	PR00213C 15.94 3.969e-
222	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 1.947e-09
224	7700000	proteins proteins.	144-155
224	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e-
225	BL00636	Nt-dnaJ domain proteins.	09 901-913 BL00636B 15.11 8.200e-
		acimain proteins.	19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e-
			21 21-38 BL00636B
229	PR00301	70 KD HEAT SHOCK PROTEIN	15.11 8.200e-19 45-66
		SIGNATURE	PR00301F 13.98 7.563e- 13 329-346 PR00301G
		1	13.78 4.300e-12 361-
230	DI OCA CO	<u> </u>	382
230	BL00460	Glutathione peroxidases	BL00460A 28.67 8.773e-
		selenocysteine proteins.	20 35-70 BL00460B 9.73 7.429e-16 78-96
			BL00460C 14.35 2.831e-
	j		12 111-134 BL00460D
	1		16.89 8.773e-11 140-
231	PR00647	SEMP ODDUAY DECEME	160
	1	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e- 09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-
			27 244-275 BL00292A
	•		22.87 7.750e-27 201-
234	PR00449	TRANSFORMING PROTEIN P21	235
		RAS SIGNATURE	PR00449A 13.20 6.308e- 13 7-29 PR00449C
			, 27 + 1004430

SEQ ID	NO: ACCESSION	DESCRIPTION	L DECOM MA
	NO.	DDDCKIT I TOW	RESULTS*
ł			17.27 4.462e-11 47-70
			PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 7.300e-
1		SIGNATURE	10 251-265 PR00019B
	}	1	11.36 5.320e-09 119-
-		)	133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 7.300c-
1		SIGNATURE	10 245-259 PR00019B
			11.36 5.320e-09 113-
1			127 PR00019B 11.36
237	PD00289	PROTEIN SH3 DOMAIN	1.000e-08 223-237 PD00289 9.97 8.448e-09
		REPEAT PRESYNA.	67-81
240	PR00011	TYPE III EGF-LIKE	PR00011D 14.03 3.492e-
241	PR00011	SIGNATURE TYPE III EGF-LIKE	10 616-635
		SIGNATURE	PR00011D 14.03 3.492e-
244	BL00903	Cytidine and	BL00903 12.93 8.941e-
		deoxycytidylate	12 54-64
		deaminases zinc-binding region s.	
245	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 8.043e-
		T-CELL.	09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-
1			40 186-239 BL00246E
			20.32 1.000e-40 305- 351 BL00246B 13.69
		ľ	4.176e-36 105-140
			BL00246A 15.75 2.286e-
•		1	24 70-90 BL00246C
	į	İ	15.56 4.857e-22 150-
250	PR00927	ADENINE NUCLEOTIDE	PR00927E 14.93 5.114e-
254	BL00674	TRANSLOCATOR 1 SIGNATURE	10 253-275
	DECCO / 4	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE	PD01796 15.01 6.045e-
255		COBALT ZINC CADMIU.	09 61-88
255	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e-
259	PR00094	ADENYLATE KINASE	10 421-435 PR00094C 12.94 2.200e-
	·	SIGNATURE	18 87-104 PR00094D
	l		12.52 2.731e-14 161-
•	1	1	177 PR00094A 10.31
			5.500e-14 11-25 PR00094B 11.01 4.115e-
	į		13 39-54 PR00094E
	İ		11.25 7.333e-13 178-
259	BL00892	HIT family	193
	2200372	HIT family proteins.	BL00892A 18.17 5.500e- 13 60-91
262	BL00388 ·	Proteasome A-type	BL00388A 23.14 1.000e-
		subunits proteins.	40 8-54 BL00388B
		1	31.38 3.864e-33 66-108
			BL00388D 20.71 1.000e- 21 153-184 BL00388C
			18.79 8.147e-16 126-
264	- Presses		148
264	BL00903	Cytidine and	BL00903 12.93 5.821e-
	Į	deoxycytidylate deaminases zinc-binding	09 91-101
		region s.	
267	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
270	Pt 00222	binding region proteins.	09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e-
	<del></del> _L	Proteins.	37 362-409 BL00226B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e- 16 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e- 09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07

SEQ ID N	0: ACCESSION	DESCRIPTION	
	NO.	- Joseph Trans	RESULTS*
			BL00028 16.07 4.086e-
	ļ		09 517-534 BL00028
		į	16.07 7.429e-09 489-
296	BL00215	Mitochondrial energy	BL00215A 15.82 8.333e-
		transfer proteins.	16 111-136 BL00215A
		[	15.82 2.723e-11 10-35
			BL00215B 10.44 9.526e-
	ĺ		11 152-165 BL00215B 10.44 7.375e-10 59-72
	ļ		BL00215A 15.82 9.824e-
302			10 205-230
302	PP00953	Glycosyl transferase.	PF00953C 19.70 8.773e-
			34 236-269 PF00953A
			19.68 5.000e-25 102- 129 PF00953B 6.17
			1.000e-13 182-194
304	PF00152	tRNA synthetases class	PF00152D 21.30 8.364e-
		II.	28 422-461 PF00152C
		İ	28.03 9.250e-21 220-
			257 PF00152B 15.67 2.658e-13 159-184
		· ·	PF00152A 19.68 5.714e-
305	ppodess		11 44-67
303	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 8.250e-
	i	BINDING NU.	35 37-76
305	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 5.840e-
307		RIBONUCLEOPROTEIN.	09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
30B	PR00237	RHODOPSIN-LIKE GPCR	09 1167-1186
		SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e- 13 188-212 PR00237G
			19.63 7.207e-13 268-
			295 PR00237A 11.48
			4.375e-11 24-49
			PR00237C 15.69 3.057e- 10 101-124 PR00237D
			8.94 4.750e-10 137-159
			PR00237F 13.57 5.364e-
			10 230-255 PR00237B
309	BL00522	DNA polymerase family X	13.50 9.438e-10 57-79
		proteins:	BL00522C 11.90 7.577e- 24 315-339 BL00522F
			14.90 1.310e-15 470-
	ļ		494 BL00522A 25.52
		1	1.265e-14 179-226
			BL00522E~19.63 8.615e- 14 430-460 BL00522B
		•	27.30 9.625e-12 267-
310			313
	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e-
312	BL00290	Immunoglobulins and	10 856-897
		major histocompatibility	BL00290A 20.89 4.706e- 14 151-174 BL00290B
		complex proteins.	13.17 9.000e-12 211-
313	BL00345	Dia 1	229
	BD00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
		İ	40 34-85 BL00345A 13.96 9.217e-16 1-20
15	PF00651	BTB (also known as BR-	PF00651 15.00 5.091e-
17	DV 07 07 0	C/Ttk) domain proteins.	15 63-76
	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e-
18	BL00216	Sugar transport	17 79-130
		proteins.	BL00216B 27.64 4.696e- 11 164-214
20	PR00109	TYROSINE KINASE	PR00109B 12.27 4.814e-
		CATALYTIC DOMAIN	10 216-235

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain	BL00027 26.43 5.688e-
722	-200027	proteins.	10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
		CATALYTIC DOMAIN SIGNATURE	12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-
		Ĭ.	30 183-236 BL01241
		į.	35.81 3.222c-13 282-
	77.00.17.0	12 (CDD 42)	335 BL00412D 16.54 4.000e-
326	BL00412	Neuromodulin (GAP-43) proteins.	12 515-566 BL00412D
		proceins.	16.54 5.705e-11 516-
	1		567 BL00412D 16.54
			7.848e-10 518-569
	Ì		BL00412D 16.54 1.827e-
	1		09 514-565 BL00412D
	Ì		16.54 1.918e-09 513-
			564 BL00412D 16.54
326	DY 00222	Cadherins extracellular	2.102e-09 520-571 BL00232B 32.79 9.557e-
328	BL00232	repeat proteins domain	20 151-199 BL00232B
	1	proteins.	32.79 2.246e-18 41-89
			BL00232B 32.79 5.985e-
			18 370-418 BL00232B
			32.79 5.500e-16 258-
			306 ВЬ00232В 32.79
			9.384e-15 475-523
			BL00232C 10.65 2.537e-
			10.65 4.326e-11 368-
			386 BL00232C 10.65
			7.261e-11 473-491
			BL00232C 10.65 7.457e-
			11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-
331	5500550	Circuio domara processio.	18 27-49
333	BL01016	Glycoprotease family	BL01016C 22.84 3.925e-
		proteins.	32 70-115 BL01016E
			14.88 5.286e-19 149-
			177 BL01016H 13.71
			7.577e-13 291-301 BL01016D 8.86 3.298e-
		1	11 127-140 BL01016G
}			7.14 5.622e-10 261-271
1		i	BL01016A 5.65 7.167e-
1	1		10 4-19 BL01016F
1	1		13.34 1.563e-09 200-
		1	212 BL01016B 8.93
770	Drozza	Cmp binding and	8.855e-09 38-50 BL01115A 10.22 5.500e-
339	BL01115	GTP-binding nuclear protein ran proteins.	11 17-61
340	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 1.231e-
	1202000	ZINC-FINGER METAL-	33 10-49
		BINDING NU.	1
341	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 55-109
342	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.400e-
	1	ZINC-FINGER METAL-	30 16-55
		BINDING NU.	
343	DM00031	IMMUNOGLOBULIN V REGION.	
1306	DDCCTCC	BYDOCINE VINCE	40 20-68 PR00109B 12.27 4.764e-
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	11 135-154
1		SIGNATURE	1223-133
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID N		DESCRIPTION	RESULTS*
	NO.	CATALYTIC DOMAIN	
		SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29
			BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00065 13.92 6.500e-13 233- 246 PD00066 13.92
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	4.300e-09 289-302 PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109-
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	131 PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR.00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 9.000e- 15 30-49 PRO0011A 14.06 9.830e-15 30-49 PRO0011B 13.08 4.500e- 14 30-49 PRO0011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e-
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	12 410-425 PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

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			10 88-118
380	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 1.000e- 23.276-307 BL00107B 13.31 1.692e-12 342- 358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e- 12 50-66
382	PR00624	HISTONE HS SIGNATURE	PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e- 10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e- 13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.657e- 09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e- 11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e- 09 272-285 BL00215B 10.44 8.500e-09 165- 178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e-
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e-
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e- 10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e- 18 331-369 PF00676D 14.40 3.854e-15 486- 506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G 15.98 6.092e-14 4555- 4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e- 10 4519-4534 BL00514H 14.95 4.955e-10 4584- 4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e- 10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e- 09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repcat proteins domain proteins.	BL00232B 32.79 9.557e- 20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e- 18 358-406 BL00232B 32.79 5.500e-16 246-

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			294 BL00232B 32.79
	1		9.384e-15 463-511
			BL00232C 10.65 2.537e-
		[	12 244-262 BL00232C 10.65 4.326e-11 356-
	}		374 BL00232C 10.65
			7.261e-11 461-479
		į	BL00232C 10.65 7.457e-
	1		11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
		(Hemagglutinin).	09 902-940
409	BL01160	Kinesin light chain	BL01160B 19.54 9.695e-
410	77.00	repeat proteins.	09 126-180
410	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
		dissociation stimulators	09 252-275
411	PF00646	CDC24 family sign. F-box domain proteins.	DR006463 14 27 6 24
	1100040	r-box domain proceins.	PF00646A 14.37 6.344e- 09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
		cellular-type proteins.	09 542-557
415	BL00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
		synthase subdomain	31 245-291 BL00866C
		proteins.	23.26 9.000e-25 331-
			366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
421	DDOOGO	TERMINAL TAIL SIGNATURE	09 590-602
421	PF00791	Domain present in 20-1	PF00791B 28.49 7.955e-
		and Unc5-like netrin	14 23-78 PF00791B
	1	receptors.	28.49 3.653e-12 273- 328 PF00791B 28.49
		·	4.273e-11 156-211
			PF00791B 28.49 7.818e-
			11 89-144 PF00791B
		1	28.49 1.524e-10 56-111
			PF00791C 20.98 3.559e-
	•		09 37-76 PF00791C
			20.98 5.235e-09 170-
	1	1	209 PF00791C 20,98
			5.235e-09 381-420 PF00791B 28.49 6.202e-
		1	09 189-244 PF00791B
			28.49 7.028e-09 435-
		1	490 PF00791B 28.49
			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
425	77707170		28 1645-1679
263	PR00109	TYROSINE KINASE	PR00109D 17.04 5.881e-
	1	CATALYTIC DOMAIN SIGNATURE	10 228-251
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
	1	(RING finger), proteins.	11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
		dependent helicases	34 490-536 BL00039A
		proteins.	18.44 5.615e-19 205-
	1		244 BL00039B 19.19
	1		8.920e-16 251-277
	1		BL00039C 15.63 5.781e-
432	PR00452	SH3 DOMAIN SIGNATURE	15 333-357
	1	SIS DOINTIN SIGNATURE	PR00452B 11.65 7.652e- 12 169-185
	i .	•	
433	PR00828	FORMIN SIGNATURE	DD00828B 5 22 0 2104
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
433	PR00828		10 382-405
<u> </u>		FORMIN SIGNATURE  Synapsins proteins.	10 382-405 BL00415N 4.29 8.643e-
436			10 382-405
<u> </u>			10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N
436	BL00415	Synapsins proteins.	10 382-405 BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853

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		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	ВЬ00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR0038C	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	ВЬ00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	ВЬ00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e-
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

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SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	+	polyprotein).	15 21-71
498	BL00120	Lipases, serine	BL00120B 11.37 7.923e-
1		proteins.	09 185-200
500	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.353e-
		region RNP-1 proteins.	11 299-318
501	BL01159	WW/rsp5/WWP domain	BL01159 13.85 8.579e-
1		proteins.	12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e-
L	_1		17 492-510
508	PR00120	H+TRANSPORTING ATPASE	PR00120C 9.90 5.800e-
		(PROTON PUMP) SIGNATURE	19 705-722
509	DM01417	6 kw INDUCING XPMC2	DM01417E 20.62 2.938e-
		MUSHROOM SPAC22G7.04.	16 362-395 DM01417D
			11.08 3.800e-13 322-
510	DEGOGO		338
310	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
511	PF00534	group 1.	09 346-370
1 321	FEC00334	Glycosyl transferases	PF00534B 14.47 6.625e-
512	PF00534	group 1.	09 293-317
	1100334	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-
513	PD01841	PHOSPHORYLASE KINASE	09 366-390 PD01841A 21.71 1.000e-
		ALPHA MUSCL:	40 110-160 PD01841B
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ļ			222 PD01841D 17.87
			1.000e-40 243-295
i		i	PD01841F 13.36 1.000e-
	ļ	i	40 333-382 PD01841G
			24.26 1.000e-40 386-
ļ			440 PD01841L 18.42
	1		1.000e-40 968-1010
			PD01841I 23.00 4.545e-
	1		37 762-804 PD01841E
			18.60 3.750e-36 295-
			333 PD01841J 14.94
•			6.023e-35 851-888
	1		PD01841H 21.30 2.909e-
			33 490-527 PD01841K
	1	[	14.81 7.088e-33 924-
			954 PD01841C 13.78
	ĺ	<b>,</b>	9.386e-23 222-243
		I	PD01841M 10.82 8.594e-
	İ		21 1054-1073 PD01841I
		1	23.00 2.667e-13 549- 591
514	PR00153	CYCLOPHILIN PEPTIDYL-	-I -
		PROLYL CIS-TRANS	PR00153C 11.01 7.188e-
·		ISOMERASE SIGNATURE	9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
		1	12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
			12 1018-1052
517	BL00242	Integrins alpha chain	BL00242C 16.86 8.320e-
		proteins.	09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
ĺ		1	39 20-68 DM00031B
-505		1	15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic	BL00319C 17.12 8.375e-
		glycoprotein	10 61-95
		extracellular domain	
526	DECORA .	proteins.	
526	PF00789	Domain present in	PF00789B 19.70 3.308e-
1		ubiquitin-regulatory	12 322-343 PF00789C
ĺ		proteins.	20.98 5.269e-09 367-
528	D1.011.60		392
760	BL01162	Quinone oxidoreductase /	BL01162C 22.80 1.500e-
ļ		zeta-crystallin	16 120-164
ı		proteins.	l i

No.	SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SIGNATURE	DEQ ID NO.		i bibekii i ion	KB50B10
transfer proteins.   17 11-36 BL00215A   15.82 8.60e-11 123-148	529	PR00910	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
15.82 8.660-11 123-148	532	BL00215		
148   BL00215   Mitochondrial energy transfer proteins   17 11-36 BL00215A   15.82 4.000e-17 11-36 BL00215A   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 97-122   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-11 98-12   15.82 8.60e-1			transfer proteins.	,
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204 PR00370F 17, 75 6,559e-21 376-396   PR00370B 10.91 9.591e-21 27-46 PR00370C 11.27-23.500e-20 140-157 PR00370B 3.35 6,42e-17 4-20   Elogo			1	22 321-340 PR00370D
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Proteins.   15 844-881				1
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Description	539	BL00762		
SIGNATURE   10 357-375		-		
PD02102   SUBUNIT E V-ATPASE   PD02102A 16.74 1.000e-VACUOLAR ATP SYNTHASE   HYDROL.   18.28 4.375e-34 57-100   PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146   PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146   PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146   PD02102D 21.69 1.000e-10 146   PD02102D 21.69 1.000e-10 146   PD02102D 21.69 1.000e-10 146   PD02102D 21.69 1.000e-10 193-210 BL00028 16.07 1.000e-09 343-360   PD0028 16.07 6.914e-09 78-95   PD02102D 21.24 8.000e-31 293-329 PD00250B 27.37 5.286e-24 354-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.24 8.000e-390   PD02102D 21.2	540	PR00985		1 "
HYDROL.  18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146  543  BL00028  Zinc finger, C2H2 type, domain proteins.  BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95  BL00250 TGF-beta family proteins.  BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390	541	PD02102		
PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146  Sinc finger, C2H2 type, domain proteins.    BL00028			I .	
30 179-218 PD02102C 26.34 8.929e-26 100- 146  543  BL00028  Zinc finger, C2H2 type, domain proteins.  BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95  BL00250  TGF-beta family proteins.  BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390			HYDROL.	
146				<b>1</b> ·
543  BL00028  Zinc finger, C2H2 type, domain proteins.  BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95  BL00250  TGF-beta family proteins.  TGF-beta family 31 293-329 BL00250B 27.37 5.286e-24 354- 390			i	ſ
domain proteins.    10 48-65 BL00028   16.07 6.400e-10 193-210 BL00028 16.07   1.000e-09 343-360   BL00028 16.07 6.914e-09 78-95     545   BL00250   TGF-beta family   BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390   390	E43	   BT-00029	Zino Firmar Covo har	Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl
16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95  545 BL00250 TGF-beta family proteins.  BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390	C#C	5000028		
1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95  545  BL00250  TGF-beta family proteins.  BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390			,	16.07 6.400e-10 193-
BL00028 16.07 6.914e- 09 78-95  545  BL00250  TGF-beta family proteins.  BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390				
545 BL00250 TGF-beta family BL00250A 21.24 8.000e- proteins. 31 293-329 BL00250B 27.37 5.286e-24 354- 390				,
proteins. 31 293-329 BL00250B 27.37 5.286e-24 354-390		1		- F
27.37 5.286e-24 354- 390	545	BL00250	,	
390		1	proteins.	
	547	PR00319	BETA G-PROTEIN	

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
}	NO.	(TRANSDUCIN) SIGNATURE	
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B
549	PR00326	GTP1/OBG GTP-BINDING	15.41 4.333e-16 102- 116
F.F.3		PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e- 15 255-276
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e-
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183-
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	199 PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
· · · · · · · · · · · · · · · · · · ·		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e-
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.196e-11 784-804
586	PFC0013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO	: ACCESSION	DESCRIPTION	RESULTS*
<u> </u>	NO.		
			5.000e-11 61-73 BL00242D 13.57 4.986e- 10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-
608	PF00855	PWWP domain proteins.	13 335-358 PF00855 13.75 5.167e-
609	PF00855	PWWP domain proteins.	15 265-282 PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.411e- 10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10.69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879- 899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e- 09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	1.000e-17 158-182 PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455.
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PRO0380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM012C6B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e-
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543-
		į –	1 5 6 6
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	566 PR00407K 9.94 8.448e- 09 326-339

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23 9.308e-29 216-240
	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 B.500e- 14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
	<u> </u>	<u> !</u>	20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN	PD01719A 12.89 4.452e-
	1	SIGNAL RE.	11 969-997 PD01719A
			12.89 3.961e-10 128-
		·	156 PD01719A 12.89
			7.395e-10 1276-1304
			PD01719A 12.89 1.222e-
CER	DY 00054	VINCE T 4 VINCE V DAYS	09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins	BL00354C 6.61 8.397e- 09 563-578
		(Ahook).	09 363-378
658	BL00354	HMG-I and HMG-Y DNA-	BL00354C 6.61 8.397e-
636	BE00334	binding domain proteins	09 580-595
		(Ahook).	05 500-555
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e-
635	DM00213	PROBING-RICH PROTEIN 3.	13 539-572 DM00215
	1		19.43 4.750e-12 549-
			582 DM00215 19.43
			9.824e-11 551-584
	1		DM00215 19.43 2.929e-
	1	Ì	10 548-581 DM00215
			19.43 4.054e-10 550-
			583 DM00215 19.43
	-		5.339e-10 552-585
	1		DM00215 19.43 7.107e-
	ł		10 544-577
660	PR00688	XYLOSE ISOMERASE	PR00688I 13.78 9.518e-
*		SIGNATURE	09 224-236
661	BL00027	'Homeobox' domain	BL00027 26.43 5.950e-
	1	proteins.	23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
			10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.1582-
		<u> </u>	10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
			10 596-610
666	PR00819	CEXX/CFQX SUPERFAMILY	PR00819B 10.83 8.988e-
	<u> </u>	SIGNATURE	10 704-720
667	BL50040	Elongation factor 1	BL50040C 22.62 2.143e-
		gamma chain profile.	16 135-178
66B	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.360e-
		SIGNATURE	09 139-153 PR00019A
		1	11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-
		i	09 163-177
670	BL00018	FF band galoium binding	
570	2000018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41
		domain proceins.	6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT	PD00131B 34.97 1.000e-
	1 200131	TRANSMEMBR.	34 356-410 PD00131C
		TIGHOLDINE.	19.59 1.346e-26 504-
	Ì		542
673	PR00667	RETINAL PIGMENT	PRC0667G 15.33 7.557e-
- · <del>-</del>	1	EPITHELIUM-RETINAL GPCR	10 106-123
	1	SIGNATURE	
674	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 4.857e-
· <del>-</del>		REPEAT SIGNATURE	13 593-608 PR00320B
			12.19 4.115e-12 635-
			650 PR00320C 13.01
		1	8.435e-11 717-732
		<b> </b>	PR00320C 13.01 2.800e-
			10 635-650 PR00320C
			13.01 6.400e-10 593-
			608 PR00320B 12.19
		1	3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 4.857e-
		REPEAT SIGNATURE	13 572-587 PR00320B
	I	1	12.19 4.115e-12 614-
		<del></del>	· · · · · · · · · · · · · · · · · · ·

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		629 PR00320C 13.01
			8.435e-11 696-711
		1	PR00320C 13.01 2.800e-
		İ	10 614-629 PR00320C
			13.01 6.400e-10 572-
			587 PR00320B 12.19
45.4			3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 3.700e-
0.5	1100012	x3-H type (and similar).	16 225-236 PF00642
	}	1	11.59 7.900e-12 187-
		İ	198
680	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 8.754e-
	<u> </u>	PROTEIN SIGNATURE	10 286-296
681	BL00019	Actinin-type actin-	BL00019D 15.33 4.200e-
682	PR00700	binding domain proteins.  PROTEIN TYROSINE	19 227-257 PR00700D 12.47 4.000e-
682	PR00700	PHOSPHATASE SIGNATURE	09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN	PR03049D 0.00 8.500e-
- • •		SIGNATURE	10 538-553
689	BL01024	Protein phosphatase 2A	BL01024A 10.26 1.000e-
	1	regulatory subunit PR55	40 22-69 BL01024B
		proteins.	8.91 1.000e-40 86-127
	1		BL01024C 7.80 1.000e-
			40 146-185 BL01024D 13.22 1.000e-40 185-
			222 BL01024E 11.96
			1.000e-40 222-266
			BL01024F 9.42 1.000e-
			40 266-317 BL01024G
			11.09 1.000e-40 317-
	1		349 BL01024H 13.88
691	BL00027	'Homeobox' domain	1.000e-40 389-442 BL00027 26.43 8.071e-
031	BEOUGET	proteins.	31 152-195
692	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 45-57
693	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 45-57
694	BL00211	ABC transporters family	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	proteins. Methionine	BL00680 14.37 5.304e-
030	PE00680 .	aminopeptidase subfamily	17 173-195
		1 proteins.	
697	BL00741	Guanine-nucleotide	BL00741B 14.27 3.418e-
	1	dissociation stimulators	11 242-265
		CDC24 family sign.	
698	DM01930	2 kw FINGER SMCX SMCY	DM01930E 15.41 1.367e-
		YDR096W.	37 170-215 DM01930F 14.16 8.232e-28 267-
İ		1	1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
		1	9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X	PR00869A 12.80 1.281e-
		SIGNATURE	16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.174e-
	1	SIGNATURE	10 77-91 PR00048A
			10.52 6.870e-10 133-
	-		147 PR00048A 10.52
	[		8.826e-10 105-119
			PR00048A 10.52 5.320e-
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-
	220023	Autrarases brocerus.	25 326-356 BL00523A
		1	
		1	13.36 5.050e-16 38-55
			13.36 5.050e-16 38-55 BL00523B 8.64 5.909e-
			1

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e- 10 513-523 BL00523F 10.85 6.351e-09 413-
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	09 364-374 PD00767A 14.84 8.941e- 14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e-
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	10 822-841  DM01354Y 10.69 4.977e- 38 425-465 DM01354X 13.86 7.300e-34 376- 415 DM01354V 12.97 4.923e-17 311-358  DM01354W 12.64 5.596e- 10 356-376
713	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.545e- 27 450-496 BL00039A 18.44 2.537e-18 147- 186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-
715	BL00383	Tyrosine specific protein phosphatases proteins.	13 194-220 BL00383E 10.35 4.981e- 10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e-
718	DM00031	IMMUNOGLOBULIN V REGION.	21 106-161 DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e-
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	12 131-142  BL00243B 17.54 1.000e- 40 131-172 BL00243C 16.42 1.000e-40 172- 208 BL00243D 24.07 1.000e-40 222-274  BL00243F 22.63 1.000e- 40 314-358 BL00243I 31.77 6.571e-39 607- 650 BL00243E 16.70 3.077e-35 274-304, BL00243G 21.38 3.625e- 34 358-400 BL00243H 17.53 5.235e-29 567- 593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e- 16 477-503 BL00243H 17.53 2.304e-11 524- 550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-
720	PR00217	43 KD POSTSYNAPTIC	09 610-653 PR00217C 10.91 8.022e-
222	PR00704	PROTEIN SIGNATURE  CALPAIN CYSTEINE  PROTEASE (C2) FAMILY  SIGNATURE	09 20-36 PR00704D 11.05 5.909e- 34 135-161 PR00704F 13.61 7.000e-26 190- 218 PR00704E 12.55 8.071e-26 165-189

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PRO0704B 17.94 2.241e-
		Ì	23 75-98 PR00704A
		i	14.68 4.094e-19 30-54
			PR00704C 11.88 1.871e-
			18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PRO0194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.125e-
121	TROOSEO	REPEAT SIGNATURE	13 277-292 PR00320A
			16.74 1.310e-11 277-
		1	292 PR00320C 13.01
			4.522e-11 323-338
		Ī	PR00320A 16.74 6.586e-
			11 323-338 PR00320B
		Ì	12.19 4.343e-10 323-
			338 PR00320B 12.19
			6.914e-10 277-292 PR00195A 11.94 8.627e-
731	PR00195	DYNAMIN SIGNATURE	16 288-307 PR00195E
			9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.082e-
, 33	1100047	x3-H type (and similar).	10 787-798
738	BL00039	DEAD-box subfamily ATP-	BL00039A 18.44 2.565e-
		dependent helicases	28 26-65 BL00039D
		proteins.	21.67 2.105e-20 338-
			384 BL00039C 15.63
			9.100e-13 160-184
	İ		BL00039B 19.19 9.617e-
			11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B
		ramity proteins.	10.45 9.571e-17 353-
			383
742	BL01019	ADP-ribosylation factors	BL01019A 13.20 7.078e-
		family proteins.	12 41-81
743	BL00965	Phosphomannose isomerase	BL00965C 23.78 1.000e-
		type I proteins.	40 256-305 BL00965B
			17.77 1.600e-25 126-
	1		153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-
/1/	BHOODEL	Kringle domain process.	25 231-273 BL00021B
1		1	13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain	BL00612B 11.35 2.034e-
]		proteins.	11 93-126
749	PR00450	RECOVERIN FAMILY	PR00450C 12.22 6.880e-
		SIGNATURE	10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C
Ì			1
1		į	17.06 9.444e-11 370-
754	BL00051	Ribosomal protein L39e	BL00051 20.92 1.935e-
1		proteins.	16 4-50
755	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.723e-
1		ENDOSOMAL III.	09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-
			12 99-150
762	3L00046	Histone H2A proteins.	BL00046 12.95 1.000e-
			40 33-88
763	PD02411	PROTEIN TRANSCRIPTION	PD02411 21.89 9.137e- 10 206-240
764	DT.00022	REGULATION NUCLEAR.	BL00027 26.43 8.800e-
764	BL00027	'Homeobox' domain proteins.	29 417-460
L	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-
767			
767	2201200		10 309-324 BL01208B

SEQ ID NO:	ACCESSION	DESCRIPTION	
	NO.	DESCRIPTION .	RESULTS*
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding	32 -208-241 BL00031B
		region proteins.	22.25 5.500e-27 242- 274
772	PRO0449	TRANSFORMING PROTEIN P21	
	İ	RAS SIGNATURE	18 4-26 PR00449E
			13.50 3.520e-14 142-
1	1	[	165 PR00449C 17.27 3.032e-13 44-67
ł	İ		PR00449D 10.79 8.579e-
			13 107-121 PR00449B
773	BL00523	Sulfatases proteins.	14.34 3.455e-11 27-44
		Julia cases processing.	BL00523E 19.27 9.333e- 23 299-329 BL00523A
			13.36 2.200e-13 47-64
	i		BL00523B 8.64 2.607e-
			13 91-103 BJ,00523D
i		1	9.89 7.923e-12 224-236 BLC0523C 12.64 4.512e-
		}	10 141-152 BL00523F
		1	10.85 5.821e-10 373-
775	BL00028	Zinc finger, C2H2 type,	384 BL00028 16.07 7.686e-
776	-	domain proteins.	09 568-585
776	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-
777	BL00028	Zinc finger, C2H2 type,	09 621-638 BL00028 16.07 7.686e-
		domain proteins.	09 595-612
778	BP00030	Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
	ļ	region RNP-1 proteins.	11 322-341 BL00030A
			14.39 7.000e-10 220- 239
779	PR00079	GLUCOSE-6-PHCSPHATE	PR00079B 12.98 2.929e-
	1	DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
		İ	16.65 4.150e-23 348~ 375 PR00079C 8.68
	[	,	6.351e-16 246-264
	1	1	PR00079D 13.51 7.070e-
			16 264-281 PR00079A 16.12 6.769e-13 169-
781	BL00215		183
,01	BD00212	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e-
		process.	17 10-35 BL00215A 15.82 6.000e-16 221-
•			246 BL00215A 15.82
_			7.857e-12 108-133
<u> </u>			BL00215B 10.44 9.526e- 11 168-181
783	PD00239	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
785	BL00690	REPEAT PRESYNA.  DRAH-box subfamily ATP-	159-173
		dependent helicases	BL00690B 13.38 1.000e- 12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
i		1	BL00690C 7.51 3.189e-
786	PR00449	TRANSFORMING PROTEIN P21	09 218-228 PR00449C 17.27 8.500e-
		RAS SIGNATURE	16 50-73 PRO0449A
		[	13.20 5.235e-14 8-30
ļ			PR00449E 13.50 2.853e-
		1	11 150-173 PR00449D . 10.79 1.545e-09 111-
700	Diag		125
788	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 8.767e-
790	BL00915	PROTEIN. Phosphatidylinositol 3-	10 1-21 PL00015C 22 42 0 100
	-	and 4-kinases proteins.	BL00915C 22.43 9.182e- 39 725-764 BL00915B
		<del></del>	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	,		22.78 5.050e-33 633- 671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e- 13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e- 10 120-138 PR00208A 12.59 6.294e-10 121- 139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e- 10 123-141 PR00208A 12.59 6.294e-10 124- 142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e- 10 126-144 PR00208A 12.59 6.294e-10 127- 145 PR00208A 12.59 6.294e-10 127- 145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e- 10 129-147 PR00208A 12.59 7.411e-09 130- 148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e- 09 132-150 PR00208A 12.59 8.274e-09 118- 136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e- 16 302-320 PR00205A 14.73 1.257e-11 284- 300 PR00205C 13.65 1.333e-11 337-352
	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000c- 12 196-247 BL00412D 16.54 5.705e-11 197- 248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e- 13 40-58
799	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e- 09 197-240
801	BL00309	Vertebrate galactoside- binding lectin proteins.	BL00309C 18.65 1.621e- 09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e- 09 187-199
	PF00774	Dihydropyridine	PF00774A 16.47 8.457e-
804		sensitive L-type calcium channel (Beta subuni.	10 110-156
808	PR00667		PR00667C 11.71 9.875e- 09 12-28 PD02346F 12.89 4.340e-

SEQ ID NO:	ACCESSION	DESCRIPTION	L DECLU MC+
32x 15 10:	NO.	DISCRIPTION	RESULTS*
	<del></del>	PHOTOSYNTHESIS.	<del> </del>
811	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A
03.2	777		11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE	PR00080A 9.32 9.419e-
813	BL00357	SUPERFAMILY SIGNATURE Histone H2B proteins.	10 93-105 BL00357 7.74 1.988e-17
	DECOSS,	mastone has proteins.	22-65
815	PD00056	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
		METAL-BINDI.	15 158-171 PD00066
		İ	13.92 5.200e-14 46-59
		1	PD00066 13.92 7.000e- -14 18-31 PD00066
	ļ		13.92 7.000e-13 130-
	i	1	143 PD00066 13.92
			7.500e-13 214-227
		1	PD00066 13.92 9.000e-
			13 102-115 PD00066
			13.92 4.429e-12 186- 199 PD00066 13.92
			1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase	BL01195C 20.12 3.348e-
828	-	proteins.	20 100-139
820	BLC0520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-
822	BL00972	Ubiquitin carboxyl-	09 1-14 BL00972A 11.93 8.113e-
		terminal hydrolases	09 224-242
		family 2 proteins.	
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
829	PD02855	SIGNATURE	10 101-115
023	1002033	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732c- 28 88-124 PD02855B
			8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
	1	PROTEIN SIGNATURE	21 44-62 PR00405C
			19.41 1.000e-13 65-87
			PR00405A 17.71 7.283e-
831	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
	1		11.36 1.720e-09 136-
			150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.438e-
		SIGNATURE	16 164-183 PR00011D
	1		14.03 6.850e-16 164-
	1	1	183 PRO0011A 14.06
			8.364e-14 164-183 PR00011C 24.25 5.415e-
			12 231-260 PR00011D
		1	14.03 9.852e-11 212-
834	DD00306	DDOMETN GT VC	231
034	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-
835	PD00306	PROTEIN GLYCOPROTEIN	12 232-246 PD00306A 10.26 4.000e-
·		PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
837	DMOOSIE	PRECURSOR RE.	12 216-230
	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 8.302e-
		RIBONUCLEOPROTEIN.	09 73-116
840	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
	}	PHOSPHATASE SIGNATURE	22 369-390 PR00700D
	1		12.47 5.765e-21 491- 510 PR00700C 13.17
			4.750e-14 449-467
			PR00700F 11.18 8.500e-
		·	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ IS NO.	NO.		
	<del> </del>		11 538-549 PR00700E
			17.57 3.100e-10 522-
			538
841 .	PR00109	TYROSINE KINASE	PR00109B 12.27 5.404e-
	1	CATALYTIC DOMAIN	13 134-153
	5000205	PROTEIN RIBOSOMAL 60S	PD02785B 14.43 1.000e-
844	PD02785	L22 RNA-BINDING HEP.	40 58-112 PD02785A
	İ	122 RNA-BINDING REF.	15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e-
043	2200020	122000	09 203-230
846	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.429e-
		(RING finger), proteins.	10 15-24
849	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
	1	(RING finger), proteins.	08 340-349
850	PR00308	TYPE I ANTIFREEZE	PR00308A 5.90 6.506e-
		PROTEIN SIGNATURE	09 12-27
851	PD02411	PROTEIN TRANSCRIPTION	PD02411 21.89 7.000e-
		REGULATION NUCLEAR.	16 246-280
852	BL00420	Speract receptor repeat	BL00420B 22.67 1.000e- 40 723-778 BL00420B
		proteins domain proteins.	22.67 1.321e-38 933-
	1	process:	988 BL00420B 22.67
			8.457e-28 482-537
		ļ	BL00420B 22.67 4.500e-
			27 587-642 BL00420B
			22.67 9.625e-27 270-
			325 BL00420B 22.67
			4.205e-26 163-218
			BL00420B 22.67 5.731e- 23 55-110 BL00420B
			22.67 6.464e-20 377-
			432 BL00420B 22.67
<u> </u>			2.800e-15 830-885
			BL00420C 11.90 1.900e-
			13 355-366 BL00420C
		1	11.90 1.900e-12 808-
ĺ	l		819 BL00420C 11.90
· ·	ł		3.550e-12 248-259 BL00420C 11.90 2.831e-
			11 141-152 BL00420C
	}	ļ <sup>:</sup>	11.90 5.119e-11 1018-
1	1		1029 BL00420C 11.90
1			7.955e-10 567-578 ·
853	BL00420	Speract receptor repeat	BL00420B 22.67 1.000e-
	1	proteins domain	40 756-811 BL00420B
	1	proteins.	22.67 1.321e-38 966-
Į.	1	į.	1021 BL00420B 22.67 8.457e-28 482-537
1			BL00420B 22.67 4.500e-
1			27 620-675 BL00420B
1		1	22.67 9.625e-27 270-
1			325 BL00420B 22.67
l .	1		4.205e-26 163-218
			BL00420B 22.67 5.731e-
1		1	23 55-110 BL00420B
		ļ	22.67 6.464e-20 377-
1		1	432 BL00420B 22.67 2.800e-15 863-918
		<u> </u>	BL00420C 11.90 1.900e-
1			13 355-366 BL00420C
1			11.90 1.900e-12 841-
1		1	852 BL00420C 11.90
1	1	1	3.550e-12 248-259
1			BL00420C 11.90 2.831e-
1	1		11 141-152 BL00420C
1			11.90 5.119e-11 1051-
1	I	·	1062 BL00420C 11.90

857 859 861 863	ACCESSION NO.  PR00388  BL00030  PR00988	J',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE Eukaryotic RNA-binding region RNP-1 proteins.  URIDINE KINASE SIGNATURE	RESULTS*  7.955e-10 567-578  PR00388A 10.45 2.778e-09 64-83  BL00030A 14.39 2.929e-13 37-56 BL00030B  7.03 1.900e-11 167-177  BL00030A 14.39 2.000e-10 128-147  PR00988A 6.39 4.250e-17 23-41 PR00988C  13.64 8.714e-16 107-123 PR00988F 12.23  7.828e-15 198-212  PR00988E 8.27 9.769e-12 176-188 PR00988D
861	BL00030	CLASS II PHOSPHODIESTERASE SIGNATURE Eukaryotic RNA-binding region RNP-1 proteins.	PR00388A 10.45 2.778e-09 64-83  BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147  PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR0098BF 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-
861	BL00030	CLASS II PHOSPHODIESTERASE SIGNATURE Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147 PR00988A 6.39 4.250e- 17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-
861		region RNP-1 proteins.	13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147 PR00988A 6.39 4.250e- 17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-
863	PR00988	URIDINE KINASE SIGNATURE	17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-
			5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-
864	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e- 12 41-54
	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e- 24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e- 17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e- 17 153-171 PR00775G 10.64 6.850e-15 267- 286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.596e- 29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e- 26 16-48
	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e- 32 665-711
	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 298-315
	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e- 10 97-141
	BL01189	Ribosomal protein S12e proteins.	Bi01189A 14.27 1.000e- 40 35-71 Bi01189B 13.49 1.000e-40 71-125
	BL00284	Serpins proteins.	BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
	3L00216	Sugar transport proteins.	BL00216B 27.64 4.375e- 21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A
1	R00327	ICE NUCLEATION PROTEIN	7.83 5.390e-11 16-36 PR00327C 6.37 5.247e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	SIGNATURE	09 313-328
000	ВР00033	DEAD-box subfamily ATP-	BL00039D 21.67 7.800e-
898	BE00033	dependent helicases	26 386-432 BL00039A
		proteins.	18.44 6.674e-16 113-
		procesns.	152 BL00039B 19.19
	1		1.947e-13 153-179
	}	<b>!</b>	BL00039C 15.63 9.460e-
			11 236-260
901	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 8.200e-
301	1000000	METAL-BINDI.	16 254-267 PD00066
		WEIGHT BINDI.	13.92 8.200e-16 282-
			295 PD00066 13.92
	1		8.200e-16 310-323
	1		PD00066 13.92 8.200e-
•			16 366-379 PD00066
	}	ł	13.92 8.200e-16 394-
			407 PD00066 13.92
	1		8.200e-14 338-351
902	BL01115	GTP-binding nuclear	BL01115A 10.22 9.321e-
902	PIOTITIE	protein ran proteins.	11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-
903	PROUBUS	VINCOLIN SIGNATURE	09 97-111
004	PR00381	KINESIN LIGHT CHAIN	PR00381E 8.75 6.586e-
904	PR00381	SIGNATURE	25 335-356 PR00381B
		SIGNATURE	18.17 2.667e-24 204-
			224 PR00381A 9.55
		Ī	2.800e-24 107-125
			PR00381C 12.48 4.522e-
		İ	24 226-245 PR00381D
		}	13.94 1.084e-22 291-
			309 PR00381F 9.13
			3.288e-22 370-392
			PR00381F 9.13 7.181e-
			13 286-308 PR00381E
	1		8.75 4.066e-11 251-272
	1	!	PR00381E 8.75 7.033e-
	Ĭ.	!	11 293-314 PR00381E
			8.75 8.364e-10 377-398
			PR00381D 13.94 5.230e-
		·	09 333-351 PR00381C
			12.48 7.120e-09 310-
			329
906	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
100		SIGNATURE	09 525-549
907	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
		SIGNATURE	09 513-537
908	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11
	1	proteins proteins.	144-155
910	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.800e-
1		ZINC-FINGER METAL-	30 48-87
1		BINDING NU.	
912	BL01104	Ribosomal protein L13e	BL01104C 15.14 6.000e-
		proteins.	09 364-392
922	3L00678	Trp-Asp (WD) repeat	BL00678 9.67 3.842e-09
1	1	proteins proteins.	500-511
I	1		
923	PR00320		PR00320C 13.01 2.500e-
923	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.500e- 09 323-338 PR00320C
923	PR00320		09 323-338 PR00320C
923	PR00320	G-PROTEIN BETA WD-40	09 323-338 PR00320C 13.01 5.500e-09 187-
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE	09 323-338 PR00320C 13.01 5.500e-09 187- 202
923	PRO0320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE PROTOCHLOROPHYLLIDE	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e-
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-64
		G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDB REDUCTASE PHOTOSYNT. Actinin-type actin-	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-64 BL00019C 14.66 7.453e-
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDB REDUCTASE PHOTOSYNT. Actinin-type actin-	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510e-11 61-84
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDB REDUCTASE PHOTOSYNT. Actinin-type actin-	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e-
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDB REDUCTASE PHOTOSYNT. Actinin-type actin-	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A
924	PD02181	G-PROTEIN BETA WD-40 REPEAT SIGNATURE  PROTOCHLOROPHYLLIDB REDUCTASE PHOTOSYNT. Actinin-type actin-	09 323-338 PR00320C 13.01 5.500e-09 187- 202 PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e-

SEQ ID N	NO: ACCESSION	DESCRIPTION	RESULTS*
ļ	NO.		
		proteins proteins:	273-284 BL00678 9.67
1			1.600e-10 314-325 BL00678 9.67 7.600e-10
		1	360-371 BL00678 9.67
929	BL00518	Zinc finger, C3HC4 type	8.579e-09 206-217
	DD00310	(RING finger), proteins.	BL00518 12.23 1.857e- 10 137-146
930	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
		epimerase family	24 134-165 BL01085B
	` <b> </b>	proteins.	10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-
			20 172-202 BL01085C
931	BL01085		21.81 2.038e-14 66-97
331	Proios	Ribulose-phosphate 3- epimerase family	BLC1085D 16.55 4.600e- 24 152-183 BL01085B
	Į.	proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
			20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE	PD00301A 10.24 6.400e-
936	DECOS	CALCIUM-BI.	09 160-171
930	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e- 12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
940	222222		10 5-49
340	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A)	PR00862D 16.17 4.086e- 09 63-84
		SIGNATURE	09 63-84
945	BL01230	RNA methyltransferase	BL01230B 11.62 2.373e-
948	BL00479	trmA family proteins. Phorbol esters /	09 407-420 BL00479B 12.57 7.429e-
	-2001/5	diacylglycerol binding	18 52-68 BL00479A
949	77.00650	domain proteins.	19.86 2.200e-13 26-49
343	BL00678	Trp-Asp (ND) repeat proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
955	PF00651	NAD INTERGENIC RE.	10 66-111
755	PF00851	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.250e- 12 47-60
956	PF00651 ·	BTB (also known as BR-	PF00651 15.00 3.250e-
957	BL00379	C/Ttk) domain proteins. CDP-alcohol	12 47-60
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	BE00379	phosphatidyltransferases	BL00379 24.64 1.610e- 15 111-148
		proteins.	13 111 110
959	BL01115	GTP-binding nuclear	BL01115A 10.22 1.884e-
960	BL01115	GTP-binding nuclear	10 31-75 BL01115A 10.22 3.438e-
		protein ran proteins.	14 110-154
962	BL00061	Short-chain	BL00061B 25.79 6.586e-
		dehydrogenases/reductase s family proteins.	13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-
966	PR00308	TOUR I DIMITED TO	11 210-225
200	FR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e- 09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 1.286e-
		PROTEIN.	12 104-124 DM01206B
	1	1	10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-
			10 73-93 DM01206B
		1	10.69 3.962e-09 108-
			128 DM01206B 10.69
969	PF01008	Initiation factor 2	5.671e-09 38-58 PF01008B 25.59 4.724e-
		subunit.	31 417-460 PF01008C
			12.25 5.333e-18 506-
			526 PF01008A 20.14 5.875e-15 369-390
	·	<del></del>	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		27.01.0220 10 10 7 6400
970	BL01277	Ribonuclease PH	BL01277C 10.18 7.648e- 10 112-143 BL01277A
		proteins.	17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain	BL01159 13.85 3.605e-
373	2001233	proteins.	12 130-145 BL01159
		•	13.85 4.122e-10 171-
			186
977	PF00791	Domain present in ZO-1	PF00791C 20.98 2.235e-
		and Unc5-like netrin	09 55-94
		receptors. Ribosomal protein L17	BL01167B 20.66 8.258e-
978	BL01167	proteins.	19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-
919	BLOOT	Diri dometri produtti	13 33-48 BL00478B
	1	į	14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PRO0312E 8.32 3.423e-
		i	36 169-199 PR00312I
			15.78 5.286e-35 332-
	İ		361 PR00312F 15.06 5.865e-35 199-229
		1	PRO0312H 13.31 8.313e-
	Ì	<b>\</b>	35 263-291 PR00312J
	1	1	13.73 5.688e-34 363-
	1		392 PR00312D 9.43
			2.636e-33 128-158
			PR00312C 15.14 8.839e-
			33 92-122 PR00312B 15.08 8.941e-33 62-92
	1		PR00312G 11.11 6.657e-
		1	32 230-258 PR00312A
		1	11.70 6.914e-27 35-59
981	PF00992	Troponin.	'PF00992A 16.67 8.816e-
302	1	<u> </u>	09 414-449
982	PR00299	ALPHA CRYSTALLIN	PR00299F 13.20 2.367e-
		SIGNATURE	09 127-149
983	BL01150	Respiratory-chain NADH	BL01150B 17.16 1.000e- 40 156-202 BL01150A
	ļ	dehydrogenase 20 Kd	14.10 8.200e-39 100-
		subunit proteins.	138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-
700	2200.22		14 4-49 BL00795C
			17.06 1.778e-11 1-46
		1	BL00795C 17.06 3.407e-
	1		10 14-59 BL00795C
			BL00795C 17.06 8.640e-
1			10 19-64 BL00795C
]		1	17.06 7.400e-09 11-56
1	ł		BL00795C 17.06 7.800e-
1	1		09 3-48
987	BL00939	Ribosomal protein Lle	BL00939F 17.27 5.393e-
		proteins.	09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
		OUT DOWNER OF OUR OFFICE	11 525-541 PR00452B 11.65 6.538e-
989	PR00452	SH3 DOMAIN SIGNATURE	11 497-513
994	BL00027	'Homeobox' domain	BL00027 26.43 2.500e-
994	BLOUDZI	proteins.	25 146-189
997	BL01304	ubiH/COQ6 monooxygenase	BL01304A 8.05 3.893e-
1	1 2201303	family proteins.	11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-
1			09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER	PR00926C 16.07 1.750e-
		PROTEIN SIGNATURE	24 73-94 PR00926D
1	1		10.53 3.250e-23 126-
1	1		145 PR00926F 17.75
			6.211e-23 217-240
1			PR00926E 11.70 6.625e-

SEQ ID NO:		DESCRIPTION	RESULTS*
	NO.		
			20 174-193 PR00926B 16.07 2.125e-18 24-39
			PR00926A 10.41 1.00Ce-
			15 11-25 PR00926F
	1		17.75 5.565e-09 120-
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e-
			40 88-143 BL00406C
	İ		6.75 1.000e-40 147-202
			BL00406D 12.58 3.700e-
			40 270-325 BL00406E 8.44 7.375e-38 327-377
			BL00406A 9.95 3.348e-
1006	DY COACC		29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e-
		•	40 88-143 BL00406C 6.75 1.000e-40 147-202
			BL00406E 8.44 1.000e-
			35 248-298 BL00406A
1007	PR00304	TATLIECE COMPLEY	9.95 3.348e-29 11-46
	1.00304	TAILLESS COMPLEX POLYPEPTIDE 1	PR00304D 11.04 8.714e- 22 384-407 PR00304C
		(CHAPERONE) SIGNATURE	8.69 4.667e-20 98-118
			PR00304B 11.60 7.577e-
	İ		19 68-87 PR00304A
			9.20 3.382e-16 46-63 PR00304E 7.79 6.870e-
			13 418-431
1009	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.929e-
		ZINC-FINGER METAL BINDING NU.	32 9-48
1011	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.929e-
•		ZINC-FINGER METAL-	32 68-107
1012	BL00518	BINDING NU.	
	2500318	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE	PD01168H 12.08 1.000e-
1018	PD00930	PROTEIN ALANYL.	11 174-194
1010	F500930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e- 32 261-302 PD00930A
			25.62 9.550e-22 157-
1022			183
1022	BL00175	Phosphoglycerate mutase	BL00175A 15.42 5.179e-
		family phosphohistidine proteins.	12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA	PR00305D 16.34 1.439e-
1026	BL00353	SIGNATURE	10 158-185
1026	PF00323	HMG1/2 proteins.	BL00353B 11.47 2.436e-
			18 238-288 BL00353C 14.83 8.844e-11 288-
			335
1028	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.310e-
1033	2F00580	enzymes proteins. UvrD/REP helicase.	33 43-91
		STEDINGE HELICASE.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID	PR00413E 15.78 3.429e-
	1	DEHALOGENASE/EPOXIDE	09 154-171
		HYDROLASE FAMILY SIGNATURE	
1037	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.657e-
		ZINC-FINGER METAL-	09 5-44
1038	2001200	BINDING NU.	
TA30	PD01796	PROTEIN TRANSMEMBRANE	PD01796 15.01 4.259e-
1039	BL00299	COBALT ZINC CADMIU. Ubiquitin domain	11 55-82 BL00299 28.84 9.036e-
		proteins.	09 17-69
1040	PR00970	ARGININE ADP-	PR00970A 17.73 6.143e-
	<u> </u>	RIBOSYLTRANSFERASE	20 56-78 PR00970D

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e- 16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e- 13 86-105 PR00970C 11.05 1.643e-11 115- 130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR0004BA 10.52 6.786e- 13 114-128 PR0004BA 10.52 1.000e-09 172- 186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B 12.25 1.857e-10 317- 331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e- 10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e- 28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e- 12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e- 11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e- 13 280-296
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e- 08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e- 12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

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		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-
1094	BI-00460	Glutathione peroxidases selenocysteine proteins.	10 23-57 BL00460A 28.67 3.204e- 18 57-92 BL00460B
			9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133-
			14.35 5.500e-09 133-
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	5.696e-13 154-167 PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	5.696e-13 147-160 BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	8.364e-09 131-145 PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-
1116	BL00355	HMG14 and HMG17 proteins.	10 63-85 BL00355 5.97 2.528e-25
1117	BL00355	HMG14 and HMG17	20-51 BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-
1129	BL00170	Cyclophilin-type peptidyl-prolyl cistrans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09
1133	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 6.211e-09
1136	BL00990	proteins proteins.  Clathrin adaptor complexes medium chain proteins.	29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear	BL01115A 10.22 6.364e-
		protein ran proteins.	13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.00Ce-
	1	binding region proteins.	19 451-482 BL00107B
		·	13.31 3.077e-12 519-
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
~~~~	1.00000	FACTOR IIB SIGNATURE	09 21-42
1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
	}	GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
			8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR	PD02894A 21.96 7.873e-
	}	PROTEIN SIGNAL BE.	28 81-127 PD02894B
	1		13.93 1.188e-27 178-
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
		proteins.	20 391-414 BL00623C
			10.86 4.240e-20 155~
			176
1161	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
11.60	PD01032	ENDONUCLEASE DNA	09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e- 09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
2200	IROUGET	MISTORE HS SIGNATORE	10 214-239 PR00624D
			11.94 1.961e-09 312-
	Į		337
1167	BL00226	Intermediate filaments	BL00226B 23.86 7.384e-
		proteins.	09 302-350
1177	BL01032	Protein phosphatase 2C	BL01032G 8.33 1.422e-
1178	PR00320	proteins. G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
2270	1100320	REPEAT SIGNATURE	10 205-220 PR00320C
	į		13.01 7.840e-10 205-
			220 PR00320B 12.19 .
			8.457e-10 35-50
			PR00320A 16.74 7.146e-
			09 35-50 PR00320B 12.19 9.100e-09 79-94
1180		ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
	PR00454		
	PR00454	EIS DOMAIN SIGNATURE	19 765-784
1181	PR00454 BL00291	Prion protein.	19 765-784 BL00291A 4.49 8.962e-
1181	BL00291		
1181		Prion protein.  Guanine-nucleotide	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e-
	BL00291	Prion protein.  Guanine-nucleotide dissociation stimulators	BL00291A 4.49 8.962e- 11 152-187
1184	BL00291 BL00720	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113
	BL00291	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e-
1184	BL00291 BL00720	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A
1184	BL00291 BL00720	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e-
1184	BL00291 BL00720 BL00215	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36
1184	BL00291 BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e-
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign.  Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93
1184	BL00291 BL00720 BL00215	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e-
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225-
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67
1184	BL00291  BL00720  BL00215  BL00983	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-
1184 1185 1187 1188	BL00291 BL00720 BL00215 BL00983 BL00878	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e- 09 270-289 PD02939B 10.10 2.723e- 12 203-220 PD02939C
1184 1185 1187 1188	BL00291 BL00720 BL00215 BL00983 BL00878	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.  PROTEIN GLUTATHIONE	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113  BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e- 09 270-289 PD02939B 10.10 2.723e- 12 203-220 PD02939C 20.01 1.000e-11 224-
1184 1185 1187 1188	BL00291 BL00720 BL00215 BL00983 BL00878	Prion protein.  Guanine-nucleotide dissociation stimulators CDC25 family sign. Mitochondrial energy transfer proteins.  Ly-6 / u-PAR domain proteins.  Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.  PROTEIN GLUTATHIONE	BL00291A 4.49 8.962e- 11 152-187 BL00720B 16.57 4.103e- 18 1089-1113 BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129 BL00983C 12.69 2.761e- 10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e- 09 270-289 PD02939B 10.10 2.723e- 12 203-220 PD02939C

SEQ ID NO:	ACCESSION	DESCRIPTION	
520 25 30.	NO.	DESCRIPTION	RESULTS*
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D
			10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-
			28 108-137 PR00345E 8.54 7.652e-28 185-210
			PR00345C 4.54 9.100e- 28 137-161 PR00345D
			10.97 1.964e-24 161- 185 PR00345A 13.46
1195	PF00995	Sec1 family.	5.645e-16 79-98 PF00995B 17.37 1.120e-
1196	BL00982	Bacterial-type phytoene	13 224-264
1197	BL01298	dehydrogenase proteins.	BL00982A 18.41 6.738e- 11 15-47
		Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959c- 09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase	BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	s family proteins. BETA-LACTAMASE CLASS A	PR00118F 16.42 9.386e-
1206	BL01183	SIGNATURE	09 213-229
1200	201103	<pre>ubiE/COQ5 methyltransferase family</pre>	BL01183B 21.31 1.429e- 37 184-229 BL01183D
		proteins.	27.71 8.535e-27 264- 307 BL01183A 13.25
			3.250e-23 51-73 BL01183C 10.77 5.295e-
1208	BL00979	G-protein coupled	09 246-258 .
		receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-
		SIGNATURE	14 227-241 PR00048A 10.52 4.316e-11 199- 213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e- 10 20-42 PR00450C
			12.22 3.506e-09 56-78
1216	BL00412		PR00450D 16.58 6.769e- 09 44-64
		Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e- 10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e- 11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066
			13.92 7.231e-15 406-
1			419 PD00066 13.92 2.286e-12 378-391
			PD00066 13.92 7.857e- 12 434-447 PD00066
	}		13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e-
1226	BL00412	Neuromodulin (GAP-43)	40 13-61 BL00412D 16.54 8.439e-
1227	BL00437	proteins.   Catalase proximal heme-	09 279-330 BL00437A 18.82 1.000e-
		ligand proteins.	40 49-101 BL00437B 16.28 1.000e-40 114-
	L		168 BL00437C 21.86

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			1.000e-40 190-239 BL00437D 25.72 1.000e- 40 248-301 BL00437E 23.95 1.000e-40 327-
			379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e- 10 5-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e- 09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.776e- 09 75-121
1237	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.818e- 21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e- 11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e- 10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e- 10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e- 36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e- 11 8-52
1256	BL00373	Phosphoribosylglycinamid e formyltransferase proteins.	BL00373C 10.35 3.348e- 12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e- 10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e- 10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e- 15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e- 12 16-27
1262	BL00462	Gamma- glutamyltranspeptidase proteins.	BL00462A 20.89 6.438e- 24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347
1263	BL00038	Myc-typc, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 9.455e- 11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e- 11 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e- 22 40-63 PR00449E 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming colicins proteins.	BL00276A 8.87 1.500e- 09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 9.769e- 09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

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		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e- 10 81-105
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82
1308	PRC0898	VASOPRESSIN V2 RECEPTOR SIGNATURE	2.658e-13 107-132 PR00898H 11.34 4.682e-
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	09 552-572 PD00301B 5.49 2.731e-
1310	BL00983	Ly-6 / u-PAR domain proteins.	09 390-401 BL00983C 12.69 9.654e- 13 73-89 BL00983B
1313	BL00194	Thioredoxin family proteins.	8.19 3.132e-09 12-22 BL00194 12.16 1.900e-
1314	BL00594	Aromatic amino acids permeases proteins.	11 15-28   BL00594A 16.75 8.969e-   10 53-97
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	7.03 4.789e-09 168-178 PR00497A 6.92 7.239e-
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	09 25-43 PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
	L	PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE	PR00860A 5.46 5.034e-
		METALLOTHIONEIN SIGNATURE	13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE	DM00099B 14.73 8.313e-
		TERMINAL	09 417-427
	ł	DIHYDROPTERIDINE.	
1345	BL00923	Aspartate and glutamate	BL00923B 11.41 5.935e-
	-	racemases proteins.	10 135-146
1348	PF00651	BTB (also known as BR-	PF00651 15.00 7.231e-
	<u> </u>	C/Ttk) domain proteins.	13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN	PR00193D 14.36 3.571e-
	1	SIGNATURE	32 416-445 PR00193C
		1	12.60 6.318e-31 179-
			207 PR00193B 11.69
	1	1	3.571e-24 133-159
			PR00193E 19.47 9.069e- 22 470-499 PR00193A
	1		15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE-	PR00447E 9.73 1.554e-
		ASSOCIATED MACROPHAGE	15 299-319 PR00447D
		PROTEIN SIGNATURE	13.54 3.408e-15 200-
			224 PR00447A 12.73
			6.357e-11 97-124
		1	PR00447G 6.69 9.877e-
	1		10 353-373
1353	BL00303	S-100/ICaBP type calcium	BL00303A 21.77 6.667e-
r		binding protein.	26 45-82 BL00303B
			26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 5.950e-
		dependent helicases	29 375-421 BL00039A
		proteins.	18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-
	ì		18 225-249 BL00039B
			19.19 3.182e-14 141-
			167
1357	PF00615	Regulator of G protein	PF00615B 16.25 2.216e-
		signalling domain	12 84-101 PF00615C
		proteins.	10.06 8.412e-12 162-
			176
1360	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.234e-
		ZINC-FINGER METAL-	29 10-49
1361	PR00925	BINDING NU.  NONHISTONE CHROMOSOMAL	DD000053 5 45 5 55
1301	FR00323	PROTEIN HMG17 FAMILY	PR00925A 5.47 5.091e- 18 14-29 PR00925B
_		SIGNATURE	3.73 5.143e-14 29-42
•			PR00925C 5.57 4.789e-
		· ·	12 53-64 PR00925D
			6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory	BL01272B 19.61 6.870e-
		protein family proteins.	30 136-171 BL01272C
	1	_	11.68 3.314e-25 249-
			274 BL01272A 6.49
	1		1.231e-18 99-117
1363	BL01272	Glucokinase regulatory	BL01272B 19.61 6.870e-
		protein family proteins.	30 113-148 BL01272C
			11.68 3.314e-25 226-
	]	1	251 BL01272A 6.49
1364	DM00179	w KINASE ALPHA ADHESION	1.231e-18 76-94 DM00179 13.97 5.304e-
	211001/9	T-CELL.	09 167-177
1368	PR00169	POTASSIUM CHANNEL	PR00169A 16.77 1.592e-
-		SIGNATURE	09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-
<u> </u>			

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	· NO.		
1371	BL00242	Integrins alpha chain	10 1-19
ļ	5250242	proteins.	BL00242B 8.13 8.615e-
1372	PR00625	DNAJ PROTEIN FAMILY	PR00625B 13.48 7.353e-
	l l	SIGNATURE	19 46-67 PR00625A
1373	7.00		12.84 1.391e-16 14-34
13/3	BL00434	HSF-type DNA-binding	BL00434C 23.85 3.778e-
1374	PR00962	domain proteins.  LETHAL (2) GIANT LARVAE	09 90-130
	11100502	PROTEIN SIGNATURE	PR00952C 8.00 6.337e- 09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-	PD02475A 23.18 8.552e-
		ASSOCIATE.	10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.571e-
•		ZINC-FINGER METAL-	32 24-63
1380	BL00194	BINDING NU. Thioredoxin family	
		proteins.	BL00194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 1.458e-
		ENDOSOMAL III.	15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1384	BL00678	proteins proteins.	243-254
	5103676	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10
1385	BL00303	S-100/ICaBP type calcium	271-282 BL00303B 26.15 6.203e-
		binding protein.	10 95-132
1386	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
1387	- DY 00510	repeat proteins.	09 1574-1628
1301	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
1389	PD01066	(RING finger), proteins.  PROTEIN ZINC FINGER	11 52-61
		ZINC-PINGER METAL-	PD01066 19.43 3.600e-
1300		BINDING NU.	30 20 25
1390	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.512e-
		ZINC-FINGER METAL- BINDING NU.	31 32-71
1392	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 9.723e-
		PROTEIN SIGNATURE	10 127-137
1393	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.625e-
		SIGNATURE	25 88-110 PR00380D
	-		9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-
	Ì		16 208-226 PR00380C
			13:18 6.538e-16 243-
1394	PD00066	DECOMPANY OF THE PARTY OF THE P	262
	1200000	PROTEIN ZINC-FINGER METAL-BINDI	PD00066 13.92 3.400e- 14 462-475 PD00066
			13.92 8.800e-14 348-
			361 PD00066 13.92
			9.571e-12 405-418 ·
			PD00066 13.92 6.087e-
	J	ł	11 490-503 PD00066 13.92 8.043e-11 320-
			333 8.043e-11 320-
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786c-
	1	ZINC-FINGER METAL-	32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10 60 B 022
		PROTEIN.	DM01206B 10.69 7.038e- 09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN	PD00930A 25.62 7.324e-
1407	BL00030	ACTIVATION.	15 363-389
•	1 2200030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e-
1408	PR00019	LEUCINE-RICH REPEAT	10 457-476 PR00019A 11.19 9.550e-
		SIGNATURE	11 179-193 PRO0019A
			11.19 8.826e-10 228-
		İ	242 PR00019B 11.36
	1		1.360e-09 199-213
		<u> </u>	PR00019B 11.36 4.960e-

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
002 10 101	NO.	255512112017	1255212
			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-
		1	12 182-202 PR00510B
			12.96 8.767e-12 210-
			230 PR00510F 9.88
	1	İ	8.172e-10 58-75 PR00510D 9.21 2.367e-
			09 251-267
1410	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.696e-
2220	1 2200.0	NUCLEAR ANKYR.	09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.00Ce-
1		proteins.	40 57-103 BL00358C
	İ	1	13.75 6.087e-14 122-
			136 BL00358D 14.26
		]	5.500e-13 143-158
			BL00358A 13.06 1.931e-
			11 33-44
1414	BL00282	Kazal serine protease	BL00282 16.88 7.338e-
		inhibitors family proteins.	10 511-534
1415	BL00023	Type II fibronectin	BL00023 24.31 4.300e-
-470	0000023	collagen-binding domain	29 40-77
		proteins.	1 10 //
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
		SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
		YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
ļ		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B
·			15.02 7.049e-30 400- 447 PD01941E 15.92
ł			2.475e-20 817-864
			PD01941C 19.96 3.118e-
į.			19 488-543 PD01941D
1			27.18 9.614e-18 641-
İ	ł		690 PD01941F 28.52
L			5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
1.00		27 2772 (2022)	12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e- 11 1009-1028
1424	BL50002	Src homology 3 (SH3)	BL50002A 14.19 8.200e-
		domain proteins profile.	14 367-386 BL50002A
j .	1	process.	14.19 9.250e-12 298-
	1		317 BL50002A 14.19
l	1		4.462e-11 208-227
l	1		BL50002B 15.18 1.000e-
			09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-
1436	DDOGGO	DUD 6	12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-
1427	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.114e-
1 ****	1.00403	PROTEIN SIGNATURE	16 281-299 PR00405A
1	1		17.71 4.306e-14 262-
1			282
1428	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 5.219e-
1	1	dependent helicases	34 147-193
		proteins.	
1429	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.920e-
		REPEAT SIGNATURE	10 577-592
1430	PR00378	INOSITOL PHOSPHATASE	PR00378D 16.86 7.563e-
1		SIGNATURE	12 295-314 PR00378B
1	l		13.80 8.650e-10 166-
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-
	- FR00320	GRAVES DISEASE CARRIER	1 FAUUSZOD 13.33 3.7698-

SEQ ID NO:	ACCESSION	DESCRIPTION	T DOLLY MO.
	NO.	DESCRIPTION	RESULTS*
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e-
			15 14-50 BL01113C
1434	PR00319	BETA G-PROTEIN	13.18 7.000e-12 82-102
1	1200313	(TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e-
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
		region RNP-1 proteins.	12 84-103
1438	BL00290	Immunoglobulins and	BL00290B 13.17 2.500e-
		major histocompatibility	
		complex proteins.	20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
			09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
144			09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-
1445	PD01841	PHOSPHORYLASE KINASE	08 114-138
	1 202032	ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 73-123 PD01841B
			14.35 1.000e-40 144-
}			185 PD01841D 17.87
			1.000e-40 206-258
		ĺ	PD01841F 13.36 1.000e- 40 296-345 PD01841G
			24.26 1.000e-40 349-
			403 PD01841I 23.00
			1.000e-40 494-536
			PD01841J 14.94 1.000e-
			40 895-932 PD01841L 18.42 1.000e-40 1083-
			1125 PD01841E 18.60
			9.719e-38 258-296
	ľ		PD01841K 14.81 1.000e-
		1	35 1041-1071 PD01841H
			21.30 3.189e-31 435- 472 PD01841C 13.78
			1.000e-25 185-206
			PD01841M 10.82 1.250e-
1446	PF00816		20 1175-1194
77.40	1100916	H-NS histone family.	PF00816B 13.84 8.875e- 09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.080e-
		SIGNATURE	09 402-416
1448	DM00315	072 RIBONUCLEASE	DM00315D 18.40 7.393e-
1451	BL00030	INHIBITOR.	09 23-67
1431	PT00020	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e-
1454	DM01688	2 POLY-IG RECEPTOR	10 94-104 DM01688D 13.44 7.146e-
			09 382-405
1455	PF00777	Sialyltransferase	PF00777C 18.60 2.929e-
1457	BL00927	family.	22 4-59
~2.57	P70027	Trehalase proteins.	BL00927C 10.83 8.085e-
1460	BL00545	Aldose 1-epimerase	09 42-53 BL00545C 11.28 7.353e-
	-	proteins.	17 169-182 BL00545A
			10.20 2.071e-15 73-89
			BL00545B 13.10 3.942e-
1466	PR00097	ANTHDANTI AMD CONTROL OF	09 140-153
,	- 100007	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e- 09 233-245
1472	BL01129	Hypothetical	BL01129E 13.25 5.250e-
		yabO/yceC/sfhB family	22 170-195 BL01129C
1450		proteins.	25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase	BL007901 20.01 2.821e-
1475	PF00686	class V proteins. Starch binding domain	09 2114-2145
-		proteins.	PF00686A 13.45 9.100e- 09 267-277
		TEcermo.	U2 401-411

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ ID NO.	NO.		
1477	PF00566	Probable rabGAP domain	PF00566A 12.64 7.333e-
1478	BL00030	proteins.  Eukaryotic RNA-binding	BL00030B 7.03 9.400e-
2.7.0	220000	region RNP-1 proteins.	10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10
1480	BL00290	Immunoglobulins and	292-305 BL00290B 13.17 2.385e-
1400	5200250	major histocompatibility	15 69-87 BL00290A
		complex proteins.	20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1-	PF00780I 14.69 4.825e-
		like kinases, mouse	09 107-137
1483	BL01160	citron and yeast ROM. Kinesin light chain	BL01160B 19.54 1.153e-
1403	BEOTIO	repeat proteins.	09 108-162
1485	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.909e-
		ZINC-FINGER METAL- BINDING NU.	25 17-56
1486	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
		binding region proteins.	09 34-50
1488	Вь00039	DEAD-box subfamily ATP-	BL00039D 21.67 9.586e-
		dependent helicases proteins.	10 116-162
1490	BL00166	Enoyl-CoA	BL00166D 22.87 2.607e-
		hydratase/isomerase	24 190-226 BL00166C
		proteins.	18.93 5.500e-14 140- 167 BL00166B 16.92
	İ		9.357e-11 93-115
1491	BL00452	Guanylate cyclases	BL00452D 28.59 3.700e- 31 63-106 BL00452E
	}	proteins.	11.92 3.045e-13 115-
	ļ		131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP-	BL00107B 13.31 1.000e-
		binding region proteins.	11 384-400 BL00107A
	<b>!</b>		18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-
			10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1503	BL00027	'Homeobox' domain	BL00027 26.43 4.789e-
		proteins.	24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e- 24 448-475 BL01177C
		process.	17.39 5.333e-19 402-
		ł	421 BL01177B 13.61
			7.840e-16 155-171 BL01177D 17.50 1.900e-
			15 427-445
1506	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 5.500e-
		terminal hydrolases family 2 proteins.	14 311-336 BL00972A 11.93 7.429e-14 48-66
	1	,	BL00972E 20.72 8.759e-
1510	DT 00500		10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e- 22 76-106 BL00523D
[	1		9.89 1.563e-11 40-52
		1	BL00523F 10.85 4.162e-
	1		09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin	BL00914 24.91 7.045e-
		family proteins.	14 168-218
1518	BT00000	Aminotransferases class- III pyridoxal-phosphate	BL00600A 17.98 6.143e- 19 98-122 BL00600E
		attachment si.	16.43 1.771e-17 302-

CPO TO NO	1 NOODOOTOV	I DESCRIPTION	L DECIM TO
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL006C0G 12.43
			9.625e-17 377-396
			BL00600B 19.60 5.091e-
			16.18 6.040e-12 190-
			206 BL006COF 8.77
		1	1.000e-11 343-356
	i	i	BL00600D 8.71 1.000e-
			10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 9.600e-
		ACTIVATION.	18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e-
		REPEAT SIGNATURE	11 192-207 PR00320B 12.19 8.839e-11 272-
	i	·	287 PR00320B 12.19
		1	9.743e-10 106-121
	l	i	PR00320A 16.74 1.878e-
		ł	09 192-207 PR00320A
		ļ•	16.74 2.317e-09 106-
			121 PRO0320A 16.74
	]		8.683e-09 272-287 PR00320C 13.01 8.800e-
	1	1	09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 4.508e-
	i	ENDOSOMAL III.	15 171-184
1539	PF00781	Diacylglycerol kinase	PF00781D 11.11 7.593e-
	ĺ	catalytic domain	10 103-127
1540		proteins (presumed).	
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e-
		PROTEIN SIGNATURE	12.93 5.846e-29 172-
			195 PR00965F 5.98
			1.123e-28 209-231
	İ	•	PR00965C 15.04 1.000e-
			27 131-151 PR00965D
			5.84 1.000e-27 150-170
			PR00965G 8.52 2.440e- 27 258-279 PR00965B
			4.80 8.650e-26 88-109
			PR00965A 12.52 1.000e-
	ł		25 35-55 PR009651
<u> </u>			3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding	BL01013D 26.81 9.719e-
1543	DD02600	protein family proteins.	17 163-207
1343	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A
		Daniel Dan.	8.91 2.286e-34 219-248
			PD02699B 18.28 6.143e-
	·		21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.857e-
		SIGNATURE	10 182-197 PR00049D
1542	77.00053	77	0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein	BL00951C 19.35 1.000e-
		retaining receptor proteins.	40 93-142 BL00951D 13.94 8.714e-40 142-
			177 BL00951A 15.10
	ľ		1.000e-38 2-38 .
			BL00951B 14.23 6.250e-
			33 38-69
1548	BL00536	Ubiquitin-activating	BL00536F 13.65 8.920e-
		enzyme proteins.	30 279-318 BL00536D
			22.91 5.737e-24 21-65
			BL00536E 16.94 4.696e-
1549	PR00139	ASPARAGINASE/GLUTAMINASE	PR00139C 11.72 9.679e-
		FAMILY SIGNATURE	09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 5.119e-
		SIGNATURE	09 58-73

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
DEQ ID NO.	NO.		[
1556	BL00061	Short-chain dehydrogenases/reductase	BL00061B 25.79 6.276e- 13 67-105
	1	s family proteins.	
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1562	BL00522	DNA polymerase family X	BL00522C 11.90 6.600e-
2502		proteins.	18 412-436 BL00522B 27.30 1.738e-16 364-
			410 BL00522A 25.52 6.000e-16 279-326
			BL00522E 19.63 6.123e-
			14 502-532 BL00522F
i			14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR-	PF00651 15.00 1.947e-
	L	C/Ttk) domain proteins.	11 46-59
1564	BL00299	Ubiquitin domain	BL00299 28.84 2.823e-
1556	DT 01033	proteins.	10 324-376 BL01013D 26.81 8.594e-
1566	BL01013	Oxysterol-binding protein family proteins.	17 184-228 BL01013C
		process raminy process.	9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 3.400e-10
		proteins proteins.	378-389 BL00678 9.67
	1		5.800e-10 418-429 BL00678 9.67 8.800e-10
	İ		295-306
1570	BL00479	Phorbol esters /	BL00479B 12.57 5.235e-
		diacylglycerol binding	17 297-313 BL00479Å
ļ	İ	domain proteins.	19.86 6.625e-15 271-
		1	294 BL00479A 19.86
		<u> </u>	2.667e-14 147-170 BL00479B 12.57 6.294e-
			12 173-189
1576	PR00665	OXYTOCIN RECEPTOR	PR00665G 12.36 4.673e-
		SIGNATURE	24 364-384 PR00665D
			9.93 1.200e-22 138-155
			PR00665F 11.73 4.000e- 22 337-354 PR00665C
			5.89 1.000e-20 65-80
	}		PR00665B 5.29 4.337e-
			19 24-39 PR00665E
ľ			5.60 2.929e-15 246-260
}	1	İ	PR00665A 5.99 5.622e-
1577	DM00099	4 kw A55R REDUCTASE	DM00099B 14.73 9.308e-
1 ***	DE100039	TERMINAL	10 127-137
		DIHYDROPTERIDINE.	
1579	BL00524	Somatomedin B domain	BL00524A 9.65 6.776e-
	1 225555	proteins.	14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR	PD02894B 13.93 6.959e- 16 182-215 PD02894A
l	•	PROTEIN SIGNAL BE.	21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain	BL00411C 15.04 5.292e-
1		proteins.	12 32-54 BL00411H
	1		15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB	PR00604A 11.13 2.440e-
		CYTOCHROME C SIGNATURE	09 79-87
1584	PF00651	BTB (also known as BR-	PF00651 15.00 1.000e-
1505	DMOIFES	C/Ttk) domain proteins.	10 225-238 DM01551C 14.62 9.455e-
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE	DM01354S 11.61 7.750e-
L		II ORF2.	09 474-495

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
L	NO.	DESCRIPTION	RESULIS-
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e-
ľ		1	33 180-210 PR00072A
			12.75 6.040e-25 120- 145 PR00072C 11.42
			2.286e-24 216-239
		i	PR00072D 10.77 3.400e-
			22 276-295 PR00072E
			10.54 1.360e-19 301~
			318 PR00072G 10.45
			5.304e-19 433-450
1			PR00072F 8.87 5.935e-
1589	BL00191	Cytochrome b5 family,	BL00191H 15.64 1.537e-
		heme-binding domain	22 51-113 BL00191K
		proteins.	17.38 9.027e-12 398-
			442
1590	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.716e-
		ENDOSOMAL III.	13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1	DM00517B 10.96 6.625e-
ĺ		CHROMOSOME.	16 1175-1193 DM00517A
			8.21 1.000e-11 1015-
			1026
1592	BL00037	Myb DNA-binding domain	BL00037B 15.92 3.250e-
	ì	proteins repeat proteins proteins.	27 116-142 BL00037A
		proceins.	16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-
	İ		12 31-55 BL00037B
	·		15.92 3.526e-11 64-90
			BL00037C 16.86 9.654e-
1595	BL00028	Rian films College	10 146-164
1333	BB00028 .	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-
	<u> </u>		11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III	PR00014D 12.04 5.500e-
1600	BL00518	REPEAT SIGNATURE	09 980-995
1800	PD00219	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.402e-
		proteins.	10 136-187
1605	PF00651	BTB (also known as BR-	PF00651 15.00 3.571e-
1.600		C/Ttk) domain proteins.	10 44-57
1607	BL00252	Interferon alpha, beta	BL00252A 18.49 6.657e-
		and delta family proteins.	23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-
<u></u>		<u>.</u> .	08 61-94
1611	BL00904	Protein	BL00904C 8.98 7.353e-
	I	prenyltransferases alpha	10 91-125 BL00904D
		subunit repeat proteins	1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e-
-		- domain processis.	09 365-391
1613	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 6.051e-
	1	proteins.	09 932-983 BL00412D
	1	l	16.54 7.153e-09 933-
1614	BL00559	Parks	984
2023	1 3500339	Eukaryotic molybdopterin oxidoreductases	BL00559I 13.63 3.531e-
		proteins.	25 54-83 BL00559K 13.17 2.957e-18 197-
		1.	224 BL00559J 19.63
	]		6.870e-16 124-176
			BL00559L 13.60 9.000e-
1615	PD01422	MID X VOICE A SH	16 266-284
1013	PD01427	TRANSFERASE	PD01427B 22.45 3.025e-
		METHYLTRANSFERASE BI.	22 500-541 PD01427A 19.94 8.773e-18 439-
	·	_t	U. //JG-10 433-

550 TO NO.	NOCECCION	DESCRIPTION	RESULTS*
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	
			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
	ļ	polymerase II	09 152-201 BL00115Z 3.12 9.603e-09 145-194
	}	heptapeptide repeat proteins.	3.12 9.603e-09 145-194
	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
1617	BE00202	binding protein.	32 51-88 BL00303A
		, , , , , , , , , , , , , , , , , , ,	21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
	j		09 137-147
1619	PD01888	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C 21.56 7.000e-30 125-
		}	155 PD01888A 12.84
		į	8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
1022		TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
		1	1.58 4.580e-09 697-709
ł	1		PR00239E 1.58 4.580e- 09 702-714 PR00239E
1			1.58 5.193e-09 703-715
	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
1622	PROUBBU	METALLOTHIONEIN	18 27-41 PRO0860C
		SIGNATURE	9.61 1.474e-14 41-51
]			PR00860A 5.46 1.720e-
			14 5-18
1624	PR00734	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
	į	UNCOUPLING PROTEIN	11 77-95
- 506	BL00325	SIGNATURE Actin-depolymerizing	BL00325B 21.66 1.000e-
1626	BL00325	proteins.	40 93-139 BL00325A
		1	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
1		proteins.	40 82-130 3L00064C
ł	j		17.28 1.000e-40 137- 182 BL00064E 27.20
1	1	ļ	1.000e-40 223-275
1			BL00064F 25.14 7.882e-
1	1	}	36 286-331 BL00064A
1	ļ	· ·	21.16 1.000e-33 22-60
			BL00064D 14.19 6.500e-
	7770000	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
1632	PR00063	SIGNATURE	11 59-84 PRO0063A
		SIGNATURE	11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
			3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e- 10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
1637	BT00385	dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
		methyltransferase family	12 132-177
		proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
	1	SURFACE PROTEIN ANCHOR	10 128-149
<u> </u>	DD00330	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
1641	PR00320	REPEAT SIGNATURE	11 364-379 PRO0320A
1	1		16.74 7.828e-11 364-
1			379 PR00320C 13.01
1	1		2.800e-10 279-294
	1		PR00320C 13.01 2.800e-
i	1		10 364-379 PR00320B 12.19 5.114e-10 279-
		1	294 PRO0320A 16.74
	1	1	1.659e-09 279-294
1	_ <del> </del>		

SEQ ID NO:	ACCESSION	DESCRIPTION	T near and
024 12 110.	NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e- 09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e-
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e-
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	17 56-89   PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e-
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

PR00747   GLYCOSYL HYDROLASE   PR00747H 12.76 8.636e-	SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2INC-FINGER METAL-BINDING NU.   38 7-46	1664			
PRO0678   PI3 KINASE P85   PR00678H 9.13 3.100e- 10 13 37   PR00678   PI3 KINASE P85   PR00678H 9.13 3.100e- 10 1146-1169   PR00678   PI3 KINASE P85   PR00678H 9.13 3.100e- 10 1146-1169   PR00678   PR00678H 9.13 3.100e- 10 1146-1169   PR00678   PR00678H 9.13 3.100e- 10 1146-1169   PR00678   PR00747   PR00678H 9.13 3.100e- 10 1146-1169   PR00678   PR00747   PR00678H 9.13 3.100e- 10 127-49   PR00747   PR00747   PR00747   PR007478   PR007478   PR007479   PR007479   PR007479   PR007479   PR007479   PR007474   PR007478   PR007476   PR007476   PR007476   PR007476   PR007478   PR007476   PR007478   PR0074568   PR0	1667	PD01066	ZINC-FINGER METAL- BINDING NU.	
REGULATORY SUBUNIT   10 1146-1169	1669	BL01153	• -	17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e- 10 13-37
1673   PR00326   GTP1/OBG GTP-BINDING   PR0326A 8.75 8.329e-   1674   PR00049   WILM'S TUMOUR PROTEIN   PR00049D 0.00 7.580e-   SIGNATURE   1343-358 PR00049D 0.00 1.286e-10 342-357     1676   PR00747   GLYCOSYL HYDROLASE   PR00747H 12.76 8.636e-   FAMILY 47 SIGNATURE   PR00747H 12.06 6.7.500e-18 112-131     PR00747	1671	PR00678	REGULATORY SUBUNIT	10 1146-1169
PROTEIN FAMILY SIGNATURE   09 686-707	1672	BL00598	Chromo domain proteins.	
SIGNATURE	1673	PR00326	t ·	09 686-707
FAMILY 47 SIGNATURE  19 427-448 PR00747G 14.50 2.2866-18 368- 393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747D 15.23 8.759e-17 163- 183 PR00747B 7.65 5.355e- 13 75-90 PR00747F 13.56 8.714e-10 311- 328  1677  PR00747  GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE  19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 13.56 8.714e-10 311- 328  1680  BL00678  Trp-Asp (WD) repeat Proteins proteins.  1681  BL00678  Trp-Asp (WD) repeat Proteins proteins.  1681  BL00678  Trp-Asp (WD) repeat Proteins proteins.  1684-17 BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331  1681  BL00678  Trp-Asp (WD) repeat Proteins proteins.  1685  PR00326  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE 13 389-410 1685  PR00456  RIBOSOMAL PROTEIN P2 RP00456  RIBOSOMAL PROTEIN P2 RP00456 RIBOSOMAL PR0TEIN P2 RP00456 RIBOSOMAL PR0TEIN P2 RP00456 RIBOSOMAL PR0TEIN P	1674	PR00049	•	
FAMILY 47 SIGNATURE  19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210  1680  BL00678  Trp-Asp (WD) repeat Proteins proteins.  406-417 BL00678 9.67 6.684e-09 320-331  1681  BL00678  Trp-Asp (WD) repeat Proteins proteins.  329-340 BL00678 9.67 6.684e-09 243-254  1683  PR00326  GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e- PROTEIN FAMILY SIGNATURE 13 389-410  1685  PR00646  RDC1 ORPHAN RECEPTOR SIGNATURE 09 755-771  1690  BL01160  Kinesin light chain repeat proteins. 09 75-129  1691  PR00456  RIBOSOMAL PROTEIN F2 PR00456E 3.06 7.281e- 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435  1692  PR00456  RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- 10 420-435  1692  PR00456  RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- 10 420-435 PR00456E 3.06 7.281e- 10 420-435	1676	PR00747		19 427-448 PR00747G 14.50 2.286e-18 368- 393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747D 15.23 8.759e-17 163- 183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e- 13 75-90 PR00747F 13.56 8.714e-10 311- 328
Proteins proteins.   406-417 BL00678 9.67   6.684e-09 320-331	1677	PR00747		19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-
Proteins proteins.   329-340 BL00678 9.67   6.684e-09 243-254   1683   PR00326   GTP1/OBG GTP-BINDING   PR00326A 8.75 1.346e-PROTEIN FAMILY SIGNATURE   13 389-410   1685   PR00646   RDC1 ORPHAN RECEPTOR   PR00646H 6.32 4.188e-SIGNATURE   09 755-771   1690   BL01160   Kinesin light chain   BL01160B 19.54 6.644e-repeat proteins.   09 75-129   1691   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-SIGNATURE   10 418-433   PR00456E 3.06 7.281e-10 420-435   1692   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-10 420-435   1692   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-10 420-435   1692   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-10 420-435   1692   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-10 420-435   PR00456E 3.06 7.281e-10 420	1680	BL00678		406-417 BL00678 9.67
PROTEIN FAMILY SIGNATURE 13 389-410  1685 PR00646 RDC1 ORPHAN RECEPTOR 09 755-771  1690 BL01160 Kine light chain 109 75-129  1691 PR00456 RIBOSOMAL PROTEIN F2 PR00456E 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 8.125e-10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 487-502 PR00456E	1681	BL00678		1
SIGNATURE   09 755-771	1683	PR00326	•	13 389-410
repeat proteins. 09 75-129  1691 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 487-502 PR00456E	1685	PR00646	SIGNATURE	09 755-771
SIGNATURE 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-SIGNATURE 10 487-502 PR00456E	1690	BL01160	1	BL01160B 19.54 6.644e- 09 75-129
1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 487-502 PR00456E	1691	PR00456	•	10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-
7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504	1692	PR00456		PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-
	1693	BL00674	· -	BL00674C 22.60 8.043e-

SEQ ID NO:	ACCESSION	DESCRIPTION	I proty mo-
02Q 13 NO.	NO.	DESCRIPTION	RESULTS*
Į.	' -		4.46 4.000e-23 241-263
			BL00674D 23.41 8.560e-
		į.	18 338-385 BL00674E
			15.24 1.720e-15 414-
1697	PR00409	PHTHALATE DIOXYGENASE	PR00409F 12.70 4.388e-
1 -02.	1200105	REDUCTASE FAMILY	10 427-447
		SIGNATURE	10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY	PR00466C 10.17 3.443e-
		CHAIN SIGNATURE	13 187-208 PR00466B
1			5.03 5.500e-11 162-186
1			PR00466F 9.16 6.159e-
			09 498-517
1699	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 9.217e-
ł		domain proteins.	12 283-300 BL00028
ŀ			16.07 3.769e-11 255-
1			272 BL00028 16.07
1			5.154e-11 171-188
			BL00028 16.07 5.500e-
ļ			11 227-244 BL00028 16.07 1.600e-10 199-
	1		216
1700	BL01019	ADP-ribosylation factors	BL01019A 13.20 3.348e-
		family proteins.	15 62-102 BL01019B
			19.49 4.000e-15 107-
			162
1703	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.484e-
	}	ZINC-FINGER METAL-	12 200-239
1700		BINDING NU.	
1707	PR00109	TYROSINE KINASE	PR00109B 12.27 4.558e-
		CATALYTIC DOMAIN SIGNATURE	14 134-153
1710	PR00019	LEUCINE-RICH REPEAT	77000707 11 10 0 525
	INCOURT	SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B
1		Dadwii OKB	11.36 4.600e-09 113-
			127 PR00019B 11.36
		ļ	7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain	BL01159 13.85 6.523e-
		proteins.	11 232-247 BL01159
			13.85 5.408e-10 613-
1712	77700000		628
1,17	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e-
1713	PF00642	Zinc finger C-x8-C-x5-C-	10 187-203
	1100042	x3-H type (and similar).	PF00642 11.59 9.550e-
1714	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.550e-
1	]	x3-H type (and similar).	11 230-241
1715	BL01115 .	GTP-binding nuclear	BL01115A 10.22 7.129e-
	1	protein ran proteins.	09 7-51
1718	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e-
ł	1		10 136-183 BL00353B
455			11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.408e-
1721	DI DOGGO	proteins.	09 432-483
-/61	BL00038	Myc-type, 'helix-loop-	BL00038B 16.97 8.448e-
		helix' dimerization domain proteins.	12 79-100 BL00038A
1723	PD00567	PROTBIN RNA-BINDING RNA	13.61 4.000e-11 52-68
	1 - 200231	REPEAT HYD.	PD00567C 9.17 8.500e- 09 418-428
1724	BL01279	Protein-L-	BL01279A 24.27 5.663c-
= =		isoaspartate(D-	12 233-281
		aspartate) 0-	TO 500 COT
		methyltransferase signa.	
1728	BL00018	EF-hand calcium-binding	BL00018 7.41 2.059e-11
	}	domain proteins.	73-86 BL00018 7.41
		·	4.176e-11 157-170
1730	BL00594	Aromatic amino acids	BL00594A 16.75 1.089e-
	L	permeases proteins.	09 17-61

ACCESSION NO.	DESCRIPTION	RESULTS*
BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e~ 10 296-350
BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e- 22 246-279 PF00850D 14.76 6.850e-20 177- 201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-
BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook)	14 281-323 BL00354C 6.61 5.932e- 09 292-307
DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e- 10 492-502
PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e- 15 136-160
PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e- 11 45-57 PR00081E 17.54 3.935e-10 150- 168
BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e- 14 65-91 BL00439G 13.40 2.895e-12 3-14
PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e- 11 4-20
PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.750e- 35 10-49
DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e- 09 224-278
PD02929 PR00326	1	
	PRECURSOR I. GTP1/OBG GTP-BINDING	09 224-278 PR00326A 8.75 5.950e-
PR00326	PRECURSOR I. GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e-
	BL01160  BL01160  PF00850  BL00354  DM00179  PR00449  PR00449  BL00720  PR00081  BL00439  PR00819  PD00066  BL01013  BL00790	BL01160 Kinesin light chain repeat proteins.  BL01160 Kinesin light chain repeat proteins.  PF00850 Histone deacetylase family.  BL00354 HMG-I and HMG-Y DNA-binding domain proteins (Ahook).  DM00179 W KINASE ALPHA ADHESION T-CELL.  PR00449 TRANSFORMING PROTEIN P21 RAS SIGNATURE  BL00720 Guanine-nucleotide dissociation stimulators CDC25 family sign.  PR00081 GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE  BL00439 Acyltransferases ChoActase / COT / CPT family proteins.  PR00819 CBXX/CFQX SUPERFAMILY SIGNATURE  PD00066 PROTEIN ZINC-FINGER METAL-BINDI.  BL00790 Receptor tyrosine kinase class V proteins.  PD01066 PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESULTS
1778	BL00984	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

<sup>\*</sup> results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.I(%CRJ0!!.DOC)

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	ļ., <u></u>			SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH C	IMP dehydrogenase / GMP	1.6e-119	410.5
	-	reductase C terminus	1.00 113	110.5
21	IMPDH C	IMP dehydrogenase / GMP	4.3e-102	352.6
22	pkinase	reductase C terminus Eukaryotic protein kinase	2.4e-79	277.0
	1	domain		
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2 3	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2 3	Ribosomal protein L23	1e-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase	2.1e-65	230.7
54	myb_DNA- binding	Myb-like DNA-binding domain	0.096	15.2
55	voltage CLC	Voltage gated chloride channels	3 20 106	631 0
56	sugar tr	Sugar (and other) transporter	3.3e-186	631.9
57	TBC	TBC domain	0.00015	-64.3
58	ank	Ank repeat	2.2e-37	137.6
59	ank	Ank repeat	5.9e-25	96.3
67	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	7.9e-49	96.3 175.6
69	n		<u></u>	1
68	C2	C2 domain	7.9e-54	192.2
69	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72 73	ig	Immunoglobulin domain	8.2e-28	94.7
	pkinase	Eukaryotic protein kinase	8e-69	242.1

	D PFAM NAME	DESCRIPTION	T =	Lanca
NO:			p-value	PFAM SCORE
		domain	<del></del>	- CONE
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf- C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92 93	laminin_G	Laminin G domain	6.1e-27	98.5
95	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
96	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97 98	adh_short	short chain dehydrogenase	2e-61	217.5
101	kinesin	Kinesin motor domain	2.2e-86	300.4
102	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
106	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
105	ras	Ras family	8.3e-24	92.5
108	FYVE	FYVE zinc finger	5.4e-27	100.7
109	Cyt_reductas	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
113	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
116	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
117	PH	PH domain	3.1e-11	45.2
118	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
120	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF	WD domain, G-beta repeat	2.4e-14	61.1
124	2	eIF4-gamma/eIF5/eIF2-epsilon	le-32	122.2
127	ig	Immunoglobulin domain	6.5e-08	30.6
128	mito_carr PP2C	Mitochondrial carrier proteins	3e-16	58.6
129	ATPIG1 PLM M	Protein phosphatase 2C	2.2e-71	250.6
130	AT8 pfkB	ATPIGI/PLM/MAT8 family	3.1e-20	80.6
133		pfkB family carbohydrate kinase	4.5e-42	137.1
133 134	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	ACBP rrm	Acyl CoA binding protein RNA recognition motif.	4.6e-22 1.2e-31	86.7 118.5
_	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134 135	ACBP rrm IQ ATP1G1_PLM_M	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIG1/PLM/MAT8 family Wiskott Aldrich syndrome	4.6e-22 1.2e-31 2.6e-08	86.7 118.5 41.0
134 135 136	ACBP FITT IQ ATPIG1_PLM_M AT8 WH2	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2	4.6e-22 1.2e-31 2.6e-08 9.3e-22	86.7 118.5 41.0 85.7
134 135 136	ACBP rrm IQ ATPIG1_PLM_M AT8	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIG1/PLM/MAT8 family Wiskott Aldrich syndrome	4.6e-22 1.2e-31 2.6e-08 9.3e-22	86.7 118.5 41.0 85.7
134 135 136 139	ACBP  rrm  IQ  ATP1G1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
134 135 136 139 140 141	ACBP  rrm  IQ  ATP1G1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf  KRAB	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
134 135 136 139 140 141 143 146	ACBP  FIM  IQ  ATP1G1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf  KRAB  DUF6	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATP1G1/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30	86.7 118.5 41.0 85.7 23.1 287.5 35.7
134 135 136 139 140 141 43 46 48	ACBP  rrm  IQ  ATP1G1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf  KRAB	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10	86.7 118.5 41.0 85.7 23.1 287.5 35.7
134 135 136 139 140 141 141 443 46 48 49	ACBP rrm IQ ATP1G1_PLM_M AT8 WH2 zf-C2H2 Peptidase_S2 6 arf KRAB DUF6 PDEase	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATP1G1/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1
134 135 136 139 140 141 43 46 48 49 51	ACBP  FIM  IQ  ATPIG1_PLM_M  AT8  WH2  Zf-C2H2  Peptidase_S2 6 arf  KRAB  DUF6  PDEase	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80 1.1e-08	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1
134 135 136 139 140 141 143 146 148 149 151 153	ACBP rrm IQ ATP1G1_PLM_M AT8 WH2 zf-C2H2 Peptidase_S2 6 arf KRAB DUF6 PDEase	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATPIGI/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain tRNA synthetases class I (R) FAD/NAD-binding Cytochrome	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1
134 135 136 139 140 141 43 46 48 49 51	ACBP  rrm  IQ  ATP1G1_PLM_M  AT8  WH2  zf-C2H2  Peptidase_S2 6  arf  KRAB  DUF6  PDEase  S4  tRNA-synt_ld  Cyt_reductas	Acyl CoA binding protein RNA recognition motif. IQ calmodulin-binding motif ATP1G1/PLM/MAT8 family Wiskott Aldrich syndrome homology region 2 Zinc finger, C2H2 type Signal peptidase I  ADP-ribosylation factor family KRAB box Integral membrane protein DUF6 3'5'-cyclic nucleotide phosphodiesterase S4 domain tRNA synthetases class I (R)	4.6e-22 1.2e-31 2.6e-08 9.3e-22 0.0067 1.7e-82 5.7e-10 1.2e-39 7.3e-30 0.096 3.8e-80 1.1e-08 3.8e-103	86.7 118.5 41.0 85.7 23.1 287.5 35.7 145.2 112.6 8.0 231.1 42.3 356.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	PPAN NAME	DESCRIPTION	p value	SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase	5.1e-67	236.1
	F	domain		
167	zf-C3IIC4	Zinc finger, C3HC4 type (RING	5.3e-07	27.0
		finger)		1 1
168	Ribosomal_S1	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function	0.07	-17.4
		DUF59		
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	qlobin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	le-31	118.8
178	ATPIG1 PLM M	ATPIG1/PLM/MAT8 family	2.5e-17	71.0
	AT8		ļ	
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y phosphatas	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase	6.5e-82	285.6
	[ ]	domain	1	1
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha t	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP-	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	synt_AC39 ldl_recept_a	Low-density lipoprotein	2.4e-25	97.6
1200	<u> </u>	receptor domain	1 42 32	70 4
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhombold family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme Ubiquitin-conjugating enzyme	7.4c-74 1e-53	191.9
213	UQ_con		1.8e-43	140.4
215	DEAD	DEAD/DEAH box helicase PMP-22/EMP/MP20/Claudin family	1.8e-43 4.5e-21	83.4
216	PMP22_Claudi n		<u> </u>	1
218	Glycos_trans f_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD4 0	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR or GLGF).	1.7e-09	45.0
L		1	J	

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate	12 5 25	
	m	deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito carr	Mitochondrial carrier proteins	1.3e-55	1,02 5
254	adenylatekin	Adenylate kinase		193.6
255	ase		1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid	2.6e-52	187.2
	1	transporter protein		1 -5
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	0.25.02	
260	Bacterial PQ	PQQ enzyme repeat	8.2e-07	25.3
	Q	1	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal S7	Pib		
279	pkinase	Ribosomal protein S7p/S5e	3.3e-20	80.6
_		Eukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f 4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	12-73	1
306	rrm	RNA recognition motif.	2e-44	161.0
308	7tm_1	7 transmembrane receptor	2.7e-44 5.2e-39	160.6
309	DNA polymera	(rhodopsin family)	L	
	seX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	771 6
326	ARID	ARID DNA binding domain		331.5
327	HMG box	HMG (high mobility group) box	5.1e-37	136.4
328	cadherin	Cadherin domain	6.7e-29	109.4
331	chromo	'chromo' (CHRromatin	8.1e-81 4e-18	281.9 66.7
Į.	1	Organization MOdifier)		
333	Peptidase M2	Glycoprotease family		

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			<u> </u>	SCORE
335	vwa	von Willebrand factor type A domain	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	iq	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase		
		domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	
361	ank	Ank repeat		79.4
362		Ank repeat	6.6e-34	126.1
	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	46.6
367	LRR -	Leucine Rich Repeat	8.8e-44	158.9
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0 .
376	ion trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase	1.6e-94	327.5
		domain		
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank .	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-05	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.le-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	1222
397	zf-C2H2		L	237.3
399	fn3	Zinc finger, C2H2 type	0.0066	23.1
400		Fibronectin type III domain	4.1e-102	352.6
	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrcg fn3	Dehydrogenase E1 component	3e-119	409.6
		Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410				T = 2
	RhoGRF	RhoGEF domain	1.1e-23	92.1
411	F-box	RhoGEF domain F-box domain.	1.1e-23 4.2e-06	33.7
411	1	F-box domain. SNF2 and others N-terminal		
	F-box SNF2_N CPSase_L_cha	F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase	4.2e-06	33.7
412	F-box SNF2_N CPSase_L_cha in	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)	4.2e-06 5.8e-16 1.5e-172	33.7
412 415 418	F-box SNF2_N CPSase_L_cha in LRR	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat	4.2e-06 5.8e-16	33.7
412 415 418 419	F-box SNF2_N CPSase_L_cha in	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain	4.2e-06 5.8e-16 1.5e-172	33.7 61.6 586.6
412 415 418	F-box SNF2_N CPSase_L_cha in LRR	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain	4.2e-06 5.8e-16 1.5e-172 3.8e-24	33.7 61.6 586.6
412 415 418 419	F-box SNF2_N CPSase_L_cha in LRR DENN	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain  RasGEF domain	4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43	33.7 61.6 586.6 93.6 207.5 155.7
412 415 418 419 420	F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank	F-box domain.  SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat	4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153	33.7 61.6 586.6 93.6 207.5 155.7 523.7
412 415 418 419 420 421 424	F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank G-patch	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain  RasGEF domain  Ank repeat  G-patch domain	4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	33.7 61.6 586.6 93.6 207.5 155.7 523.7 78.9
412 415 418 419 420 421 424 425	F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank G-patch pkinase	F-box domain.  SNF2 and others N-terminal domain  Carbamoyi-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain  RasGEF domain  Ank repeat  G-patch domain  Eukaryotic protein kinase domain	4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153	33.7 61.6 586.6 93.6 207.5 155.7 523.7
412 415 418 419 420 421 424	F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank G-patch	F-box domain.  SNF2 and others N-terminal domain  Carbamoyl-phosphate synthase (CPSase)  Leucine Rich Repeat  DENN (AEX-3) domain  RasGEF domain  Ank repeat  G-patch domain  Eukaryotic protein kinase	4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	33.7 61.6 586.6 93.6 207.5 155.7 523.7 78.9

No:	SEQ ID	PFAM NAME	DESCRIPTION		
Temporal political political principle   Temporal political political principle   Temporal political principle   Temporal political principle   Temporal political principle   Temporal political principle   Temporal political principle   Temporal politica			DESCRIPTION	p-value	PFAM
Singer)   Section   Sect		E		<del></del>	SCORE
Singer   DEAD/DEAH box helicase   1e-66   214.0	429	zf-C3HC4	Zinc finger, C3HC4 tyme (DINC	0.6- 17-	
ASAD   DEAD   DEAD/DEAH box helicase   1e-66   234.0	1		finger)	8.66-11	39.2
433   GFF CDC   Cell division protein   3.4e-16   67.7   678   CDC   Cell division protein   2.1e-114   393.5   658.1   Collagen	431	DEAD		10-66	<del>                                      </del>
436   Collagen   Collagen triple helix repeat   4.6e-194   558.1     438   Ricin_B_lect   Collagen triple helix repeat   4.6e-194   558.1     438   Ricin_B_lect   Similarity to lectin domain of in ricin b   Alpha_adapti   Alpha_a	432				
A36		GTP_CDC	Cell division protein		
Ricin_B lect   Similarity to lectin domain of in ricin h   Alpha_adapti   Alpha_adaptin carboxyl-terminal   1.2e-256   866.0   442   Alpha_adaptin   Alpha_adaptin carboxyl-terminal   1.8e-235   795.7   442   Alpha_adaptin   Alpha_adaptin carboxyl-terminal   1.8e-235   795.7   443   PDZ   PDZ   PDZ   Gomain (Also known as DHR   1.9e-65   230.9   PDZ   Gomain (Also known as DHR   1.9e-65   230.9   PDZ   Gomain (Also known as DHR   1.9e-65   230.9   PDZ   Gomain (Also known as DHR   1.9e-65   230.9   445   LON   APP-dependent protease La (LON)   0.00012   -17.1   446   ig   Immunoglobulin domain   0.00011   20.1   20.1   446   ig   Immunoglobulin domain   1.5e-06   35.2   452   fn3   Pibzonectin type III domain   1.5e-06   35.2   452   fn3   Pibzonectin type III domain   1.5e-06   35.2   456   Kinesin   Kinesin motor domain   4.9e-217   734.4   457   Reur_chan   Neurotransmitter-gated ion-channel   4.9e-217   734.4   458   Josephin   Josephin   Josephin   0.0002   18.7   468   BZIP   EZIP transcription factor   1.7e-07   31.8   470   NTP_transfer   ase   Nuclectidyl transferase   6.3e-06   -26.3   471   MD40   ND domain, G-beta repeat   2e-28   107.9   473   LDM   LIM domain containing proteins   0.00021   20.7   2f-RanbP   Zn-finger in Ran binding   0.028   22.0	436	Collagen	Collagen triple helix repeat		
Albha adapti   Alpha adaptin carboxyl-terminal   1.2e-256   866.0   n.C   domain   n.C   domain   domain   n.C   domain   domain   n.C   domain   domain   domain   n.C   domain   domain   domain   n.C   domain   domain   domain   domain   domain   domain   n.C   domain	L		(20 copies)	1.00 154	038.1
Alpha_adapti	438		Similarity to lectin domain of	0.0085	10.5
Alpha_adapti			ricin b		
Alpha adapti	441		Alpha adaptin carboxyl-terminal	1.2e-256	866.0
1.0   1.90   1			domai		
PDZ   PDZ	442		Alpha adaptin carboxyl-terminal	1.8e-235	795.7
ATP-dependent protease La (LON)   0.00012   -17.1		· –			J
ATP-dependent protease La (LON)   0.00012   -17.1	443	PDZ	PDZ domain (Also known as DHR	1.9e-65	230.9
Afficient processe	445	TON			
146	***3	LON	ATP-dependent protease La (LON)	0.00012	-17.1
ASSISTANT   Sushi	446	110			1
452   fn3		_1	Immunoglobulin domain		20.1
A54			Sushi domain (SCR repeat)		75.2
Social			Fibronectin type III domain		35.2
A56	7.77	_	Pyridoxal-dependent	8.3e-14	50.3
1.   1.   1.   1.   1.   1.   1.   1.	456		decarboxylase conse	1	1
Second   Channel   Chann			Kinesin motor domain	4.9e-217	734.4
Josephin   Josephin   Josephin   Diliphin	13,	Hear_Chan	Neurotransmitter-gated ion-	le-175	597.1
18.7   18.7	458	Josephin	Channel	<u>                                     </u>	
A70			Josephin		18.7
A			DZIP transcription factor		31.8
471	1,0		Nucleotidy1 transferase	6.3e-06	-26.3
A73	471		WD domein G		
2f-RanBP			TIM dendin, G-beta repeat	1	
A79   WD40   WD domain, G-beta repeat   6.5e-18   73.0	477		72 financial containing proteins	1	
Wilson   W		- italibi	protein and others	0.028	21.0
RRB	479	WD40	WD domain Chiers.		
### ArfGap	480	KRAB	KRAR box		
Protein for Arf   232.0   23	481	ArfGap			
A85		1	protein for Arf	8.4e-66	232.0
A86   Clq   Clq domain   A.3e-74   259.6	485	SH2	Src homology domain 2	0.013	<del> </del>
dsrm	486	Clq	Clg domain		1.
### ### ### ### ### #### #############	487	dsrm	Double-stranded RNA binding		
Alpha_adapti   Alpha_adapti   Alpha_adaptin carboxyl-terminal   3.4e-222   751.6     492			motif	1.16-4/	1/1.9
Alpha_adapti		zf-C2H2	Zinc finger, C2E2 type	A 80 153	L-21 0
Age	490	Alpha_adapti	Alpha adaptin carboxyl-terminal		
### Shift and ### ### ### ### ### #### #### ####		<u> </u>	domai	3.40-222	/31.0
ENV_polyprot ein			Shikimate kinase	1.2e-10	49 9
dahydrolase	497		ENV polyprotein (coat		
abhydrolase			polyprotein)		''''
2	498		Phospholipase/Carboxylesterase	0.041	~48.1
Soli				<del>-</del>	
WW   WW domain   4.6e-18   73.4			RNA recognition motif.	5.4e-34	126.4
1g					
Solution   Solution			Immunoglobulin domain		
505         vwa         von Willebrand factor type A domain         7.1e-62         219.0           508         Na_K_ATPase condition         2.3e-145         496.3           509         Exonuclease Exonuclease condition         1.3e-56         201.5           510         Glycos_trans followsyl transferases group 1 condition         2.9e-06         27.0           511         Glycos_trans followsyl transferases group 1 condition         2.9e-06         27.0           512         Glycos_trans followsyl transferases group 1 condition         1.9e-09         38.5           514         pro_isomeras         Cyclophilin type peptidyl-         1.8e-63         221.4			alpha/beta hydrolase fold		
domain	505	vwa	von Willebrand factor type A		
C   C   C   C   C   C   C   C   C   C			domain	· ••	
C   C   C   C   C   C   C   C   C   C	508		Na+/K+ ATPase C-terminus	2.3e-145	496.3
510 Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0  511 Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0  512 Glycos_trans Glycosyl transferases group 1 1.9e-09 38.5  514 pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4					
Glycos_trans   Glycosyl transferases group 1   2.9e-06   27.0				1.3e-56	201.5
Sil	510		Glycosyl transferases group 1		
f_1 2.9e-06 27.0  f_1 2.9e-06 27.0  Glycos_trans Glycosyl transferases group 1 1.9e-09 38.5  f_1 pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4					- ' - '
Glycos_trans Glycosyl transferases group 1 1.9e-09 38.5  f_1 pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4	511		Glycosyl transferases group 1	2.9e-06	27.0
f_1   1.9e-09   38.5   1.9e-63   221.4				_,	~ / . •
pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4	212		Glycosyl transferases group 1	1.9e-09	38.5
1.8e-63   221.4			1		
e prolyl cis-tr	P14		Cyclophilin type peptidyl-	1.8e-63	221.4
		е	prolyl cis-tr		

SEQ 10   PPAM NAME   DESCRIPTION   P-value   PPAM   SCORE					
Sic   FGF	SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
Surp					,
19		Į.		1	
UBX					1
SAM				3.3e-06	25.0
SAM	526	UBX	UBX domain	1.le-34	128.6
motif	528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
331	530	SAM	SAM domain (Sterile alpha	0.046	10.0
		1	motif)		
	531	adh_short	short chain denydrogenase	0.0025	-34.1
	532	mito carr	Mitochondrial carrier proteins	2.5e-81	281.7
Second   S	533	mito carr		2e-61	213.5
Signature	534	thiolase		3.5e-183	622.0
1   1   1   1   1   1   1   1   1   1	535	FMO-like	Flavin-binding monooxygenase-	L	1153.7
Signature   Canal Synthetases class   (I, L, 3.1e-136   466.0   M and V)		1	,		
Signature   Canal Synthetases class   (I, L, 3.1e-136   466.0   M and V)	536	SCAN	SCAN domain	4e-55	196.6
Mand V    1	537	tRNA-synt 1	I control of the cont	ľ	
TRNA synt				3.20 200	1
Mand V    1	538	tRNA-synt 1		3 10-136	466 0
Sample	-50	0		3.16 130	100.0
Mand V	539	tRNA-synt 1	<u> </u>	1 90-117	403 6
TRNA-synt	222	craise synte_1		1.96-11/	403.6
Mand V    S4TP-synt_E	540	FDMA-great 1		3 10 136	166 0
541         VATP-synt_E         ATP synthase (E/31 kDa) subunit         5.9e-85         295.7           543         2f-C2H2         Zinc finger, C2H2 type         5.5e-69         242.6           544         DUF101         Protein of unknown function         8.5e-38         119.0           545         TGFb_propept ide         1.1e-67         238.2           547         WD40         WD domain, G-beta repeat         2.6e-32         120.8           548         RHD         Rel homology domain (RHD)         1.5e-238         606.2           549         MNR HSR1         GTPase of unknown function         5.4e-67         236.0           551         HECT         HECT-domain (ubiquitin-transferase).         4.3e-127         435.6           551         HECT         HECT-domain (ubiquitin-transferase).         3.5e-74         259.8           552         Zf-UBR1         Putative zinc finger in N-recognin         3.3e-16         67.3           555         zf-UBR1         Putative zinc finger in N-recognin         3.3e-16         67.3           561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           <	240	-ww-patter_T		3.16-136	1 400.0
544         Zinc finger, C2H2 type         5.5e-69         242.6           544         DUF101         Protein of unknown function         8.5e-38         139.0           545         TGFD propept ide         1.1e-67         238.2           547         MD40         WD domain, G-beta repeat         2.6e-32         120.8           548         RHD         Rel monology domain (RHD)         1.6e-238         686.2           549         MNR HSR1         GTPase of unknown function         5.4e-67         236.0           551         HECT         HECT-domain (ubiquitin-transferase).         4.3e-127         435.6           551         HECT         HECT-domain (ubiquitin-transferase).         4.3e-127         435.6           554         MHC_II_alpha         Class II histocompatibility antique of transferase).         3.5e-74         259.8           555         zf-UBR1         Putative zinc finger in N-recognin         3.3e-16         67.3           556         Kelch         Kelch motif         5.5e-29         109.7           561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           562         PABP         Poly-adenylate binding protein, unique domain         4.9e-38         139.8           564<	5/1	I MATE CAME R		5 00 05	206 7
DUF101				,	
DUF101   TGFb_propept   TGF-beta propeptide   1.1e-67   238.2	_ : : : : : : : : : : : : : : : : : : :			1	
TGFb_propept   TGF-beta propeptide   1.1e-67   238.2	344	DOLIOT		8.5e-38	139.0
ide	FAE	morph	I		I
547         WD40         WD domain, G-beta repeat         2.6e-32         120.8           548         RHD         Rel homology domain (RHD).         1.6e-238         686.2           549         MNR HSR1         GTPase of unknown function         5.4e-67         236.0           551         HECT         HECT-domain (ubiquitin-transferase).         4.3e-127         435.6           551         HECT         HECT-domain (ubiquitin-transferase).         3.5e-74         259.8           554         MHC_II_alpha         Class II histocompatibility         3.5e-74         259.8           555         Zf-UBR1         Putative zinc finger in N-recognin         3.3e-16         67.3           556         Kelch         Kelch motif         5.5e-29         109.7           561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           562         PABP         Poly-adenylate binding protein, unique domain         4.9e-38         139.8           564         Gag_p30         Gag F30 core shell protein         1.2e-67         238.2           566         PWMP         PWWP domain         8.1e-16         66.0           567         SCAN         SCAN domain         7.3e-68         238.9           57	343		TGF-beta propeptide	1.1e-67	238.2
548         RHD         Rel homology domain (RHD)         1.6e-238         686.2           549         MNR HSR1         GTPase of unknown function         5.4e-67         236.0           551         HECT         HECT-domain (ubiquitin-transferase)         4.3e-127         435.6           554         MHC_II_alpha         Class II histocompatibility         3.5e-74         259.8           555         Zf-UBR1         Putative zinc finger in N-recognin         3.3e-16         67.3           556         Kelch         Kelch motif         5.5e-29         109.7           561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           562         PABP         Poly-adenylate binding protein, unique domain         4.9e-38         139.8           564         Gag_p30         Gag P30 core shell protein         1.2e-67         238.2           565         PWWP         PWWP domain         8.1e-16         66.0           567         SCAN         SCAN domain         7.3e-68         238.9           569         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         0.00081         -79.7	E42		MD 1	<u> </u>	1
MMR_HSR1   GTPase of unknown function   5.4e-67   236.0					
HECT					1 1
transferase .					
S54	221	HECT		4.3e-127	435.6
antigen, alp		1000 77			
S55	554	MHC_II_alpha		3.5e-74	259.8
recognin		-2 11000			<u> </u>
S56   Kelch   Kelch motif   S.5e-29   109.7	222	21-UBRI		3.3e-16	67.3
561         AMP-binding         AMP-binding enzyme         2.8e-06         -163.7           562         PABP         Poly-adenylate binding protein, unique domai         4.9e-38         139.8           564         Gag p30         Gag p30 core shell protein         1.2e-67         238.2           566         PWWP         PWWP domain         8.1e-16         66.0           567         SCAN         SCAN domain         7.3e-68         238.9           569         pkinase         Eukaryotic protein kinase         1.5e-84         294.3           569         pkinase         Eukaryotic protein kinase         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase         1.5e-84         294.3           571         CN hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin head         Myosin head (motor domain)         0         1495.2           573         myosin head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           578         PDZ         DNA					
PABP					
Unique domai   1.2e-67   238.2				•	
564         Gag_p30         Gag_P30 core shell protein         1.2e-67         238.2           566         PWWP         PWWP domain         8.1e-16         66.0           567         SCAN         SCAN domain         7.3e-68         238.9           569         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           571         CN_hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin_head         Myosin head (motor domain)         0         1490.4           573         myosin_head         Myosin head (motor domain)         0         1490.4           573         surp         Surp module         1.7e-23         91.5           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA_pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLEF)         8.3e-09         42.7           579         LRR         Leucine Rich Repeat	562	PABP		4.9e-38	139.8
566         PWWP         PWWP domain         8.1e-16         66.0           567         SCAN         SCAN domain         7.3e-68         238.9           569         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           571         CN hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin_head         Myosin head (motor domain)         0         1495.2           573         myosin_head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA_pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           584         DEAD <td< td=""><td></td><td></td><td></td><td><u> </u></td><td><u> </u></td></td<>				<u> </u>	<u> </u>
567         SCAN         SCAN domain         7.3e-68         238.9           569         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           571         CN hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin head         Myosin head (motor domain)         0         1495.2           573         myosin head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           584					
569         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           570         pkinase         Eukaryotic protein kinase domain         1.5e-84         294.3           571         CN hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           571         CN hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin head         Myosin head (motor domain)         0         1495.2           573         myosin head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586				1	1
domain	L .				
Pkinase	569	pkinase		1.5e-84	294.3
domain					
571         CN_hydrolase         Carbon-nitrogen hydrolase         0.00081         -79.7           572         myosin_head         Myosin head (motor domain)         0         1495.2           573         myosin_head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA_pol_B         DNA polymerase family B         0         1138.6           578         PDZ         DDA polymerase family B         0         1138.6           578         PDZ         DDA polymerase family B         0         1138.6           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.	570	pkinase		1.5e-84	294.3
572         myosin head         Myosin head (motor domain)         0         1495.2           573         myosin head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain <td></td> <td><u> </u></td> <td></td> <td></td> <td></td>		<u> </u>			
573         myosin head         Myosin head (motor domain)         0         1490.4           575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA pol B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7				0.00081	
575         Surp         Surp module         1.7e-23         91.5           576         Surp         Surp module         1.7e-23         91.5           577         DNA pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7		myosin_head		0	
576         Surp         Surp module         1.7e-23         91.5           577         DNA_pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7					
577         DNA_pol_B         DNA polymerase family B         0         1138.6           578         PDZ         PDZ domain (Also known as DHR or GLGF).         8.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7		<u>^</u>	1		91.5
FDZ         PDZ domain (Also known as DHR or GLGF).         B.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7				1.7e-23	
FDZ         PDZ domain (Also known as DHR or GLGF).         B.3e-09         42.7           579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7			DNA polymerase family B	0	1138.6
579         LRR         Leucine Rich Repeat         4.9e-21         83.3           580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7	578	PDZ	PDZ domain (Also known as DHR	8.3e-09	42.7
580         neur_chan         Neurotransmitter-gated ion-channel         5.9e-177         601.3           583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7		<u> </u>			
channel     1673.0       583     sushi     Sushi domain (SCR repeat)     0     1673.0       584     DEAD     DEAD/DEAH box helicase     7.3e-36     116.3       586     KH-domain     KH domain     2.9e-13     57.5       587     G-patch     G-patch domain     2.3e-14     61.2       589     LIM     LIM domain containing proteins     2.3e-36     133.4       590     bromodomain     Bromodomain     6.6e-32     114.7		LRR	Leucine Rich Repeat	4.9e-21	83.3
583         sushi         Sushi domain (SCR repeat)         0         1673.0           584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7	580	neur_chan	Neurotransmitter-gated ion-	5.9e-177	601.3
584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7		1	channel		į į
584         DEAD         DEAD/DEAH box helicase         7.3e-36         116.3           586         KH-domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7	583	sushi	Sushi domain (SCR repeat)	0	1673.0
586         KH-domain         KH domain         2.9e-13         57.5           587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7	584	DEAD		7.3e-36	
587         G-patch         G-patch domain         2.3e-14         61.2           589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7	586	KH-domain			1
589         LIM         LIM domain containing proteins         2.3e-36         133.4           590         bromodomain         Bromodomain         6.6e-32         114.7				1	
590 bromodomain Bromodomain 6.6e-32 114.7		1			
			<del></del>		1
0.08-32   114./					1
					1

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SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	.3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3 •
608	PWWP	PWWP domain	2.6e-28	107.5
609	PMMb	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	205.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632 635	rrm	RNA recognition motif.	4e-05	30.5
	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain ,	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
643	efhand	TPR Domain  EF hand	4.8e-08	40.1
647	SNF2 N	SNF2 and others N-terminal	1.9e-27	104.6
648	PseudoU synt	domain  RNA pseudouridylate synthase	1.2e-101	351.1
650	h_2	Zinc finger, C2H2 type	1.9e-55	197.6
651	ank	Ank repeat	0.0087 1.3e-17	22.7
652	I LWEQ	1/LWEQ domain	9.5e-101	71.9
653	neur_chan	Neurotransmitter-gated ion- channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter WD domain, G-beta repeat	5.3e-60	212.8
674	WD40		4.8e-24	93.3

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat	0.0015	25.2
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPC	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
6B3	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M2	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl transf	Acyl transferase domain	1.le-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran BP1	RanBP1 domain.	8.4e-06	-7.3
		DEAD/DEAH box helicase	9.9e-42	134.9
713	DEAD	PH domain	1.6e-09	39.0
714	PH		1.5e-37	138.2
715	DSPc	Dual specificity phosphatase, catalytic doma		115.9
717	Sialyltransf	Sialyltransferase family	7.5e-31	
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP- OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI typeI	Phosphomannosc isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like	6.le-11	49.8
754	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
755	PH ·	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8
761	CIDE-N	CIDE-N domain	2.2e-40	147.6
1 ,07	CIDE-M	CTDD-14 COMMOTH	2.20-40	1 - 2 /

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			-	SCORE
762 763	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
764	zf-MYND	MYND finger	4.1e-14	60.3
767	pou	Pou domain - N-terminal to homeobox domain	1e-52	188.6
		von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.le-12	55.5
779	rrm	RNA recognition motif.	2.1e-32	121.1
	G6PD .	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782 783	SCAN	SCAN domain	1.3e-24	95.2
	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786 787	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
	PI3_PI4_kina se	Phosphatidylinositol 3- and 4- kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797 799	trypsin	Trypsin	9.9e-20	64.8
801	CH Gal-	Calponin homology (CH) domain	3.7e-15	63.8
803	bind_lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
806 .	TBC	WD domain, G-beta repeat	0.00082	26.1
807	TBC	TBC domain TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	1.8e-26	101.4
811	CBFD NFYB HM	Histone-like transcription	8.8e-80 6e-14	278.5
	F	factor	96-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hy dro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	100 5
840	Y_phosphatas e	Protein-tyrosinc phosphatase	2.60-119	88.5 409:8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2 2e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	TRP domain	10.00	<u> </u>
849	zf-C3HC4	IBR domain	9e-15	62.5
		Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR	Scavenger receptor cysteine-	0	1025.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
	<del></del>	rich domain	<del> </del>	SCORE
853	SRCR	Scavenger receptor cysteine-	D	1005
		rich domain	1	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
B58	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
B59	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha	Carbamoyl-phosphate synthase	2.1e-218	739.0
	in	(CPSase)		
879	Ribosomal_S1 2e	Ribosomal protein Sl2e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6)	0.044	8.0
		domain	1	1
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function	1.3e-43	158.3
896	IP trans	DUF28 Phosphatidylinositol transfer		
898		protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
900	KE2 KE2	KE2 family protein	7e-61	215.7
900	zf-C2H2	KE2 family protein	4.3e-51	183.2
902	ras	Zinc finger, C2H2 type	2.7e-57	203.8
904	TPR	Ras family	2.3e-75	263.8
906	GBP	TPR Domain	3.2e-22	87.2
907	GBP	Guanylate-binding protein	8.9e-253	853.1
908	WD40	Guanylate-binding protein WD domain, G-beta repeat	1.1e-239	809.6
909	PH	PH domain	2.6e-26	100.8
910	2f-C2H2	Zinc finger, C2H2 type	1.3e-09 2.5e-39	39.4
913	Epimerase	NAD dependent	5e-07	144.1
		epimerase/dehydratase family	36-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like	2.9e-05	29.1
	1	hydrolase	1	1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e-53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul P 3 ep	Ribulose-phosphate 3 epimerase	1.2e-96	334.4
	im	family	7.20.30	133.3
936	C2	C2 domain	2.2e-62	220.7
	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
937	1			<u> </u>
	abhydrolase	alpha/heta hydrolaga fold	1 0 011	127
940	abhydrolase	alpha/beta hydrolase fold	0.011	3.1
940 944	Tropomyosin	Tropomyosins	3.2e-07	25.1
940 944 948	Tropomyosin pkinase	Tropomyosins Eukaryotic protein kinase domain	3.2e-07 3.4e-75	25.1 263.2
937 940 944 948 949	Tropomyosin	Tropomyosins Eukaryotic protein kinase	3.2e-07	25.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			7	SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO_IDH_MOCA	Oxidoreductase family	1.3e-11	52.0
955 956	BTB	BTB/POZ domain	7e-22	86.1
956	BTB CDP-	BTB/POZ domain	7e-22	86.1
1 957	OH P transf	CDP-alcohol	0.053	-22.2
959	ras	phosphatidyltransferase Ras family		
960	ras	Ras family	2.4e-97	336.8
961	Acetyltransf	Acetyltransferase (GNAT) family	8.4e-43 1.2e-08	155.6
962	adh short	short chain dehydrogenase	2.4e-31	42.2
963	mutT	Bacterial mutT protein	5.6e-06	117.6 26.2
969	IF-2B	Initiation factor 2 subunit	8.4e-193	653.9
1	1	family	0.46-155	653.9
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR	3.6e-21	83.7
ļ		or GLGF).		1
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri n	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6)	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.7e-15	53.1
1016	tRNA-synt 2c	finger)		1
1018	RhoGAP	tRNA synthetases class II (A) RhoGAP domain	2.3e-15	55.2
1022	PGAM	Phosphoglycerate mutase family	1.6e-78	274.3
1026	HMG box	HMG (high mobility group) box	3.8e-18	69.7
1027	TBC	TBC domain	8.4e-20	79.2
1028	UQ_con	Ubiquitin-conjugating enzyme	7.3e-45	162.5
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	1.4e-49 0.028	178.1
1034	Hydrolase	haloacid dehalogenasc-like	2e-21	84.6
1037	KRAB	hydrolase KRAB box	4 8	
1038	Cation_efflu x	Cation efflux family	4.8e-06 7.1e-42	32.4 152.5
	ART	NAD:arginine ADP-	4.7e-47	169.1
1040				
		ribosyltransferase		
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1042 1043	WD40 zf-C2H2	WD domain, G-beta repeat Zinc finger, C2H2 type	3.7e-24	93.7
1042	WD40	WD domain, G-beta repeat		

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	iq	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1030	4e	RIDOSOMAL PROCESS DATE		
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22 Claudi	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1033	n	PMF-22/BMF/M220/Claddin Zamily	0.023	
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
		GTP1/OBG family	4.8e-41	141.8
1066	GTP1_OBG		8.4e-48	159.1
1071	ig	Immunoglobulin domain		
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077 .	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	le-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPC	Dual specificity phosphatase,	3.3e-63	223.4
		catalytic doma		
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreducta	Nitroreductase family	1.3e-13	58.6
	se		2 20 270	610.1
1106	PTE	Phosphotriesterase family	1.3e-179	19.6
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14 17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14 17	HMG14 and HMG17	9.9e-12	52.4
1117	FAA hydrolas	Fumarylacetoacetate (FAA)	2e-83	290.6
1119	e	hydrolase fam		<u> </u>
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro isomeras	Cyclophilin type peptidyl-	2.2e-56	197.1
	e	prolyl cis-tr	1	1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
		Adaptor complexes medium	1.2e-256	866.0
1136	Adap_comp_su b	subunit family		
1137	Adap_comp_su	Adaptor complexes medium	2.5e-209	708.8
	b	subunit family		<u> </u>
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1		Down down (TDC 1 harry)	E 40 FF	196.1
1153	IRS	PTB domain (IRS-1.type)	5.4e-55	
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	AN1-like Zinc finger	0.00021	27.9
		<del></del>		

CEO TD	1 20004		_	
SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
1163	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
	ne			1
1164	DED IRS	Death effector domain	3.9e-05	30.5
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	PTB domain (IRS-1 type)	2.6e-43	157.3
1100	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	IIM	RNA recognition motif.	2.1e-40	147.7
1220	DUF6 SCAN	Integral membrane protein DUF6	0.015	21.5
1223	G-gamma	SCAN domain	1.5e-71	251.1
1227	catalase	GGL domain	3.6e-36	129.5
1232	PX	PX domain	0	1158.9
1233	PX	PX domain	2.2e-15 2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_trans f 2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	EF hand	40. 11	150 4
1254	UQ con	Ubiquitin-conjugating enzyme	4e-11 2.1e-73	50.4 257.3
1255	ras	Ras family	2.1e-73 2.2e-62	257.3
1256	formyl_trans	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	DiHfolate_re	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transp ept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

NO: 1266 1267 1269 1275 1276 1277 1279 1280	SCP K_tetra ras zf-C3HC4 abhydrolase abhydrolase trypsin	SCP-like extracellular protein K+ channel tetramerisation domain Ras family Zinc finger, C3HC4 type (RING finger) alpha/beta hydrolase fold alpha/beta hydrolase fold	1.3e-85 4.2e-10	108.0 104.0 297.9 37.0
1267 1269 1275 1276 1277 1279 1280	ras zf-C3HC4 abhydrolase abhydrolase trypsin	domain Ras family Zinc finger, C3HC4 type (RING finger) alpha/beta hydrolase fold	1.3e-85 4.2e-10 5.4e-23	297.9 37.0
1275 1276 1277 1279 1280	zf-C3HC4 abhydrolase abhydrolase trypsin	Zinc finger, C3HC4 type (RING finger) alpha/beta hydrolase fold	4.2e-10 5.4e-23	37.0
1275 1276 1277 1279 1280	zf-C3HC4 abhydrolase abhydrolase trypsin	Zinc finger, C3HC4 type (RING finger) alpha/beta hydrolase fold	5.4e-23	
1277 1279 1280	abhydrolase trypsin	alpha/beta hydrolase fold		
1277 1279 1280	abhydrolase trypsin	alpha/beta hydrolase fold		89.8
1279 1280	trypsin		5.6e-21	83.1
1280		Trypsin	4.4e-41	132.0
1005	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1297	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
		Mitochondrial carrier proteins	2.1e-53	186.0
1307	mito_carr	WD domain, G-beta repeat	1.6e-17	71.6
1308	WD40	u-PAR/Ly-6 domain	7.1e-20	75.5
1310	UPAR_LY6		3.6e-05	21.6
1313	thiored	Thioredoxin	1.5e-67	237.9
1314	Aa_trans	Transmembrane amino acid transporter protein	4.4e-41	132.0
1316	trypsin	Trypsin		219.8
1320	Ribosomal_L1	Ribosomal protein L13	3.9e-62	
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_syntheta	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPC	Dual specificity phosphatase, catalytic doma	2,3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band 41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1373	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1347	1		5.3e-28	106.5
1347	BTB	BTB/PUZ domain		
1347	BTB	BTB/POZ domain Integral membrane protein DUF6	0.033	15.8
1347 1348 1349	DUF6	Integral membrane protein DUF6	0.033	1088.7
1347		Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated		
1347 1348 1349 1350	DUF6 myosin_head	Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium	0	1088.7
1347 1348 1349 1350 1352	DUF6 myosin_head Nramp S_100	Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain	0 1.2e-202	1088.7
1347 1348 1349 1350 1352 1353	DUF6 myosin_head Nramp S_100 DEAD	Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DEAD/DEAH box helicase	0 1.2e-202 5.3e-23	1088.7 686.6 89.9
1347 1348 1349 1350 1352	DUF6 myosin_head Nramp S_100	Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain	0 1.2e-202 5.3e-23 3.6e-65	1088.7 686.6 89.9

SEO ID	PFAM NAME			
NO:	Pram Name	DESCRIPTION	p-value	PFAM
1362	SIS	SIS domain	3.8e-30	SCORE
1363	SIS	SIS domain		113.6
1364	ig	Immunoglobulin domain	1.3e-28 0.00026	108.5
1368	K_tetra	K+ channel tetramerisation	1.1e-16	19.0
		domain	1.16-16	68.9
1371	Collagen	Collagen triple helix repeat	2.2e-113	390.1
		(20 copies)	2.26-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	92.9
		finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type		<del></del>
1390	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1393	kinesin	Kincsin motor domain	2.5e-85	296.9
1394	zf-C2H2	Zinc finger, C2H2 type	7.8e-188	637.4
1398	KRAB	KRAB box	1.2e-49	178.4
1402	bZIP	bZIP transcription factor	5.1e-22	86.6
1405	sugar tr	Sugar (and other) transporter	0.035	13.1
1406	RhoGAP	RhoGAP domain	0.003	-101.5
1407	rrm		8.9e-47	168.8
1408	LRR	RNA recognition motif. Leucine Rich Repeat	le-35	132.1
1409	Nebulin repe		2.1e-13	58.0
	at	Nebulin repeat	6e-54	192.6
1410	ank	Anie		
1412	Ribosomal L5	Ank repeat	1.6e-17	71.6
	C	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin		
1416	aminotran 1	Aminotransferases class-I	4.7e-85	.270.4
1417	S1	Aminotransierases class-I	4.4e-05	-91.2
1419	WD40	S1 RNA binding domain	1.6e-07	33.1
1422	cadherin	WD domain, G-beta repeat	2.2e-09	44.6
1424	SH3	Cadherin domain SH3 domain	8.3e-42	152.3
1425	PHD		2.5e-80	280.3
1426	PHD	PHD-finger PHD-finger	3.2e-17	70.6
1427	ArfGap	Pho-linger	3.2e-17	70.6
,	ALLGap	Putative GTP-ase activating	le-37	138.8
1428	helicase C	protein for Arf		<u> </u>
	""" Lase_C	Helicases conserved C-terminal domain	le-26	102.2
1429	WD40		<u> </u>	
1430	inositol P	WD domain, G-beta repeat	3.9e-07	37.2
1431	mito_carr	Inositol monophosphatase family	2.5e-10	40.2
1433	Clq	Mitochondrial carrier proteins	4.3e-83	287.7
1434	WD40		2.9e-16	66.2
1435	Inos-1-	WD domain, G-beta repeat	1.6e-13	58.3
	P_synth	Myo-inositol-1-phosphate	7e-228	770.4
1436	rrm	synthase		<u> </u>
1438	ig	RNA recognition motif.	1.4e-34	128.3
1440	G Adapt CT	Immunoglobulin domain	1.3e-12	45.6
1441	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Gamma-adaptin, C-terminus	3.4e-67	236.7
1446		Kelch motif	0.00013	28.7
1447	ARID	ARID DNA binding domain	1.8e-21	84.7
1448	zf-C2H2	Zinc finger, CZH2 type	9.4e-28	105.6
	AMP-binding	AMP-binding enzyme	2.6e-07	-145.1
1451	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
L460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1461	C2	C2 domain	4e-18	73.6
470	TIG	IPT/TIG domain	3.1e-19	77.3
472	PseudoU_synt	RNA pseudouridylate synthase	4.3e-16	66.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
	h_2			
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflu x	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_al pha	Telomere-binding protein alpha subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cy c	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1.492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.le-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox EGF	Homeobox domain	0.084	13.8
1505 1506	UCH-2	EGF-like domain	2.7e-23 2.7e-21	84.2
		Ubiquitin carboxyl-terminal hydrolase family		
1508	Peptidase_M2 0	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35 0.011	130.7
1516 1518	Syntaxin aminotran_3	Syntaxin Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKC	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidas e	Flavin containing amine oxidase	3.2e-43	157.0
1655	Amino_oxidas e	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1 UCH-2	GTPase of unknown function Ubiquitin carboxyl-terminal	0.0011 2.5e-11	-45.5 51.1
1660	actin	hydrolase family Actin	6.6e-21	69.9
~000	BAH	BAH domain	1.7e-82	287.5
1661		L Derr Collecti	1 4.75-02	
1661 1662	vwa	von Willebrand factor type A	0	1909.4
1662	vwa	domain		
1662 1663	WD40	domain WD domain, G-beta repeat	1.4e-67	237.9
1662	vwa	domain		

SEO ID	I Down was			
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
1672	chromo	'chromo' (CHRromatin	2.1e-18	SCORE 67.7
L		Organization MOdifier)	2.16-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
		type		1 -7.0
1676	Glyco_hydro_	Glycosyl hydrolase family 47	1.8e-187	636.2
	47	_		1 333.5
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
L	47		1	
1680	WD40	WD domain, G-beta repeat	1.le-27	105.5
1681	WD40 .	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various	1.3e-81	284.5
1		cellular act		
1697	Ferric_reduc	Ferric reductase like	8.4e-82	285.2
	t	transmembrane com		
1698	Ferric_reduc	Ferric reductase like	3.5e-53	190.1
	t	transmembrane com	i	]
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase	1.2e-88	307.9
		domain		1 307.5
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
	_ł	type	1 0 - 0 -	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
		type		[ 30.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	FLH	Helix-loop-helix DNA-binding	9.2e-10	45.9
		domain		}
1723	cisrm	Double-stranded RNA binding	2.9e-05	30.9
		) motif	1	1
1724	RrnaAD	Ribosomal RNA adenine	0.045	9.2
1000	<u> </u>	dimethylases	ļ	
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1725	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	1			1
	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific	0.0023	16.1
	ļ	phospholipase		1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	328.8
1769	CN hydrolase	Carbon-nitrogen hydrolase		149.4
1775	ank	Ank repeat	3e-06	-43.9
1779	Oxysterol BP	Oxysterol-binding protein	4.1e-07	37.1
1783	RhoGEF	RhoGEF domain	4.7e-56	199.6
1784	RhoGEF	RhoGEF domain	1.6e-23	91.6
		WOUNTIE	1.6e-23	91.6

WO 01/53312 PCT/US00/34263

SEQ ID PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO:	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

	I CTCNINI TNI NMTNIO		
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		
2	1-21	0.991	0.955
3	1-31	0.995	0.944
4	1-33	0.949	0.736
5	1-19	0.970	0.951
6	<del></del>	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.971	0.863
10	1-21	0.982	0.901
11	1-23	0.991	0.955
12	1-25	0.989	0.899
13	1-18	0.955	0.803
14	1-18	0.932	0.625
15	1-25	0.941	0.876
16	1-17	0.972	0.811
17	1-27	0.964	0.939
18	1-16	0.914	0.777
19	1-19	0.914	0.657
20	1-20	0.935	0.840
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.570	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75 88	1-29	0.958	0.854
94	1-20	0.986	0.945
97	1-33	0.994	0.943
103	1-46	0.964	0.595
108	1-49	0.983	0.570
111	1-26	0.978	0.885
126	1-25	0.989	0.899
129	1-19	0.955	0.803
138	1-29	0.963	0.918
143	1-18	0.971	0.844
148	1-20	0.914	0.628
156	1-25	0.969	0.904
158	1-22	0.941	0.811
1.60	1-17	0.979	0.927
161	1-48	0.972	0.939
162	1-25	0.903	0.571
L68	1-16	0.937	0.729
171	1-27	0.939	0.826
178	1-21	0.945	0.777
180	1-27	0.945	0.825
L87	1-28	0.981	0.941
90	1-19	0.982	0.936
	<del></del>	0.953	0.840
196	1-22	0.975	0.916

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-27	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
	1-24	0.953	0.739
272	1-21	0.906	0.688
283	1-29	0.997	0.854
	1-31	0.986	0.841
290	1-31	0.980	0.893
302	1-16	0.907	0.635
304	1-16	0.993	0.976
312		0.930	0.753
313	1-17	0.998	0.909
323	1-22	0.982	0.954
324	1-17	0.971	0.865
328	1-19	0.963	0.924
329		0.978	0.841
330	1-33	0.520	0.712
331		0.975	0.881
332	1-24	0.984	0.941
333	1-20	0.899	0.567
334		0.942	0.813
335	1-27	0.952	0.850
336	1-38	0.942	0.653
337	1-38	0.973	0.772
	1-36	0.979	0.804
339	1-27	0.888	0.597
340	1-19	0.971	0.865
	1-22	0.994	0.928
344	1-22	0.966	0.687
345		0.936	0.822
346	1-19	0.963	0.924
347	1-22	0.982	0.966
349	1-24	0.918	0.815
351	1-21	0.988	0.912
352	1-31	0.974	0.839
354	1-31	0.932	0.632
355	1-29	0.932	0.969
356	1-15	0.935	0.726
357	1-33		0.728
360	1-27	0.938	0.674
361	1-25	0.954	0.788
362	1-22	0.929	
363	1-21	0.881	0.715
364	1-33	0.978	
365	1-33	0.978	0.841

	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	
367	1-19	0.936	0.820
368	1-29	0.972	0.822
370	1-24	0.920	0.874
371	1-24	0.961	0.712
372	1-27	0.919	0.773
373	1-19	0.986	0.768
375	1-32		0.945
376	1-34	0.994	0.932
377	1-17	0.987	0.810
378	1-49	0.995	0.950
380	1-20	0.971	0.749
381	1-20	0.968	0.874
382	1	0.928	0.782
383	1-19	0.986	0.934
	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	
411	1-38	0.977	0.962
412	1-20	0.944	0.827
413	1-20	0.988	0.768
414	1-46	0.993	0.965
415	1-23	0.981	0.638
417	1-29	0.941	0.940
418	1-20		0.672
419	1-19	0.952	0.850
420	1-29	0.986	0.967
421	1-22	0.965	0.861
422	1-48	0.889	0.785
424	1-19	0.982	0.862
428	1-38	0.979	0.933
430		0.942	0.653
432	1-18	0.947	0.595
	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
143	1-15	0.966	0.940
148	1-36	0.979	0.804
153	1-41	0.958	0.609
55	1-33	0.943	0.606
157	1-27	0.888	0.597
162	1-16	0.925	0.681
86	1-27	0.972	0.845
95	1-24	0.917	0.636
198	1-26	0.993	
505	1-20	0.976	0.890
507	1-17	0.966	0.926
10	1-23		0.687
-	1	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
	1-21	0.918	0.815
571	1-31	0.988	0.912
574	1-39	0.925	0.556
580		0.974	0.839
594	1-31	0.932	0.632
608	1-29		0.632
609	1-29	0.932	
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.850	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
	1-46	0.903	0.598
735		0.916	0.730
746	1-14	0.965	0.876
747	1-22	0.968	0.785
748	1-29		0.773
759	1-24	0.961	0.768
767	1-27	0.919	0.585
768	1-33	0.900	
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
	1-29	0.957	0.845
950 963	1-29	0.981	0.900
		0.886	0.558
964	1-20		0.890
973	1-16	0.968	0.749
980	1-34	0.961	
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
	1-22	0.993	0.935

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	<del> </del>
1080	1-19	0.931	0.934
1092	1-19	0.991	0.829
1094	1-46	0.992	<u></u>
1095	1-30	0.974	0.653
1105	1-23	0.994	0.929
1123	1-35	0.987	0.921
1138	1-32		0.658
1140	1-39	0.954	0.613
1142	1-33	0.989	0.789
1152	1-25	0.897	0.570
1170		0.990	0.962
1176	1-38	0.977	0.827
1187	1-20	0.944	0.768
	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	
1266	1-20	0.885	0.785
1276	1-48	0.982	0.809
1292	1-19	0.982	0.862
1296	1-21	0.919	0.933
1297	1-19		0.944
1332	1-38	0.984	0.953
1358	1-18	0.942	0.653
1371	1-33	0.947	0.595
1380		0.957	0.789
1397	1-26	0.979	0.904
1399	1-27	0.962	0.777
1404	1-23	0.997	0.960
1410	1-24	0.998	0.977
1414	1-15	0.946	0.845
1415	1-24	0.913	0.588
	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0 500
1428	1-25	0.957	<del></del>
1430	1-34	0.977	0.899
1431	1-28	0.979	0.819
1432	1-36	0.957	0.923
1433	1-32		0.613
1434	1-39	0.921	0.753
1435	1-25	0.983	0.621
1436	1-42	0.910	0.631
1437	<b></b>	0.988	0.868
1442	1-22	0.998	0.980
1448	1-20	0.918	0.753
	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	
1561	1-25	0.967	0.891
1580	1-17	0.923	0.899
1593	1-28	<del></del>	0.824
	<u> </u>	0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

SEQ 1D NO:   SEQ 1D NO:   Of config   Friority   No: of contig   Ingish	IABLEO					
of full- nucleotide sequence sequence sequence sequence sequence sequence sequence   1 1767   3573   5359   784CIP2   1103     2 1788   3574   5360   784CIP2   2673     3 1789   3575   5362   784CIP2   3576     4 1790   3576   5362   784CIP2   3576     5 1791   3577   5363   784CIP2   5556     6 1792   3578   5364   784CIP2   5556     6 1792   3578   5364   784CIP2   5556     7 1793   3579   5365   784CIP2   5556     8 1794   3580   5366   784CIP2   5556     8 1795   3581   5364   784CIP2   5556     10 1796   3582   5368   784CIP2   5556     11 1797   3581   5364   784CIP2   5556     12 1798   3584   5370   784CIP2   1556     13 1799   3586   5371   784CIP2   1556     14 1802   3588   5374   784CIP2   15577     16 1802   3588   5375   784CIP2   15577     17 1803   3599   5376   784CIP2   15577     18 1804   3590   5376   784CIP2   15577     19 1805   3581   5367   784CIP2   15577     19 1806   3592   5376   784CIP2   15577     19 1807   3593   5367   784CIP2   15577     19 1808   3594   5370   784CIP2   15577     19 1808   3594   5375   784CIP2   15577     19 1809   3589   5376   784CIP2   15577     19 1806   3592   5378   784CIP2   15577     19 1807   3593   5377   784CIP2   15577     19 1808   3594   5367   784CIP2   15577     19 1808   3594   5377   784CIP2   15577     19 1808   3594   5377   784CIP2   15577     19 1808   3595   5378   784CIP2   15577     19 1808   3593   5376   784CIP2   15577     19 1808   3594   5367   784CIP2   15577     19 1808   3593   5376   784CIP2   15577     19 1808   3594   5367   784CIP2   15577     19 1809   3595   5367   784CIP2   15577     20 1806   3592   5378   784CIP2   15577     21 1807   3593   5379   784CIP2   15577     22 1808   3594   5367   784CIP2   15577     31 1817   3605   5387   784CIP2   15577     31 1817   3605   5387   784CIP2   15577     31 1819   3606   5392   784CIP2   15577     31 1819   3607   5393   784CIP2   15577     31 1819   3607   5393   784CIP2   15577     31 1819   3607   5393   784CIP2   15577     31 1819   3607   5393   784CIP2   15577     31 18	_		SEQ ID NO:	SEQ ID	Priority	SEQ ID
nucleotide   sequence   sequence   sequence   sequence   sequence   1   1797   3573   5355   764CTP2   1   103   3648   77   37   37   37   37   37   37   3						
Sequence	1				corresponding	U.S.S.N.
Sequence		_	sequence	) - <b>-</b>	SEQ ID NO: in	09/488,725
1   1797   3573   5359   784CIP2   103	sequence			sequence		
2 1.788 3574 5360 784CIP2 2 2673 3 1789 3575 5361 784CIP2 2 2673 3 1789 3575 5361 784CIP2 3 4117 4 1780 3576 5362 784CIP2 4 5556 5 1791 3577 5363 784CIP2 5 5562 6 1792 3578 5364 784CIP2 6 5562 7 1793 3579 5365 784CIP2 7 5562 8 1794 3580 5366 784CIP2 8 5562 9 1795 3581 5367 784CIP2 9 5563 10 1796 3582 5368 784CIP2 1 5562 9 1795 3581 5367 784CIP2 9 5563 11 1797 3583 5369 784CIP2 1 5562 12 1798 3584 5370 784CIP2 1 5562 12 1798 3585 5371 784CIP2 1 5689 13 1799 3585 5371 784CIP2 11 5565 14 1800 3586 5372 784CIP2 11 5745 15 1801 3587 5373 784CIP2 12 5689 15 18 18 18 18 18 18 18 18 18 18 18 18 18			<u> </u>	<u> </u>		
3	1					1103
4 1.790 3576 5362 784CIP2 4 5555 5 1791 3577 5363 784CIP2 5 5562 6 1792 3578 5363 784CIP2 5 5562 7 1793 3579 5365 784CIP2 7 5562 7 1793 3579 5365 784CIP2 7 5562 8 1794 3580 5366 784CIP2 8 5562 9 1795 3581 5367 784CIP2 9 5563 10 1796 3582 5368 784CIP2 10 5564 11 1797 3583 5369 784CIP2 10 5564 11 1797 3583 5369 784CIP2 11 5565 12 1798 3584 5370 784CIP2 11 5565 13 1798 3585 5371 784CIP2 12 5689 13 1799 3585 5371 784CIP2 13 5729 14 1800 3586 5372 784CIP2 14 5745 15 1801 3587 5373 784CIP2 15 5777 16 1802 3588 5377 784CIP2 15 5777 17 1803 3589 5375 784CIP2 15 5777 18 18 1804 3590 5376 784CIP2 15 5777 19 1805 3589 5375 784CIP2 15 5777 20 1806 3599 5376 784CIP2 12 5804 20 1806 3592 5378 784CIP2 15 5052 21 1807 3593 5379 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5805 25 1811 3597 5383 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5804 24 1810 3596 5382 784CIP2 2 5804 25 1811 3597 5383 784CIP2 2 5805 26 1812 3598 5381 784CIP2 2 5804 27 1813 3599 5375 784CIP2 2 5804 28 1814 3600 5386 784CIP2 2 5805 30 1815 3601 5395 5381 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 2 5804 31 1807 3593 5395 784CIP2 3 5805 30 1815 3601 5397 784CIP2 3 5005 31 1817 3603 5388 784CIP2 3 6005 31 1817 3603 5389 5385 784CIP2 3 6005 31 1817 3603 5389 5395 784CIP2 3 6005 31 1818 3604 5390 784CIP2 3 6005 31 1818 3604 5390 784CIP2 3 6005 31 1819 3605 5391 784CIP2 3 6005 31 1819 3605 5391 784CIP2 3 6015 31 1817 3603 5389 784CIP2 3 6015 31 1817 3603 5389 784CIP2 3 6015 31 1817 3603 5389 784CIP2 3 6015 31 1817 3603 5389 784CIP2 3 6015 31 1817 3603 5380 784CIP2 3 6015 31 1817 3603 5380 784CIP2 3 6015 31 1817 3603 5380 784CIP2 3 6015 31 1818 3604 5390 784CIP2 3 6015 31 1819 3605 5391 784CIP2 3 6015 31 1819 3605 5391 784CIP2 3 6015 31 1819 3605 5391 784CIP2 3 6015 31 1819 3605 5391 784CIP2 3 6015 31 1819				,	<u> </u>	2673
5 1.791 3577 5363 784CIP2 55562 6 1792 3578 5364 784CIP2 6 55662 7 1793 3579 5365 784CIP2 7 5562 8 1794 3380 5366 784CIP2 8 5562 9 1795 3581 5367 784CIP2 9 5563 10 1795 3582 5368 784CIP2 10 5564 11 1 797 3583 5369 784CIP2 11 5565 12 1798 3564 5370 784CIP2 11 5565 12 1798 3564 5370 784CIP2 11 5565 13 1799 3565 5371 784CIP2 11 5565 14 1800 3566 5372 784CIP2 12 5669 13 1799 3565 5371 784CIP2 11 5565 14 1800 3566 5372 784CIP2 14 5745 15 1801 3587 5373 784CIP2 17 5789 16 1802 3588 5376 784CIP2 17 5789 17 1803 3589 5375 784CIP2 17 5789 18 18 1804 3590 5376 784CIP2 17 5789 19 1805 3591 5377 784CIP2 17 5789 19 1806 3592 5378 784CIP2 19 5805 21 1807 3593 5379 784CIP2 20 5805 21 1807 3593 5379 784CIP2 20 5805 21 1807 3593 5379 784CIP2 20 5805 21 1807 3593 5379 784CIP2 20 5805 21 1807 3593 5379 784CIP2 20 5805 21 1807 3593 5379 784CIP2 20 5805 21 1808 3594 5360 788CIP2 22 5844 24 1810 3596 5362 784CIP2 23 5844 24 1810 3596 5362 784CIP2 24 5850 25 1811 3597 5383 784CIP2 25 5844 24 1810 3596 5362 784CIP2 25 5844 24 1810 3596 5362 784CIP2 25 5844 24 1810 3596 5362 784CIP2 25 5867 26 1812 3598 5381 784CIP2 25 5867 27 1813 3599 5385 784CIP2 25 5867 28 1814 3600 5386 784CIP2 25 5973 28 1814 3600 5386 784CIP2 25 5973 30 1815 3601 5387 784CIP2 36 6005 31 1817 3603 5399 784CIP2 37 6005 31 1817 3603 5399 784CIP2 37 6005 31 1817 3603 5399 784CIP2 37 6005 31 1817 3603 5399 784CIP2 37 6005 31 1817 3603 5399 784CIP2 38 6005 31 1817 3603 5399 784CIP2 36 6015 34 1820 3606 5392 784CIP2 36 6015 35 1821 3607 5393 784CIP2 36 6015 36 1822 3608 5394 784CIP2 36 6015 37 1823 3609 5395 784CIP2 36 6015 36 1822 3608 5394 784CIP2 36 6015 37 1823 3609 5395 784CIP2 37 6018 38 1819 3605 5391 784CIP2 36 6015 36 1822 3608 5394 784CIP2 36 6015 37 1823 3609 5395 784CIP2 37 6018 39 1825 3611 5397 784CIP2 36 6015 36 1822 3608 5394 784CIP2 37 6018 39 1825 3611 5397 784CIP2 36 6015 36 1822 3608 5394 784CIP2 37 6018 39 1825 3611 5397 784CIP2 38 6015 39 1828 3614 5400 784CIP2 36 6015 39 1828 3614 5400 784CIP2 36 6015 39 1828 3614 5400 784CIP2 36 6015 39 1828 361						4117
6 1.792 3578 5364 784CIP2 6 5562 7 1793 3579 5365 784CIP2 7 5562 8 1.794 3580 5366 784CIP2 8 5562 9 1795 3581 5367 784CIP2 9 5563 10 1.796 3582 5368 784CIP2 10 5564 11 1.797 3583 5369 784CIP2 11 5565 12 1798 3584 5370 784CIP2 11 5565 13 1.799 3585 5371 784CIP2 12 5689 13 1.799 3585 5371 784CIP2 13 5729 14 1800 3586 5372 784CIP2 13 5729 15 1801 3587 5373 784CIP2 14 5745 16 1802 3588 5374 784CIP2 16 5777 16 1803 3588 5374 784CIP2 16 5777 17 1803 3589 5375 784CIP2 17 5789 18 1804 3590 5376 784CIP2 17 5789 19 1805 3591 5377 784CIP2 19 5804 20 1806 3592 5378 784CIP2 19 5804 21 1807 3593 5375 784CIP2 20 5805 21 1807 3593 5375 784CIP2 21 5805 22 1808 3594 5380 784CIP2 22 5844 24 1810 3596 5382 784CIP2 22 5844 24 1810 3596 5382 784CIP2 22 5844 24 1810 3596 5382 784CIP2 22 5844 24 1810 3596 5382 784CIP2 22 5844 24 1810 3596 5382 784CIP2 23 5844 24 1810 3596 5382 784CIP2 24 5850 25 1811 3597 5383 784CIP2 25 5867 27 1813 3599 5365 784CIP2 25 5867 27 1813 3599 5365 784CIP2 27 5995 28 1814 3600 5366 784CIP2 27 5995 29 1815 3601 5387 784CIP2 29 5995 29 1815 3601 5387 784CIP2 29 5995 29 1815 3601 5387 784CIP2 29 5995 29 1815 3601 5387 784CIP2 23 5844 31 3609 3595 5381 784CIP2 24 5850 30 1815 3601 5387 784CIP2 35 6007 31 1817 3603 5389 784CIP2 39 6007 31 1817 3603 5389 784CIP2 39 6007 31 1817 3603 5389 784CIP2 39 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6007 31 1817 3603 5389 784CIP2 31 6018 34 1820 3606 5392 784CIP2 31 6018 34 1820 3606 5392 784CIP2 31 6018 34 1820 3606 5392 784CIP2 31 6018 34 1820 3606 5392 784CIP2 31 6018 35 1821 3607 5393 784CIP2 31 6018 36 1822 3608 5394 784CIP2 36 6018 37 1823 3609 5395 784CIP2 31 6018 38 1824 3610 5396 784CIP2 31 6018 39 1825 3611 5397 784CIP2 31 6018 39 1825 3611 5397 784CIP2 31 6018 39 1825 3611 5397 784CIP2 31 6018 39 1825 3611 5397 784CIP2 31 6018 39 1825 3611 784CIP2 35 6018 39 1825 3611 784CIP2 35 6018 39 1825 3611 784CI	1			1	784CIP2_4	5556
7 1.793 3.579 5365 7.84CIP.2 8 5562 8 1794 3.580 5366 784CIP.2 8 5562 9 1795 3.581 5367 784CIP.2 8 5563 10 1.796 3.582 5368 784CIP.2 10 5564 11 1.797 3.583 5369 784CIP.2 10 5564 11 1.797 3.583 5369 784CIP.2 11 5565 12 1.798 3.584 5370 784CIP.2 12 5689 13 1.799 3.585 5371 784CIP.2 12 5689 13 1.799 3.585 5371 784CIP.2 14 5745 15 1801 3.587 5373 784CIP.2 14 5745 15 1801 3.587 5373 784CIP.2 15 5777 16 1802 3.588 5374 784CIP.2 15 5777 17 1803 3.589 5375 784CIP.2 17 5789 18 1804 3.590 5375 784CIP.2 17 5789 19 1805 3.591 5377 784CIP.2 17 5789 19 1806 3.592 5379 784CIP.2 18 5792 20 1806 3.592 5379 784CIP.2 19 5804 21 1807 3.593 5379 784CIP.2 19 5804 22 1808 3.594 5380 784CIP.2 20 5805 21 1807 3.593 5379 784CIP.2 21 5805 22 1808 3.594 5380 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 23 5844 24 1810 3.596 5382 784CIP.2 24 5850 25 1811 3.597 5383 784CIP.2 25 5867 26 1812 3.598 5381 784CIP.2 26 5973 27 1813 3.599 5.385 784CIP.2 26 5973 30 1815 3.600 5.366 784CIP.2 28 5995 30 1815 3.600 5.366 784CIP.2 28 5995 31 1817 3.603 5389 784CIP.2 30 6007 32 1818 3.601 5.387 784CIP.2 30 6007 32 1818 3.604 5.390 784CIP.2 30 6007 33 1819 3.605 5381 784CIP.2 30 6007 34 1820 3.606 5.392 784CIP.2 30 6007 35 1818 3.600 5.366 784CIP.2 30 6007 36 1822 3.608 5391 784CIP.2 37 6018 36 1822 3.608 5391 784CIP.2 37 6018 37 1823 3.609 5.395 784CIP.2 37 6018 38 1824 3.600 5.366 5392 784CIP.2 36 6018 39 1825 3.611 5.397 784CIP.2 36 6018 39 1825 3.611 5.397 784CIP.2 36 6018 30 1815 3.600 5.366 784CIP.2 36 6018 31 1817 3.603 5.399 784CIP.2 36 6018 31 1817 3.603 5.399 784CIP.2 36 6018 31 1817 3.603 5.399 784CIP.2 36 6018 31 1817 3.603 5.399 784CIP.2 36 6018 31 1819 3.605 5.390 784CIP.2 36 6018 31 1819 3.605 5.390 784CIP.2 36 6018 31 1821 3.600 5.366 784CIP.2 36 6018 31 1823 3.609 5.395 784CIP.2 36 6018 31 1824 3.600 5.396 784CIP.2 36 6018 31 1828 3.611 5.397 784CIP.2 36 6018 3			1		784CIP2_5	5562
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9 1795 3581 5367 784CIP2 9 5563 10 1796 3582 5368 784CIP2 10 5564 11 1797 3583 5369 784CIP2 11 5565 12 1798 3584 5370 784CIP2 12 5686 13 1799 3585 5371 784CIP2 12 5686 13 1799 3585 5371 784CIP2 14 5745 14 1890 3586 5372 784CIP2 14 5745 15 1801 3587 5373 784CIP2 14 5745 16 1802 3588 5374 784CIP2 15 5777 17 1803 3589 5375 784CIP2 17 5789 18 1804 3590 5376 784CIP2 18 5792 19 1805 3591 5377 784CIP2 18 5792 19 1806 3592 5378 784CIP2 19 5805 20 1806 3592 5379 784CIP2 19 5805 21 1807 3593 5379 784CIP2 19 5805 22 1808 3594 5380 784CIP2 21 5805 22 1808 3594 5380 784CIP2 22 5844 24 1810 3596 5382 784CIP2 24 5850 25 1811 3597 5383 784CIP2 24 5850 26 1812 3598 5384 784CIP2 26 5973 27 1813 3599 5385 784CIP2 27 5867 26 1812 3598 5384 784CIP2 26 5973 27 1813 3599 5385 784CIP2 27 5867 28 1814 3600 5366 784CIP2 28 5995 29 1815 3601 5367 784CIP2 29 6005 30 1816 3602 5388 784CIP2 28 5995 29 1815 3601 5367 784CIP2 29 6005 31 1817 3603 5386 784CIP2 28 5995 29 1815 3601 5367 784CIP2 29 6005 31 1817 3603 5386 784CIP2 30 6007 31 1817 3603 5386 784CIP2 31 6007 32 1818 3604 5330 784CIP2 31 6007 33 1819 3605 5381 784CIP2 32 6009 33 1819 3605 5391 784CIP2 30 6007 31 1817 3603 5389 784CIP2 31 6007 32 1818 3604 5330 784CIP2 38 6015 34 1820 3606 5392 784CIP2 36 6015 36 1822 3608 5394 784CIP2 37 6018 39 1825 3661 5397 784CIP2 36 6018 39 1825 3661 5397 784CIP2 37 6018 44 1820 3606 5392 784CIP2 36 6018 45 1821 3609 5395 784CIP2 36 6018 46 1822 3608 5394 784CIP2 36 6018 47 1823 3609 5395 784CIP2 37 6018 48 1824 3610 5396 784CIP2 36 6018 49 1836 3604 5390 784CIP2 37 6018 40 1826 3612 5398 784CIP2 36 6018 41 1827 3613 5399 784CIP2 36 6018 41 1827 3613 5399 784CIP2 37 6018 42 1828 3614 5400 784CIP2 37 6018 43 1829 3606 5392 784CIP2 37 6018 44 1830 3616 5402 784CIP2 37 6018 45 1831 3617 5603 784CIP2 37 6018 46 1832 3618 5404 784CIP2 36 6018 50 1836 3624 5400 784CIP2 47 6177 50 1836 3624 5400 784CIP2 55 6284 51 1831 3627 5605 784CIP2 55 6284 51 1831 3629 5405 784CIP2 55 6284 51 1831 3629 5405 784CIP2 55 6284 51 1831 3629 5405 784CIP2 55 6445			1	1	784CIP2_7	5562
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12			3582	5368	784CIP2 10	5564
13			3583	5369	784CIP2 11	5565
14         1800         3586         5372         784CIP2_14         5745           15         1801         3587         5373         784CIP2_15         5777           16         1802         3588         5374         784CIP2_16         5777           17         1803         3589         5375         784CIP2_17         5789           18         1804         3590         5376         784CIP2_18         5792           19         1805         3591         5377         784CIP2_19         5805           20         1806         3592         5378         784CIP2_20         5805           21         1807         3593         5379         784CIP2_21         5805           22         1808         3594         5380         784CIP2_22         5844           23         1809         3595         5381         784CIP2_22         5844           24         1810         3596         5382         784CIP2_24         5850           25         1811         3597         5383         784CIP2_25         5867           26         1812         3588         5384         784CIP2_27         5995         29			3584	5370	784CIP2 12	5689
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15	L		3586	5372		
16		1801	3587	5373		
17		1802	3588	1	<del></del>	1
18	17	1803	3589			
19	18	1804	3590	5376		
20	19	1805	3591	L		
21         1807         3593         5379         784CIP2         21         5805           22         1808         3594         5380         784CIP2         22         5844           23         1809         3595         5381         784CIP2         24         5850           24         1810         3596         5382         784CIP2         24         5850           25         1811         3597         5383         784CIP2         25         5667           26         1812         3598         5384         784CIP2         27         5995           27         1813         3599         5385         784CIP2         27         5995           28         1814         3600         5386         784CIP2         28         5995           29         1815         3601         5387         784CIP2         29         6007           30         1816         3602         5388         784CIP2         30         6007           31         1819         3605         5391         784CIP2         31         6007           32         1818         3604         5390         784CIP2         31	20	1806	3592		<u> </u>	.i
22         1808         3594         5380         784CIP2_22         5844           23         1809         3595         5381         784CIP2_23         5844           24         1810         3596         5382         784CIP2_25         5867           25         1811         3597         5383         784CIP2_25         5867           26         1812         3598         5584         784CIP2_26         5973           27         1813         3599         5385         784CIP2_27         5995           28         1814         3600         5386         784CIP2_28         5995           29         1815         3601         5387         784CIP2_29         6005           30         1816         3602         5388         794CIP2_30         6005           31         1817         3603         5389         784CIP2_31         6007           32         1818         3604         5390         784CIP2_31         6007           33         1819         3605         5391         784CIP2_31         6015           34         1820         3606         5392         784CIP2_34         6015           35	21	1807	3593			
23         1809         3595         5381         784CIP2         23         5844           24         1810         3596         5382         784CIP2         24         5850           25         1811         3597         5383         784CIP2         25         5867           26         1812         3598         5384         784CIP2         26         5973           27         1813         3599         5385         784CIP2         27         5995           28         1814         3600         5386         784CIP2         29         6005           30         1815         3601         5387         784CIP2         29         6005           30         1815         3601         5388         784CIP2         30         6007           31         1817         3603         5388         784CIP2         30         6007           32         1818         3604         5390         784CIP2         32         6009           33         1819         3605         5391         784CIP2         32         6009           34         1820         3606         5392         784CIP2         34	22	1808	3594		L	
24         1810         3596         5382         784CIP2_24         5850           25         1811         3597         5383         784CIP2_25         5867           26         1812         3598         5384         784CIP2_26         5973           27         1813         3599         5385         784CIP2_27         5995           28         1814         3600         5386         784CIP2_28         5995           29         1815         3601         5387         784CIP2_39         6005           30         1815         3602         5388         784CIP2_30         6007           31         1817         3603         5389         784CIP2_31         6007           32         1818         3604         5390         784CIP2_31         6007           33         1819         3605         5391         784CIP2_33         6012           34         1820         3606         5392         784CIP2_34         6015           35         1821         3607         5393         784CIP2_35         6016           37         1823         3609         5395         784CIP2_37         6018           38	23	1809	1			.I.
25         1811         3597         5383         784CIP2 25         5867           26         1812         3598         5384         784CIP2 26         5973           27         1813         3599         5385         784CIP2 27         5995           28         1814         3600         5386         784CIP2 28         5995           29         1815         3601         5387         784CIP2 29         6005           30         1815         3602         5388         784CIP2 30         6007           31         1817         3603         5389         784CIP2 31         6007           32         1818         3604         5390         784CIP2 32         6009           33         1819         3605         5391         784CIP2 32         6009           34         1820         3606         5392         784CIP2 33         6015           35         1821         3607         5393         784CIP2 34         6015           36         1822         3608         5394         784CIP2 35         6016           37         1823         3609         5395         784CIP2 34         6018           38	24	1810			1	
26         1.812         3598         5384         784CIP2_26         5973           27         1.813         3599         5385         784CIP2_27         5995           28         1.814         3600         5386         784CIP2_29         6005           30         1.815         3601         5387         784CIP2_29         6005           30         1.817         3603         5388         784CIP2_31         6007           31         1.817         3603         5389         784CIP2_31         6007           32         1.818         3604         5390         784CIP2_32         6009           33         1.819         3605         5351         784CIP2_32         6009           34         1.820         3606         5392         784CIP2_34         6015           35         1.821         3607         5393         784CIP2_34         6015           36         1.822         3608         5394         784CIP2_34         6016           37         1.823         3609         5395         784CIP2_37         6018           38         1.824         3610         5396         784CIP2_37         6018	25	. 1811	4		<u> </u>	
27         1813         3599         5385         784CIP2_27         5995           28         1814         3600         5386         784CIP2_28         5995           29         1815         3601         5387         784CIP2_30         6005           30         1815         3602         5388         784CIP2_30         6007           31         1817         3603         5389         784CIP2_31         6007           32         1818         3604         5390         784CIP2_31         6007           33         1819         3605         5351         784CIP2_33         6012           34         1820         3606         5392         784CIP2_33         6015           35         1821         3607         5393         784CIP2_34         6015           36         1822         3608         5394         784CIP2_35         6016           37         1823         3609         5395         784CIP2_37         6018           38         1824         3610         5396         784CIP2_38         6018           40         1826         3612         5398         784CIP2_39         6018           40	26	1812	<u> </u>			
28         1814         3600         5386         784CIP2_28         5995           29         1815         3601         5387         784CIP2_29         6005           30         1816         3602         5388         784CIP2_30         6007           31         1817         3603         5389         784CIP2_31         6007           32         1818         3604         5390         784CIP2_32         6009           33         1819         3605         5351         784CIP2_33         6012           34         1820         3606         5392         784CIP2_34         6015           35         1821         3607         5393         784CIP2_35         6016           36         1822         3608         5394         784CIP2_35         6016           37         1823         3609         5395         784CIP2_37         6018           39         1825         3611         5396         784CIP2_37         6018           40         1826         3612         5398         784CIP2_37         6018           41         1827         3613         5399         784CIP2_41         6070           42	27	1813	4			1
29         1815         3601         5387         784CIP2         29         6005           30         1815         3602         5388         784CIP2         30         6007           31         1817         3603         5389         784CIP2         31         6007           32         1818         3604         5390         784CIP2         32         6007           33         1819         3605         5391         784CIP2         33         6012           34         1820         3606         5392         784CIP2         34         6015           35         1821         3607         5393         784CIP2         35         6016           36         1822         3608         5394         784CIP2         36         6016           37         1823         3609         5395         784CIP2         37         6018           38         1824         3610         5396         784CIP2         37         6018           39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         39	28	1814	.1	<u></u>		<u> </u>
30	29	1815	I	L		J
31         1817         3603         5389         784C1P2_31         6007           32         1818         3604         5390         784C1P2_32         6009           33         1819         3605         5391         784C1P2_33         6012           34         1820         3606         5392         784C1P2_34         6015           35         1821         3607         5393         784C1P2_35         6016           36         1822         3608         5394         784C1P2_36         6016           37         1823         3609         5395         784C1P2_37         6018           38         1824         3610         5396         784C1P2_37         6018           39         1825         3611         5397         784C1P2_38         6018           40         1826         3612         5398         784C1P2_39         6018           41         1827         3613         5399         784C1P2_40         6023           41         1827         3613         5399         784C1P2_41         6070           42         1828         3614         5400         784C1P2_42         6081           43	30	1815	4			
32         1818         3604         5390         784CIP2 32         6009           33         1819         3605         5391         784CIP2 33         6012           34         1820         3606         5392         784CIP2 34         6015           35         1821         3607         5393         784CIP2 35         6016           36         1822         3608         5394         784CIP2 36         6016           37         1823         3609         5395         784CIP2 37         6018           38         1824         3610         5396         784CIP2 38         6018           39         1825         3611         5397         784CIP2 39         6018           40         1826         3612         5398         784CIP2 39         6018           41         1827         3613         5399         784CIP2 39         6018           41         1827         3613         5399         784CIP2 40         6023           41         1828         3614         5400         784CIP2 41         6070           42         1828         3615         5401         784CIP2 43         6089           44	31	1817	<u> </u>			
33         1819         3605         5391         784CIP2         33         6012           34         1820         3606         5392         784CIP2         34         6015           35         1821         3607         5393         784CIP2         35         6016           36         1822         3608         5394         784CIP2         36         6016           37         1823         3609         5395         784CIP2         37         6018           38         1824         3610         5396         784CIP2         38         6018           39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         39         6018           41         1827         3613         5399         784CIP2         40         6023           41         1827         3613         5399         784CIP2         41         6070           42         1828         3614         5400         784CIP2         42         6081           43         1829         3615         5401         784CIP2         43	32		<u>.                                    </u>			
34         1820         3606         5392         784CIP2         34         6015           35         1821         3607         5393         784CIP2         35         6016           36         1822         3608         5394         784CIP2         36         6016           37         1823         3609         5395         784CIP2         37         6018           38         1824         3610         5396         784CIP2         39         6018           39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         40         6023           41         1827         3613         5399         764CIP2         41         6070           42         1828         3614         5400         784CIP2         41         6070           42         1828         3614         5400         784CIP2         42         6081           43         1829         3615         5401         784CIP2         43         6089           44         1830         3616         5402         784CIP2         43	33		<del></del>			
35         1821         3607         5393         784CIP2         35         6016           36         1822         3608         5394         784CIP2         36         6016           37         1823         3609         5395         784CIP2         37         6018           38         1824         3610         5396         784CIP2         38         6018           39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         39         6018           40         1826         3612         5398         784CIP2         40         6023           41         1827         3613         5399         784CIP2         41         6070           42         1828         3614         5400         784CIP2         42         6081           43         1829         3615         5401         784CIP2         43         6089           44         1830         3616         5402         784CIP2         44         6118           45         1831         3617         5403         784CIP2         45	34	_1				<u> </u>
36         1822         3608         5394         784CIP2         36         6016           37         1823         3609         5395         784CIP2         37         6018           38         1824         3610         5396         784CIP2         38         6018           39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         40         6023           41         1827         3613         5399         784CIP2         41         6070           42         1828         3614         5400         784CIP2         41         6070           42         1828         3615         5401         784CIP2         42         6081           43         1829         3615         5401         784CIP2         43         6089           44         1830         3616         5402         784CIP2         44         6118           45         1831         3617         5403         784CIP2         45         6118           46         1832         3618         5404         784CIP2         46	35	1821			<u> </u>	
37         1823         3609         5395         784CIP2 37         6018           38         1824         3610         5396         784CIP2 38         6018           39         1825         3611         5397         784CIP2 39         6018           40         1826         3612         5398         784CIP2 40         6023           41         1827         3613         5399         784CIP2 41         6070           42         1828         3614         5400         784CIP2 42         6081           43         1829         3615         5401         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           45         1831         3617         5403         784CIP2 44         6118           45         1831         3617         5403         784CIP2 45         6118           46         1832         3618         5404         784CIP2 47         6177           48	36			<u></u>		
38         1824         3610         5396         784CIP2 38         6018           39         1825         3611         5397         784CIP2 39         6018           40         1826         3612         5398         784CIP2 40         6023           41         1827         3613         5399         784CIP2 41         6070           42         1828         3614         5400         784CIP2 42         6081           43         1829         3615         5401         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           44         1830         3616         5402         784CIP2 43         6089           45         1831         3617         5403         784CIP2 45         6118           46         1832         3618         5404         784CIP2 45         6118           47         1833         3619         5405         784CIP2 47         6177           48	37					1
39         1825         3611         5397         784CIP2         39         6018           40         1826         3612         5398         784CIP2         40         6023           41         1827         3613         5399         784CIP2         41         6070           42         1828         3614         5400         784CIP2         42         6081           43         1829         3615         5401         784CIP2         43         6089           44         1830         3616         5402         784CIP2         44         6118           45         1831         3617         5403         784CIP2         45         6118           46         1832         3618         5404         784CIP2         46         6130           47         1833         3619         5405         784CIP2         46         6130           47         1833         3629         5405         784CIP2         47         6177           48         1834         3620         5406         784CIP2         47         6177           49         1835         3621         5407         784CIP2         49	38					
40         1826         3612         5398         784CIP2 40         6023           41         1827         3613         5399         784CIP2 41         6070           42         1828         3614         5400         784CIP2 42         6081           43         1829         3615         5401         784CIP2 43         6089           44         1830         3616         5402         784CIP2 44         6118           45         1831         3617         5403         784CIP2 45         6118           46         1832         3618         5404         784CIP2 46         6130           47         1833         3619         5405         784CIP2 47         6177           48         1834         3620         5406         784CIP2 47         6177           48         1834         3620         5406         784CIP2 49         6191           50         1835         3621         5407         784CIP2 49         6191           50         1836         3622         5408         784CIP2 50         6204           51         1837         3623         5409         784CIP2 51         6204           52	39		<u> </u>			L (
41         1827         3613         5399         784CIP2_41         6070           42         1828         3614         5400         784CIP2_42         6081           43         1829         3615         5401         784CIP2_43         6089           44         1830         3616         5402         784CIP2_44         6118           45         1831         3617         5403         784CIP2_45         6118           46         1832         3618         5404         784CIP2_46         6130           47         1833         3619         5405         784CIP2_47         6177           48         1834         3620         5406         784CIP2_47         6177           48         1834         3620         5406         784CIP2_48         6189           49         1835         3621         5407         784CIP2_48         6189           50         1836         3622         5408         784CIP2_49         6191           50         1836         3622         5408         784CIP2_50         6204           51         1837         3623         5409         784CIP2_51         6204           52						
42         1828         3614         5400         784CIP2 42         6081           43         1829         3615         5401         784CIP2 43         6089           44         1830         3616         5402         784CIP2 44         6118           45         1831         3617         5403         784CIP2 45         6118           46         1832         3618         5404         784CIP2 46         6130           47         1833         3619         5405         784CIP2 47         6177           48         1834         3620         5406         784CIP2 47         6177           48         1835         3621         5407         784CIP2 48         6189           49         1835         3621         5407         784CIP2 49         6191           50         1836         3622         5408         784CIP2 50         6204           51         1837         3623         5409         784CIP2 51         6204           52         1838         3624         5410         784CIP2 52         6284           53         1839         3625         5411         784CIP2 53         6367           54	L					
43         1829         3615         5401         784CIP2 43         6089           44         1830         3616         5402         784CIP2 44         6118           45         1831         3617         5403         784CIP2 45         6118           46         1832         3618         5404         784CIP2 46         6130           47         1833         3619         5405         784CIP2 47         6177           48         1834         3620         5406         784CIP2 48         6189           49         1835         3621         5407         784CIP2 49         6191           50         1936         3622         5408         784CIP2 50         6204           51         1837         3623         5409         784CIP2 51         6204           52         1838         3624         5410         784CIP2 52         6284           53         1839         3625         5411         784CIP2 53         6367           54         1840         3626         5412         784CIP2 54         6436           55         1841         3627         5413         784CIP2 55         6442           56	42		L .			I
44         1830         3616         5402         784CIP2_44         6118           45         1831         3617         5403         784CIP2_45         6118           46         1832         3618         5404         784CIP2_46         6130           47         1833         3619         5405         784CIP2_47         6177           48         1834         3620         5406         784CIP2_48         6189           49         1835         3621         5407         784CIP2_49         6191           50         1836         3622         5408         784CIP2_50         6204           51         1837         3623         5409         784CIP2_51         6204           52         1838         3624         5410         784CIP2_52         6284           53         1839         3625         5411         784CIP2_52         6284           53         1839         3625         5411         784CIP2_53         6367           54         1840         3626         5412         784CIP2_55         6442           55         1841         3627         5413         784CIP2_55         6442           56	43					
45 1831 3617 5403 784CIP2_45 6118 46 1832 3618 5404 784CIP2_46 6130 47 1833 3619 5405 784CIP2_47 6177 48 1834 3620 5406 784CIP2_48 6189 49 1835 3621 5407 784CIP2_49 6191 50 1836 3622 5408 784CIP2_50 6204 51 1837 3623 5409 784CIP2_51 6204 52 1838 3624 5410 784CIP2_52 6284 53 1839 3625 5411 784CIP2_53 6367 54 1840 3626 5412 784CIP2_53 6367 55 1841 3627 5413 784CIP2_55 6442 56 1842 3628 5414 784CIP2_55 6445 57 1843 3629 5415 784CIP2_57 6457 58 1844 3630 5416 784CIP2_58 6458	44				L — ""	
46         1832         3618         5404         784CIP2_46         6130           47         1833         3619         5405         784CIP2_47         6177           48         1834         3620         5406         784CIP2_48         6189           49         1835         3621         5407         784CIP2_49         6191           50         1836         3622         5408         784CIP2_50         6204           51         1837         3623         5409         784CIP2_51         6204           52         1838         3624         5410         784CIP2_52         6284           53         1839         3625         5411         784CIP2_53         6367           54         1840         3626         5412         784CIP2_54         6436           55         1841         3627         5413         784CIP2_55         6442           56         1842         3628         5414         784CIP2_55         6445           57         1843         3629         5415         784CIP2_58         6458           58         1844         3630         5416         784CIP2_58         6458	L					
47         1833         3619         5405         784CIP2 47         6177           48         1834         3620         5406         784CIP2 48         6189           49         1835         3621         5407         784CIP2 49         6191           50         1836         3622         5408         784CIP2 50         6204           51         1837         3623         5409         784CIP2 51         6204           52         1838         3624         5410         784CIP2 52         6284           53         1839         3625         5411         784CIP2 53         6367           54         1840         3626         5412         784CIP2 54         6436           55         1841         3627         5413         784CIP2 55         6442           56         1842         3628         5414         784CIP2 55         6445           57         1843         3629         5415         784CIP2 57         6457           58         1844         3630         5416         784CIP2 58         6458	46					
48 1834 3620 5406 784CIP2 48 6189 49 1835 3621 5407 784CIP2 49 6191 50 1836 3622 5408 784CIP2 50 6204 51 1837 3623 5409 784CIP2 51 6204 52 1838 3624 5410 784CIP2 52 6284 53 1839 3625 5411 784CIP2 53 6367 54 1840 3626 5412 784CIP2 54 6436 55 1841 3627 5413 784CIP2 55 6442 56 1842 3628 5414 784CIP2 56 6445 57 1843 3629 5415 784CIP2 57 6457 58 1844 3630 5416 784CIP2 58 6458						L
49         1835         3621         5407         784C1P2_49         6191           50         1936         3622         5408         784C1P2_50         6204           51         1837         3623         5409         784C1P2_51         6204           52         1838         3624         5410         784C1P2_52         6284           53         1839         3625         5411         784C1P2_53         6367           54         1840         3626         5412         784C1P2_54         6436           55         1841         3627         5413         784C1P2_55         6442           56         1842         3628         5414         784C1P2_56         6445           57         1843         3629         5415         784C1P2_57         6457           58         1844         3630         5416         784C1P2_58         6458						
50         1836         3622         5408         784CIP2 50         6204           51         1837         3623         5409         784CIP2 51 .         6204           52         1838         3624         5410         784CIP2 52 .         6284           53         1839         3625         5411         784CIP2 53 .         6367           54         1840         3626         5412         784CIP2 54 .         6436           55         1841         3627         5413         784CIP2 55 .         6442           56         1842         3628         5414         784CIP2 56 .         6445           57         1843         3629         5415         784CIP2 57 .         6457           58         1844         3630         5416         784CIP2 58 .         6458	L	<del></del>				
51         1837         3623         5408         784CIP2_51         6204           52         1838         3624         5410         784CIP2_52         6284           53         1839         3625         5411         784CIP2_53         6367           54         1840         3626         5412         784CIP2_54         6436           55         1841         3627         5413         784CIP2_55         6442           56         1842         3628         5414         784CIP2_56         6445           57         1843         3629         5415         784CIP2_57         6457           58         1844         3630         5416         784CIP2_58         6458						
52     1838     3624     5410     784CIP2_52     6284       53     1839     3625     5411     784CIP2_53     6367       54     1840     3626     5412     784CIP2_54     6436       55     1841     3627     5413     784CIP2_55     6442       56     1842     3628     5414     784CIP2_56     6445       57     1843     3629     5415     784CIP2_57     6457       58     1844     3630     5416     784CIP2_58     6458		<del></del>				
53     1839     3625     5411     784CIP2_53     6367       54     1840     3626     5412     784CIP2_54     6436       55     1841     3627     5413     784CIP2_55     6442       56     1842     3628     5414     784CIP2_56     6445       57     1843     3629     5415     784CIP2_57     6457       58     1844     3630     5416     784CIP2_58     6458						
54     1840     3626     5412     784CIP2_54     6436       55     1841     3627     5413     784CIP2_55     6442       56     1842     3628     5414     784CIP2_56     6445       57     1843     3629     5415     784CIP2_57     6457       58     1844     3630     5416     784CIP2_58     6458						
55         1841         3627         5413         784CIP2_55         6442           56         1842         3628         5414         784CIP2_56         6445           57         1843         3629         5415         784CIP2_57         6457           58         1844         3630         5416         784CIP2_58         6458						
56     1842     3628     5414     784CIP2_56     6445       57     1843     3629     5415     784CIP2_57     6457       58     1844     3630     5416     784CIP2_58     6458						
57 1843 3629 5415 784CIP2 57 6457 58 1844 3630 5416 784CIP2 58 6458		<del> </del>				
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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sequence	peptide sequence		sequence	application	1
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61	1846			784CIP2_60 784CIP2_61	6472
	1847	3633	5419		
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIPZ_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2 70	6592
71	1857	3643	5429	784CIP2 71	6645
72	1358	3644	5430	784CIP2 72	6671
73	1959	3645	5431	784CIP2 73	6763
74	1860	3646	5432	784CIP2 74	6763
75	1861	3647	5433	784CIP2 75	6786
76	1862	3648	5434	784CIP2 76	6824
77	1863	3649	5435	784CIP2_76	6830
78	1864	3649	5435	784CIP2_77	6831
					6832
79	1865	3651	5437	784CIP2_79	
80	1866	3652	5438	784CIP2_80	6834
. 81	1857	3653	5439	784CIP2_81	6834
82	1858	3654	5440	784CIP2_82	6835
83	1869	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784CIP2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5447	784CIP2_89	6961
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91	1877	3663	5449	784CIP2 91	6973
92	1878	3664	5450	784CIP2 93	7007
93	. 1879	3665	5451	784CIP2 94	7018
94	1880	3666	5452	784CIP2 95	7019
95	1881	3667	5453	784CIP2 96	7020
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101	L		5458		
101	1887	3673		784CIP2_102	7029 7031
102		3674	5460	784CIP2_103	,
103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
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107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
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115	1901	3687	5473	784CIP2 116	7094
116	1902	3688	5474	784CIP2 117	7106
117	1903	3689	5475	784CIP2_117 784CIP2_118	7107
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119	1904	3690	5476	784CIP2_119	
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nucleotide	length	sequence	of contig	corresponding SEQ ID NO: in	U.S.S.N.
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122	1908	3694	5480	784CIP2 123	7154
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124	1910	3696	5482	784CIP2 125	7169
125	1911	3697	5483	784CIP2 126	7185
126	1912	3698	5484	784CIP2 127	7197
127	1913	3699	5485	784CIP2 128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
138	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
140	1926	3712	5498 .	784CIP2_141	7282
141	1927	3713	5499	784CIP2_142	7288
143	1928	3714	5500	784CIP2_143	7291
144	1929	3715	5501	784CIP2_144	7293
145	1930	3716	5502	784CIP2_145	7294
146	1932	3717	5503	784CIPZ_146	7299
147	1932	3718	5504	784CIP2_147	7300
148	1934	3719	5505	784CIP2_148	7312
149	1935	3720 3721	5506	784CIP2_149	7313
150	1936	3721	5507	784CIP2_150	7315
151	1937	3723	5508 5509	784CIP2_151	7318
152	1938	3724	5510	784CIP2_152	7321
153	1939	3725	5511	784CIP2_153 784CIP2_154	7330
154	1940	3726	5512	784CIP2_154 784CIP2_155	7331
155	1941	3727	5513	784CIP2_155	7333
156	1942	3728	5514	784CIP2_150	7350 7352
157	1943	3729	5515	784CIP2 158	7384
158	1944	3730	5516	784CIP2 159	7403
159	1945	3731	5517	784CIP2 160	7431
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161	1947	3733	5519	784CIP2 162	7453
162	1948	3734	5520	784CIP2 163	7467
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166	1952	3738	5524	784CIP2 167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2 169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	. 7578
172	1958	3744	5530	784CIP2_173	7583
173	1959	3745	5531	784CIP2 174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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187	1973	3759	5545	784CIP2_189	7657
188	1974	3760	5546 5547	784CIP2_190	7657
189	1975	3761		784CIP2_191	7662
190	1976	3762	5548 5549	784CIP2_192	7668
191	1977	3763		784CIP2_193	7673
192	1978	3764	5550 5551	784CIP2_194	7690
193	1979	3765	5552	784CIP2_193	7700
194	1980	3766 3767	5553	784CIP2_198	7709
195	1981	3768	5554	784CIP2 198	7736
196	1982	3769	5555	784CIP2 199	7737
197	1983 1984	3769	5556 5556	784CIP2_199	7744
198	1984	3771	5557	784CIP2_200	7771
199 200	1985	3772	5558	784CIP2_201	7786
200	1986	3773	5559	784CIP2_202	7791
201	1988	3774	5560	784CIP2_203	7797
202	1988	3775	5561	784CIP2 205	7806
203	1990	3776	5562	784CIP2 206	7812
205	1991	3777	5563	784CIP2 207	7812
205	1992	3778	5564	784CIP2 208	7818
207	1993	3779	5565	784CIP2 209	7822
208	1994	3780	5566	784CIP2 210	7827
209	1995	3781	5567	784CIP2 211	7830
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211	1997	3783	5569	784CIP2 214	7840
212	1998	3784	5570	784CIP2 215	7858
213	1999	3785	5571	784CIP2 216	7858
214	2000	3786	5572	784CIP2 217	7861
215	2001	3787	5573	784CIP2_218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137 8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5501	784CIP2_246	8161
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SEQ ID NO: of full-	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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nucleotide	length	sequence	of contig	corresponding	U.S.S.N.
sequence	peptide	sequence	peptide sequence	SEQ ID NO: in priority	09/488,729
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246	2032	3818	5604	784CIP2 249	8196
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249	2035	3821	5607	784CIP2 252	8220
250	2036	3822	5608	784CIP2 253	8238
251	2037	3823	5609	784CIP2 254	8254
252	2038	3824	5610	784CIP2 255	8255
253	2039	3825	5611	784CIP2 256	8288
254	2040	3826	5612	784CIP2 257	8296
255	2041	3827	5€13	784CIP2 258	8329
256	2042	3828	5614	784CIP2 259	8362
257	2043	3829	5615	784CIP2 260	8429
258	2044	3830	5616	784CIP2 261	8436
259	2045	3831	5617	784CIP2 262	8448
260	2046	3832	5618	784CIP2 263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264 265	2050	3836	5622	784CIP2_268	8509
266	2051	3837	5623	784CIP2_269	8515
267	2052	3838	5624	784CIP2_270	8519
268	2053	3839	5625	784CIP2_271	8530
269	2054	3840	5626	784CIP2_272	8532
270	2056	3841 3842	5627	784CIP2_273	8532
271	2057	3843	5628	784CIP2_274	B539
272	2058	3844	5629 5630	784CIP2_275	8541
273	2059	3845	5631	784CIP2_276 784CIP2_277	8543
274	2060	3846	5632	784CIP2_277	8593 8595
275	2061	3847	5633	784CIP2_278	8615
276	2062	3848	5634	784CIP2 280	8620
277	2063	3849	5635	784CIP2 281	8621
278	2064	3850	5636	784CIP2 282	8623
279	2065	3851	5637	784CIP2 283	8625
280	2066	3852	5638	784CIP2 284	8628
281	2067	3853	5639	784CIP2 285	8628
282	2068	3854	5640	784CIP2 286	8629
283	2069	3855	5641	784CIP2_287	8630
284	2070	3856	5642	784CIP2_288	8631
285 286	2071	3857	5643	784CIP2_289	8633
287	2072	3858	5644	784CIP2_290	8634
288	2073	3859	5645	784CIP2_291	8635
289	2074	3860	5646	784CIP2_292	8636
290	2075	3861 3862	5647	784CIP2_293	8659
291	2077		5648	784CIP2_294	8660
292	2078	3863 3864	5649 5650	784CIP2_295	8667
293	2079	3865	5650	784CIP2_296	8667
294	2080	3866	5652	784CIP2_297	8685
295	2081	3867	5653	784CIP2_298	8805
296	2082	3868	5654	784CIP2_299 784CIP2_300	8896 8978
297	2083	3869	5655	784CIP2_300	
298	2084	3870	5656	784CIP2_301 784CIP2_302	9046 9048
299	2085	3871	5657	784CIP2_302 784CIP2_303	9116
300	2086	3872	5658	784CIP2_303 784CIP2_304	9116
301	2087	3873	5659	784CIP2_304 784CIP2_305	9195
302	2088	3874	5660	784CIP2_305	9307
303	2089	3875	5661	784CIP2_306	9307
304	2090	3876	2665	784CIP2_307 784CIP2_308	9321
305	2091	3877	5663	784CIP2_308	9405
	2092	3878		784CIP2 310	
306	2032	30/0 1	5664	/84C1P2 410 1	9406

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nucleotide	length'	sequence	peptide	SEQ ID NO: in	09/488,725
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	sequence			application	
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152
329	2115	3901	5687	784CIP2B_2	167
330	2116	3902	5688	784C1P2B_3	205
331 332	2117	3903	5689	784CIP2B_4	210
		3904 3905	5690	784CIP2B_5	225
333	2119 2120		5691	784CIP2B_6	226
334 335	2121	3906 3907	5692 5693	784CIP2B_7 784CIP2B 8	264 268
336	2122	3908	5694	784CIP2B_8 784CIP2B_9	293
337	2122	3909	5695	784CIP2B_9	293
338	2124	3910	5696	784CIP2B 11	293
339	2125	3911	5697	784CIP2B_11 784CIP2B 12	302
340	2126	3912	5698	784CIP2B 13	311
341	2127	3913	5699	784CIP2B 14	352
342	2128	3914	5700	784CIP2B 15	358
343	2129	3915	5701	784CIP2B 16	368
344	2130	3916	5702	784CIP2B 17	393
345	2131	3917	5703	784CIP2B 18	477
346	2132	3918	5704	784CIP2B 19	508
347	2133	3919	5705	784CIP2B 20	508
348	2134	3920	5706	784CIP2B 21	515
349	2135	3921	5707	784CIP2B 22	578
350	2136	3922	5708	784CIP2B 23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
353	2139	3925	5711	784CIP2B 26	594
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B 35	838
363	2149	3935	5721	784CIP2B 36	870
364	2150	3936	5722	784CIP2B 37	891
204			5723	784CIP2B 38	891
365	2151	3937	3/23		
	2151 2152	3937	5724	784CIP2B 39	921
365					
365 366	2152	3938	5724	784CIP2B_39	921

of full-	SEQ ID NO: of	SEQ ID NO: of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number_ corresponding	NO:in
nucleotide	length	sequence	peptide	SEQ ID No: in	U.S.S.N.
sequence	peptide	1	sequence	priority	09/488,72
	sequence	i		application	1
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371	2157	3943	5729	784CIP2B 44	968
372	2158	3944	5730	784CIP2B 45	992
373	2159	3945	5731	784CIP2B 46	1025
374	2160	3946	5732	784CIP2B 47	1074
375	2161	3947	5733	784CIP2B 48	1104
376	2162	3948	5734	784CIP2B 49	1114
377	2163	3949	5735	784CIP2B 50	1144
378	2164	3950	5736	784CIP2B 51	1262
379	2165	3951	5737	784CIP2B 52	1318
380	2166	3952	5738	784CIP2B 53	1319
381	2167	3953	5739	784CIP2B 54	1328
382	2168	3954	5740	784CIP2B 55	1436
383	2169	3955	5741	784CIP2B 56	1464
384	2170	3956	5742	784CIP2B 57	1584
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386	2172	3958	5744	784CIP2B 59	1724
387	2173	3959	5745	784CIP2B 60	1728
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389	2175	3961	5747	784CIP2B 62	1809
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392	2178	3964	5750	784CIP2B 65	1926
393	2179	3965	5751	784CIP2B 66	1965
394	2180	3966	5752	784CIP2B 67	1967
395	2181	3967	5753	784CIP2B 68	1995
396	2182	3968	5754	784CIP2B 69	2005.
397	2183	3969	5755	784CIP2B 70	2027
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399	2185	3971	- 5757	784CIP2B 72	2103
400	2186	3 972	5758	784CIP2B 73	2106
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420	2205	3991	5777	784CIP2B_93	2512
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423		3994	5780	784CIPZB_96	2816
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425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
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438		4010	5797	784CIP2B 113	4090
439	2225	4011	5798	784CIP2B_113 784CIP2B 114	4105
440	2226	4012		784CIP2B_114 784CIP2B_115	4142
441	2227 .	4013	5799	<u> </u>	4142
442	2228	4014	5800	784CIP2B_116	1
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444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784C1P2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B 132	5579
459	2245	4031	5817	784CIP2B 133	5582
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464	2250	4036	5822	784CIP2B 138	5593
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490	2276	4062	5848	784CIP2B 164	5674
_491	2277	4063	5849	784CIP2B_165	5678
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499	2285	4071	5857	784CIP2B 173	5719
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501	2287	4073	5859	784CIP2B 175	5727
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503	2289	4075	5861	784CIP2B 177	5734
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507	2293	4079	5865	784CIP2B 181	5744
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520	2305	4091	5877	784CIP2B_193	5788
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522	2308	4094	5879 5880	784CIP2B_196	5807
523	2309	4095	5881	784CIP2B_197	5818
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539	2325	4111	5897	784CIP2B_214	5880
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542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5902
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554	2339 2340	4125	5911	784CIP2B_228	5947
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560	2346	4132	5918	784CIP2B_236	5980
561	2347	4133	5919	784CIP2B_237	5988
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622	2408	4193	5979	784CIP2B_298	6167
623	2409	4195	5980	784CIP2B_299	6172
624	2410	4196	5981	784CIP2B_300	6173
625	2411	4197	5982	784CIP2B_301	6190
626	2412	4197	5983	784CIP2B_302	6194
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632	2418	4204	5990	784CIP2B_309	6215
633	2419	4205	5991	784CIP2B_310	6219
634	2420	4206	5992	784CIP2B_311	6226
635	2421	4207	5992	784CIP2B 312 784CIP2B 313	6229
636	2422	4208	5994	784CIP2B_313 784CIP2B_314	6234
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638	2424	4210	5996	784CIP2B 315	6238
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642	2428	4214	6020	784CIP2B 320	6244
643	2429	4215	6001	784CIP2B 321	6245
644	2430	4216	6002	784CIP2B 322	6250
645	2431	4217	6003	784CIP2B 323	6252
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647	2433	4219	6005	784CIP2B 325	6256
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663	2449	4234	6020	784CIP2B_343	6312
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669	2455	4241		784CIP2B_350	6331
670	2456	4242	6027	784CIP2B_351	6333
671	2457	4243	6029	784CIP2B_352	6334
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674	2460	4245	6031 6032	784CIP2B_355	6346
675	2461	4246		784CIP2B_356	6348
676	2462	4248	6033 6034	784CIP2B_357	6348
677	2463	4249		784CIP2B_358	6350
678	2464	4250	6035 6036	784CIP2B_359	6351
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	2470	4256	6042	784CIP2B_366	6379
685 686	2471	4257	6043	784CIP2B_367	6380
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688	2473	4259	6045	784CIP2B_369	6392
689	2474	4260	6046	784CIP2B_370	6395
690	2475	4261	6047	784CIP2B_371	6397
691	2476	4262	6048	784CIP2B_372	6400
692	2477	4263	6049	784CIP2B_373	6401
693	2478	4264	6050	784CIP2B_374	6411
694		4265	6051	784CIP2B_375	6411
695	2480	4266	6052	784CIP2B_376	6411
696	2481	4267	6053	784CIP2B_377	6416
697	2482	4268 4269	6054 6055	784CIP2B_378 784CIP2B_379	6418
698	2484	I			. 6422
699	2485	4270	6056	784CIP2B_380	6423
700	2486	4271 4272	6057 6058	784CIP2B_381	6426
701	2486	4272		784CIP2B_382	6427
702	2487	4274	6059	784CIP2B_383	6428
703	2489	4275	6060 6061	784CIP2B_384	6429
704	2490	4276	6062	784CIP2B_385 784CIP2B 386	6430 6432
705	2491	4277	6063	784CIP2B_386 784CIP2B_387	6432
706	2492	4278	6064	784CIP2B 387	6438
707	2493	4279	6065	784CIP2B_388	6441
708	2494	4280	6066	784CIP2B_389	6446
709	2495	4281	6067	784CIP2B 391	6454
710	2496	4282	6068	784CIP2B 392	6459
711	2497	4283	6069	784CIP2B 394	6461
712	2498	4284	6070	784CIP2B 395	6467
713	2499	4285	6071	784CIP2B 396	6468
714	2500	. 4286	6072	784CIP2B 397	6487
715	2501	4287	6073	784CIP2B 398	6491
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717	2503	4289	6075	784CIP2B 401	6514
718	2504	4290	6076	784CIP2B 402	6519
719	2505	4291	6077	784CIP2B 403	6521
720	2506	4292	6078	784CIP2B 404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729					
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731	2515 2516	4301 4302	6087 6088	784CIP2B_413 784CIP2B_414	6556 6560
	2515 2516 2517	4301 4302 4303			
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733	2515 2516 2517 2518 2519	4301 4302 4303	6088 6089	784CIP2B_414 784CIP2B_415	6560 6563
733 734	2515 2516 2517 2518 2519 2520	4301 4302 4303 4304	6088 6089 6090	784CIP2B 414 784CIP2B 415 784CIP2B 416	6560 6563 6564
733 734 735	2515 2516 2517 2518 2519	4301 4302 4303 4304 4305	6088 6089 6090 6091	784CIP2B 414 784CIP2B 415 784CIP2B 416 784CIP2B 417	6560 6563 6564 6567
733 734 735 736	2515 2516 2517 2518 2519 2520 2521 2522	4301 4302 4303 4304 4305 4306	6088 6089 6090 6091 6092	784CIP2B 414 784CIP2B 415 784CIP2B 416 784CIP2B 417 784CIP2B 418	6560 6563 6564 6567 6573
733 734 735 736 737	2515 2516 2517 2518 2519 2520 2521 2522 2523	4301 4302 4303 4304 4305 4306 4307	6088 6089 6090 6091 6092 6093	784CIP2B 414 784CIP2B 415 784CIP2B 416 784CIP2B 417 784CIP2B 418 784CIP2B 419	6560 6563 6564 6567 6573 6575
733 734 735 736 737 738	2515 2516 2517 2518 2519 2520 2521 2521 2522 2523 2524	4301 4302 4303 4304 4305 4306 4307 4308	6088 6089 6090 6091 6092 6093	784CIP2B 414 784CIP2B 415 784CIP2B 416 784CIP2B 417 784CIP2B 418 784CIP2B 419 784CIP2B 420	6560 6563 6564 6567 6573 6575
733 734 735 736 737 738 739	2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525	4301 4302 4303 4304 4305 4306 4307 4308 4309	6088 6089 6090 6091 6092 6093 6094 6095	784CIP2B_414 784CIP2B_415 784CIP2B_416 784CIP2B_417 784CIP2B_418 784CIP2B_419 784CIP2B_420 784CIP2B_420	6560 6563 6564 6567 6573 6575 6577
733 734 735 736 737 738	2515 2516 2517 2518 2519 2520 2521 2521 2522 2523 2524	4301 4302 4303 4304 4305 4306 4307 4308 4309 4310	6088 6089 6090 6091 6092 6093 6094 6095	784CIP2B_414 784CIP2B_415 784CIP2B_416 784CIP2B_417 784CIP2B_418 784CIP2B_419 784CIP2B_420 784CIP2B_421 784CIP2B_421	6560 6563 6564 6567 6573 6575 6577 6593

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sequence	peptide	sequence	peptide sequence	SEQ ID NO: in	09/488,725
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744	2530	4316	6102	784CIP2B 428	6631
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747	2533	4319	6105	784CIP2B 431	6634
748	2534	4320	6106	784CIP2B 432	6638
749	2535	4321	6107	784CIP2B 433	6641
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751	2537	4323	6109	784CIP2B 435	6646
752	2538	4324	6110	784CIP2B 436	6648
753	2539	4325	6111	784CIP2B 437	6652
754	2540	4326	6112	784CIP2B 438	6654
755	2541	4327	6113	784CIP2B 439	6657
756	2542	4328	6114	784CIP2B 440	6658
757	2543	4329	6115	784CIP2B 441	6663
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759	2545	4331	6117	784CIP2B 443	6668
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762	2548	4334	6120	784CIP2B 446	6685
763	2549	4335	6121	784CIP2B 447	6687
764	2550	4336	6122	784CIP2B 448	6689
765	2551	4337	6123	784CIP2B 449	6693
766	2552	4338	6124	784CIP2B 450	6698
767	2553	4339	6125	784CIP2B 451	6699
768 .	2554	4340	6126	784CIP2B 452	6705
769	2555	4341	6127	784CIP2B 453	6711
770	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
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774	2560	4346	6132	784CIP2B_458	6727
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777	2562	4348	6134	784CIP2B_460	6730
778	2563	4349	6135	784CIP2B_461	6730
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780	2565	4351	6137	784CIP2B_463	6733
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782	2568	4353	6139	784CIP2B_465	6745
783	2569	4354	6140	784CIP2B_466	6751
784	2570	43 55 43 56	5141 6142	784CIP2B_467	6754
785	2571	4357	6143	784CIP2B_468	6758
786	2572	4350	6144	784CIP2B 469	6761
787	2573	43 59		784CIP2B_470	6765
788	2574	4360	6145	784CIP2B_471	6768
789	2575	4361	6146 6147	784CIP2B_472	6773
790	2576	4362	6148	784CIP2B_473 784CIP2B 474	6776
791	2577	4363	6149	784CIP2B_474 784CIP2B_475	6796
792	.2578	4364	6150	784CIP2B 475	6798
793	2579	4365	6151	784CIP2B_476 784CIP2B_477	6823
794	2580	4366	6152	784CIP2B 477	6825
795	2581	4367	6153		6826
796	2582	4368		784CIP2B_479	6839
797	2583	4369	6154	784CIP2B_480	6844
798	2584	4370	6155	784CIP2B_482	6849
799	2585	4371	6156	784CIP2B_483	6854
800	2586	4372	6157	784CIP2B_484	6857
801	2587	4373	6158 6159	784CIP2B_485	6861
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808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901 6904
810	2595	4382	6168	784CIP2B_495	
811	2597	4383	6169	784CIP2B_496	6907 6914
812	2598	4384	6170	784CIP2B_497	
813	2599	4385	6171	784CIP2B_498	6917
814 ·	2600	4386	6172	784CIP2B_499	6923
815	2601	4387	6173	784CIP2B_500	6929
816	2602	4388	6174	784CIP2B_501	6931
817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
81.9	2605	4391	6177	784CIP2B_504	6945
820	2606	4392	6178	784CIP2B_505	6946
821	2607	4393	6179	784CIP2B_506	6947
822	2608	4394	6180	784CIP2B_507	6949
823	2609	4395	6181	784CIP2B_508	6959
824	2610	4396	6182	784CIP2B_509	6960
825	2611	4397	6183	784CIP2B_510	6962
826	2612	4398	6184	784CIP2B_511	6963
827	2613	4399	6185	784CIP2B_512	6967
828	2614	4400	6186	784CIP2B_513	6983
829	2615	4401	6137	784CIP2B_514	6988
830	2616	4402	6138	784CIP2B_515	6996
831	2617	4403	6139	784CIP2B_516	7003
832	2618	4404	6190	784CIP2B_517	7016
833	2619	4405	6191	784CIP2B_518	7017
834	2620	4406	6192	784CIP2B_519	7025
835	2621	4407	6193	784CIP2B_520	7025
836	2622	4408	6194	784CIP2B_521	7025
837	2623	4409	6195	784CIP2B_522	7050
838	2624	4410	6196	784CIP2B_523	7051
839	2625	4411	6197	784CIP2B_524	7055
840	2626	4412	6198	784CIP2B_525	7060
841	2627	4413	6199	784CIP2B_526	7067
842	2628	4414	6200	784CIP2B_527	7071
843	2629	4415	6201	784CIP2B_528	7072
844	2630	4416	6202	784CIP2B_529	7073
845	2631	4417	6203	784CIP2B_530 784CIP2B_531	7076
846	2632	4418	6204 6205	784CIP2B 531	7078
847	2633	4419	6205	784CIP2B 533	7089
848	2634	4420		784CIP2B_533	7091
849	2635	4421	6207	784CIP2B_534 784CIP2B_535	7091
850	2636	4422	6209	784CIP2B_535	7104
851	2637	4423	6210	784CIP2B_537	7105
852	2638	4424	6210	784CIP2B 538	7105
853	2639	4425		784CIP2B_538	7109
854	2640	4426	6212	784CIP2B 540	7109
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856	2642 2643	4428	6214	784CIP2B 542	7120
857		4429		784CIP2B 543	7121
858	2644	4430	6216	784CIP2B_543	7126
859	2645	4431	6217	784CIP2B 545	7127
860	2646	4432	6218	784CIP2B 545	7130
861	2647	4433	6219		7130
862	2648	4434	6220	784CIP2B_547	7131
863	2649	4435	6221	784CIP2B_548	7159
864	2650	4436	6222	784CIP2B 549	7163
865	2651	4437	6223	784CIP2B_550	/103

of fall.    Sol. 10	SEQ ID NO:	SEQ ID	SEQ ID NO:	1 000 70	· · · · · · · · · · · · · · · · · · ·	
length   length   length   length   sequence   sequen				SEQ ID	Priority	SEQ ID
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866   2652		1	1	sequence		
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883					784CIP2B_566	7245
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885 2671 4457 6243 784CIP2B 570 7250 886 2672 4458 6244 784CIP2B 571 7265 887 2673 4459 6245 784CIP2B 572 7268 8887 2673 4459 6245 784CIP2B 572 7268 8888 2674 4460 6246 784CIP2B 573 7275 8890 2676 4461 6247 784CIP2B 573 7275 890 2676 4462 6248 784CIP2B 575 7283 891 2677 4463 6249 784CIP2B 575 7283 892 2678 4464 6250 784CIP2B 577 7287 893 2679 4465 6250 784CIP2B 577 7287 894 2680 4466 6250 784CIP2B 577 7287 895 2681 4467 6253 784CIP2B 577 7308 896 2682 4468 6254 784CIP2B 580 7308 897 2683 4464 6256 784CIP2B 580 7308 898 2684 4470 6256 784CIP2B 581 7309 899 2685 4471 6256 784CIP2B 582 7319 899 2686 4472 6258 784CIP2B 583 7326 900 2688 4474 6260 784CIP2B 587 7326 901 2687 4473 6259 784CIP2B 587 7327 902 2688 4476 6260 784CIP2B 587 7337 903 2669 4476 6260 784CIP2B 587 7337 904 2690 4476 6260 784CIP2B 587 7337 905 2691 4477 6263 784CIP2B 587 7337 906 2692 4478 6260 784CIP2B 587 7337 907 2693 4479 6266 784CIP2B 587 7359 908 2695 4480 6266 784CIP2B 587 7359 909 2695 4480 6266 784CIP2B 587 7359 900 2688 6477 6263 784CIP2B 587 7337 901 2687 7479 6263 784CIP2B 587 7337 902 2688 6477 6263 784CIP2B 587 7337 903 2669 4476 6260 784CIP2B 587 7337 904 2690 4476 6261 784CIP2B 587 7337 905 2691 4477 6263 784CIP2B 589 7345 907 2693 4478 6264 784CIP2B 589 7365 908 2695 4481 6267 784CIP2B 597 7365 909 2695 4481 6267 784CIP2B 597 7365 910 2696 4480 6266 784CIP2B 597 7365 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 596 7372 913 2699 4485 6271 784CIP2B 596 7372 914 2700 4486 6272 784CIP2B 596 7372 915 2701 4487 6273 784CIP2B 603 7391 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6277 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 607 7381 919 2705 4491 6277 784CIP2B 603 7395 919 2705 4491 6277 784CIP2B 603 7395 920 2706 4492 6278 784CIP2B 604 7395 919 2705 4491 6277 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 607 7399 922 2708 4494 6280 784CIP2B 601 7395 923 2709 4495 6281 784CIP2B 601 7406 924 2710 4496 6282 784CIP2B 601 7406			4455	6241	784CIP2B 568	7251
886 2672 4458 6244 784CIP2B_571 7265 887 2673 4459 6245 784CIP2B_572 7268 888 2674 4460 6246 784CIP2B_573 7275 889 2675 4461 6247 784CIP2B_573 7275 890 2676 4462 6246 784CIP2B_574 7279 890 2676 4462 6248 784CIP2B_576 7283 891 2677 4463 6249 784CIP2B_576 7283 892 2678 4464 6250 784CIP2B_576 7283 892 2678 4464 6250 784CIP2B_577 7287 893 2679 4465 6251 784CIP2B_577 7287 894 2680 4466 6252 784CIP2B_579 7308 895 2681 4467 6253 784CIP2B_579 7308 896 2682 4468 6252 784CIP2B_589 7309 897 2683 4469 6255 784CIP2B_581 7309 898 2684 4470 6256 784CIP2B_581 7309 899 2685 4471 6257 784CIP2B_582 7319 890 2686 4472 6258 784CIP2B_587 7326 900 2686 4472 6258 784CIP2B_587 7337 901 2687 4473 6259 784CIP2B_587 7337 902 2688 4474 6260 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_589 7334 904 2690 4476 6262 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7334 906 2686 4479 6265 784CIP2B_589 7334 907 2693 4478 6260 784CIP2B_589 7334 908 2694 4480 6266 784CIP2B_589 7363 909 2695 4481 6267 784CIP2B_599 7363 909 2695 4481 6267 784CIP2B_599 7363 909 2695 4481 6267 784CIP2B_590 7363 901 2687 4473 6259 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7349 905 2691 4478 6261 784CIP2B_599 7363 907 2693 4489 6266 784CIP2B_590 7365 908 2695 4481 6267 784CIP2B_591 7363 909 2695 4481 6267 784CIP2B_595 7363 909 2695 4481 6267 784CIP2B_595 7369 911 2697 4483 6269 784CIP2B_595 7369 912 2698 4488 6270 784CIP2B_595 7369 913 2699 4485 6271 784CIP2B_600 7381 914 2700 4488 6270 784CIP2B_600 7387 915 2701 4487 6273 784CIP2B_600 7387 917 2703 4489 6275 784CIP2B_600 7395 918 2704 4490 6276 784CIP2B_600 7395 919 2705 4491 6277 784CIP2B_600 7395 919 2705 4491 6277 784CIP2B_600 7395 910 2706 4496 6292 784CIP2B_600 7395 920 2706 4499 6275 784CIP2B_600 7395 921 2707 4493 6279 784CIP2B_600 7395 922 2708 4499 6282 784CIP2B_601 74066 923 2701 4497 6281 784CIP2B_601 74066 925 2711 4497 6284 784CIP2B_611 7409		L	4456	6242	784CIP2B 569	7255
887 2673 4459 6245 784CIP2B_572 7268 888 2674 4460 6246 784CIP2B_573 7275 889 2675 4461 6247 784CIP2B_573 7275 890 2676 4462 6248 784CIP2B_574 7279 890 2676 4462 6248 784CIP2B_575 7283 891 2677 4463 6248 784CIP2B_575 7283 892 2678 4464 6250 784CIP2B_577 7287 893 2679 4465 6250 784CIP2B_577 7287 893 2679 4465 6251 784CIP2B_577 7287 894 2680 4466 6252 784CIP2B_579 7308 895 2681 4467 6253 784CIP2B_579 7308 896 2682 4468 6254 784CIP2B_580 7308 897 2683 4469 6255 784CIP2B_580 7308 899 2685 4471 6257 784CIP2B_582 7319 899 2686 4470 6256 784CIP2B_582 7319 899 2686 4471 6257 784CIP2B_581 7326 900 2686 4472 6258 784CIP2B_583 7326 900 2686 4472 6258 784CIP2B_583 7326 900 2688 4474 6260 784CIP2B_585 7326 901 2687 4473 6259 784CIP2B_586 7334 902 2688 4476 6260 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_587 7337 904 2690 4476 6262 784CIP2B_589 7346 905 2691 4477 6263 784CIP2B_589 7349 905 2691 4477 6263 784CIP2B_589 7349 905 2693 4479 6266 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_589 7349 905 2691 4477 6263 784CIP2B_589 7349 905 2691 4478 6264 784CIP2B_589 7365 907 2693 4479 6265 784CIP2B_589 7365 909 2695 4480 6266 784CIP2B_597 7363 909 2695 4480 6266 784CIP2B_597 7365 911 2697 4483 6269 784CIP2B_597 7369 912 2698 4488 6270 784CIP2B_597 7369 913 2699 4488 6270 784CIP2B_600 7381 914 2700 4488 6271 784CIP2B_600 7389 915 2701 4489 6277 784CIP2B_600 7399 921 2706 4499 6277 784CIP2B_600 7399 922 2708 4491 6277 784CIP2B_600 7399 923 2709 4495 6281 784CIP2B_600 7399 924 2700 4489 6277 784CIP2B_600 7399 925 2701 4493 6279 784CIP2B_600 7399 921 2705 4491 6277 784CIP2B_600 7399 922 2708 4494 6280 784CIP2B_600 7399 923 2709 4495 6281 784CIP2B_600 7399 921 2707 4493 6279 784CIP2B_600 7399 922 2708 4494 6280 784CIP2B_600 7399 923 2709 4495 6281 784CIP2B_600 7399 924 2710 4496 6282 784CIP2B_601 7400		2671	4457	6243	784CIP2B 570	7260
887         2673         4459         6245         784CIP2B_573         7275           889         2675         4461         6246         784CIP2B_573         7275           890         2676         4461         6247         784CIP2B_574         7279           890         2676         4462         6248         784CIP2B_575         7283           891         2677         4463         6249         784CIP2B_576         7283           892         2678         4464         6250         784CIP2B_577         7287           893         2679         4465         6251         784CIP2B_579         7300           894         2680         4466         6252         784CIP2B_579         7300           895         2681         4467         6253         784CIP2B_580         7308           896         2682         4468         6254         784CIP2B_580         7309           897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_583         7326			4458	6244	<del>_</del>	
888         2674         4460         6246         784CIP2B_573         7275           889         2675         4461         6247         784CIP2B_575         7279           890         2676         4462         6248         784CIP2B_575         7283           891         2677         4463         6249         784CIP2B_576         7283           892         2678         4464         6250         784CIP2B_577         7287           893         2679         4465         6251         784CIP2B_579         7300           894         2680         4466         6252         784CIP2B_579         7308           895         2681         4467         6253         784CIP2B_580         7308           896         2682         4468         6254         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_581         7319           898         2684         4470         6256         784CIP2B_583         7326           899         2685         4471         6257         784CIP2B_585         7326           900         2686         4472         6258         784CIP2B_585         7326	887	2673	4459	6245	784CIP2B 572	
899 2675 4461 6247 784CIP2B_57\$ 7283 890 2676 4462 6248 784CIP2B_57\$ 7283 891 2677 4463 6249 784CIP2B_576 7283 892 2678 4464 6250 784CIP2B_577 7287 893 2679 4465 6251 784CIP2B_577 7287 894 2680 4466 6252 784CIP2B_579 7300 895 2681 4467 6253 784CIP2B_581 7301 896 2682 4468 6254 784CIP2B_581 7309 897 2683 4469 6255 784CIP2B_581 7309 899 2685 4471 6257 784CIP2B_582 7319 899 2686 4470 6256 784CIP2B_583 7320 899 2686 4471 6257 784CIP2B_584 7326 900 2686 4472 6258 784CIP2B_584 7326 901 2687 4473 6259 784CIP2B_587 7337 902 2688 4474 6260 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_588 7339 904 2690 4476 6262 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7344 905 2691 4478 6260 784CIP2B_589 7349 905 2693 4478 6264 784CIP2B_590 7355 906 2692 4478 6264 784CIP2B_591 7363 907 2693 4479 6265 784CIP2B_590 7355 908 2694 4480 6266 784CIP2B_591 7363 909 2695 4481 6267 784CIP2B_591 7363 901 2697 4483 6260 784CIP2B_591 7369 911 2697 4483 6260 784CIP2B_591 7369 912 2698 4484 6270 784CIP2B_591 7369 913 2699 4488 6264 784CIP2B_591 7369 914 2700 4488 6267 784CIP2B_591 7369 915 2691 4489 6266 784CIP2B_601 7381 916 2702 4488 6267 784CIP2B_590 7355 918 2704 4480 6266 784CIP2B_601 7381 919 2705 4481 6267 784CIP2B_601 7381 911 2697 4488 6267 784CIP2B_690 7395 912 2698 4484 6270 784CIP2B_690 7395 913 2699 4488 6267 784CIP2B_690 7395 914 2700 4488 6271 784CIP2B_600 7381 915 2701 4487 6273 784CIP2B_600 7381 916 2702 4488 6271 784CIP2B_600 7381 917 2703 4489 6275 784CIP2B_600 7381 918 2704 4490 6276 784CIP2B_600 7399 922 2708 4499 6275 784CIP2B_600 7399 922 2708 4499 6275 784CIP2B_600 7399 923 2706 4492 6278 784CIP2B_600 7399 924 2700 4496 6282 784CIP2B_600 7399 925 2711 4496 6282 784CIP2B_600 7406	888	2674	4460	6246	784CIP2B 573	<u> </u>
890 2676 4462 6248 764CIP2B_575 7283  891 2677 4463 6249 784CIP2B_576 7283  892 2678 4464 6250 784CIP2B_577 7287  893 2679 4465 6251 784CIP2B_577 7287  893 2679 4465 6251 784CIP2B_579 7301  894 2680 4466 6252 784CIP2B_579 7308  895 2681 4467 6253 784CIP2B_580 7308  896 2682 4468 6254 784CIP2B_581 7309  897 2683 4469 6255 784CIP2B_581 7309  898 2684 4470 6256 784CIP2B_581 7319  899 2685 4471 6257 784CIP2B_583 7320  899 2685 4471 6257 784CIP2B_583 7320  899 2686 4472 6258 784CIP2B_584 7326  900 2686 4472 6258 784CIP2B_585 7326  901 2687 4473 6259 784CIP2B_586 7334  902 2688 4474 6260 784CIP2B_587 7337  903 2689 4475 6261 784CIP2B_589 7334  904 2690 4476 6262 784CIP2B_589 7334  905 2691 4477 6263 784CIP2B_589 7345  906 2692 4478 6264 784CIP2B_599 7345  907 2693 4479 6265 784CIP2B_599 7366  908 2694 4480 6266 784CIP2B_591 7363  909 2695 4481 6267 784CIP2B_591 7363  901 2687 4483 6269 784CIP2B_591 7368  911 2697 4483 6269 784CIP2B_591 7368  911 2697 4483 6269 784CIP2B_591 7369  912 2698 4484 6270 784CIP2B_591 7368  911 2697 4488 6264 784CIP2B_591 7369  912 2698 4484 6270 784CIP2B_595 7369  913 2699 4485 6271 784CIP2B_595 7379  914 2700 4486 6272 784CIP2B_600 7381  915 2701 4487 6273 784CIP2B_600 7381  917 2703 4489 6275 784CIP2B_600 7395  919 2705 4489 6275 784CIP2B_600 7399  911 2697 4489 6275 784CIP2B_600 7399  922 2708 4499 6275 784CIP2B_600 7399  923 2706 4492 6276 784CIP2B_600 7399  924 2700 4498 6276 784CIP2B_600 7399  925 2706 4491 6277 784CIP2B_600 7399  927 2703 4489 6276 784CIP2B_600 7399  928 2706 4491 6277 784CIP2B_600 7399  929 2706 4491 6270 784CIP2B_600 7399  920 2706 4491 6270 784CIP2B_600 7399  921 2707 4493 6279 784CIP2B_600 7399  922 2708 4494 6280 784CIP2B_601 7406  923 2710 4496 6282 784CIP2B_601 7406  924 2710 4496 6282 784CIP2B_611 7409  925 2711 4497 6283 784CIP2B_611 7409	889	2675	4461	6247	784CIP2B 574	7279
891 2677 4463 6249 784CIP2B_576 7283 892 2678 4464 6250 784CIP2B_577 7287 893 2679 4465 6250 784CIP2B_577 7287 894 2680 4466 6252 784CIP2B_579 7300 895 2681 4467 6253 784CIP2B_579 7308 896 2682 4468 6252 784CIP2B_580 7308 897 2683 4469 6255 784CIP2B_581 7309 898 2684 4470 6256 784CIP2B_581 7309 899 2685 4471 6257 784CIP2B_583 7320 899 2685 4471 6257 784CIP2B_584 7326 900 2686 4472 6258 784CIP2B_585 7326 901 2687 4473 6259 784CIP2B_586 7334 902 2688 4474 6260 784CIP2B_586 7334 902 2688 4474 6260 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_589 7344 905 2691 4476 6262 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7344 906 2692 4478 6264 784CIP2B_589 7346 907 2693 4479 6265 784CIP2B_597 7363 908 2694 4480 6266 784CIP2B_597 7363 909 2695 4481 6267 784CIP2B_597 7368 911 2697 4483 6269 784CIP2B_595 7369 911 2696 4482 6268 784CIP2B_595 7369 911 2696 4486 6270 784CIP2B_599 7375 913 2699 4486 6270 784CIP2B_599 7375 914 2700 4486 6272 784CIP2B_590 7385 915 2701 4487 6273 784CIP2B_590 7395 916 2702 4488 6274 784CIP2B_600 7381 917 2703 4489 6275 784CIP2B_600 7381 918 2704 4490 6276 784CIP2B_600 7381 919 2705 4491 6277 784CIP2B_600 7381 919 2705 4491 6277 784CIP2B_600 7399 921 2706 4499 6275 784CIP2B_600 7399 922 2708 4491 6277 784CIP2B_600 7399 923 2709 4495 6281 784CIP2B_600 7399 924 2710 4496 6282 784CIP2B_600 7399 925 2711 4497 6283 784CIP2B_601 7309	890	2676	4462	6248	784CIP2B 575	
892         2678         4464         6250         784CIP2B_577         7287           893         2679         4465         6251         784CIP2B_578         7301           894         2680         4466         6252         784CIP2B_579         7308           895         2681         4467         6253         784CIP2B_580         7308           896         2682         4468         6254         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_585         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_589         7337           904         2690         4476         6262         784CIP2B_589         7339	891	2677	4463	6249	784CIF2B 576	
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894         2680         4466         6252         784CIP2B_579         7308           895         2681         4467         6253         784CIP2B_580         7308           896         2682         4468         6254         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_584         7326           899         2685         4471         6257         784CIP2B_584         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_599         7363	893	2679	4465			
895         2681         4467         6253         784CIP2B_580         7308           896         2682         4468         6254         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_585         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_587         7337           904         2690         4476         6262         784CIP2B_588         7339           905         2691         4477         6263         784CIP2B_589         7344           905         2691         4478         6264         784CIP2B_591         7363	894	2680	4466		<del></del>	
896         2682         4468         6254         784CIP2B_582         7309           897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_584         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_586         7334           903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_591         7363           907         2693         4478         6264         784CIP2B_591         7363           908         .2694         4480         6266         784CIP2B_592         7363	895	2681	4467	6253		
897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_584         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         '6263         784CIP2B_599         7355           906         2692         4478         6264         784CIP2B_591         7363           907         2693         4479         6265         784CIP2B_591         7363           908         2694         4480         6266         784CIP2B_593         7365           909         2695         4481         6267         784CIP2B_595         7369	896	2682	4468	6254		
898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_584         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_590         7355           906         2692         4478         6264         784CIP2B_591         7363           907         2693         4479         6265         784CIP2B_591         7363           909         2695         4481         6267         784CIP2B_593         7365           909         2695         4481         6267         784CIP2B_595         7369	897	2683	4469			
899         2685         4471         6257         784CIP2B_584         7326           900         2686         4472         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_587         7337           903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_590         7355           906         2692         4478         6264         784CIP2B_590         7355           906         2692         4478         6264         784CIP2B_591         7363           907         2693         4479         6265         784CIP2B_591         7363           908         2694         4480         6266         784CIP2B_593         7368           910         2696         4482         6268         784CIP2B_594         7368           910         2696         4483         6269         784CIP2B_595         7372	898	2684	4470	6256		L.
900 2686 4472 6258 784CIP2B_585 7326 901 2687 4473 6259 784CIP2B_586 7334 902 2688 4474 6260 784CIP2B_587 7337 903 2689 4475 6261 784CIP2B_588 7339 904 2690 4476 6262 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_590 7355 906 2692 4478 6264 784CIP2B_591 7363 907 2693 4479 6265 784CIP2B_591 7363 908 2694 4480 6266 784CIP2B_592 7363 909 2695 4481 6267 784CIP2B_593 7365 910 2696 4482 6268 784CIP2B_595 7369 911 2697 4483 6269 784CIP2B_595 7369 912 2698 4484 6270 784CIP2B_596 7372 912 2698 4484 6270 784CIP2B_590 7381 914 2700 4486 6272 784CIP2B_600 7381 915 2701 4487 6273 784CIP2B_601 7383 916 2702 4488 6274 784CIP2B_602 7367 917 2703 4489 6275 784CIP2B_604 7393 918 2704 4490 6276 784CIP2B_604 7393 919 2705 4491 6277 784CIP2B_606 7397 920 2706 4492 6278 784CIP2B_607 7399 921 2707 4493 6279 784CIP2B_607 7399 921 2707 4493 6279 784CIP2B_609 7406 923 2709 4495 6281 784CIP2B_610 7406 924 2710 4496 6282 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409	899	2685	4471	6257		<u> </u>
901         2687         4473         6259         784CIP2B 586         7334           902         2688         4474         6260         784CIP2B 587         7337           903         2689         4475         6261         784CIP2B 588         7339           904         2690         4476         6262         784CIP2B 589         7344           905         2691         4477         6263         784CIP2B 590         7355           906         2692         4478         6264         784CIP2B 591         7363           907         2693         4479         6265         784CIP2B 592         7363           908         2694         4480         6266         784CIP2B 592         7363           909         2695         4481         6267         784CIP2B 594         7368           910         2696         4482         6268         784CIP2B 595         7369           911         2697         4483         6269         784CIP2B 595         7372           912         2698         4484         6270         784CIP2B 596         7372           913         2699         4485         6271         784CIP2B 600         7381	900	2686	4472			<u> </u>
902 2688 4474 6260 784CIP2B 587 7337 903 2689 4475 6261 784CIP2B 588 7339 904 2690 4476 6262 784CIP2B 589 7344 905 2691 4477 6263 784CIP2B 589 7344 906 2692 4478 6264 784CIP2B 591 7363 907 2693 4479 6265 784CIP2B 592 7363 908 2694 4480 6266 784CIP2B 593 7365 909 2695 4481 6267 784CIP2B 594 7368 910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 595 7372 912 2698 4484 6270 784CIP2B 596 7372 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 600 7381 915 2701 4487 6273 784CIP2B 601 7383 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 606 7397 921 2707 4493 6279 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7406 923 2709 4495 6281 784CIP2B 609 7406 924 2710 4496 6282 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 612 7411	901	2687	4473			
903         2689         4475         6261         784CIP2B_588         7339           904         2690         4476         6262         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_590         7355           906         2692         4478         6264         784CIP2B_591         7363           907         2693         4479         6265         784CIP2B_592         7363           908         2694         4480         6266         784CIP2B_593         7365           909         2695         4481         6267         784CIP2B_594         7368           910         2696         4482         6268         784CIP2B_595         7369           911         2697         4483         6269         784CIP2B_595         7369           911         2698         4484         6270         784CIP2B_599         7375           913         2699         4485         6271         784CIP2B_599         7375           913         2699         4485         6271         784CIP2B_600         7381           914         2700         4486         6272         784CIP2B_600         7387	902	2688	4474	L		1
904 2690 4476 6262 784CIP2B_589 7344 905 2691 4477 6263 784CIP2B_590 7355 906 2692 4478 6264 784CIP2B_591 7363 907 2693 4479 6265 784CIP2B_592 7363 908 2694 4480 6266 784CIP2B_593 7365 909 2695 4481 6267 784CIP2B_593 7368 910 2696 4482 6268 784CIP2B_595 7369 911 2697 4483 6269 784CIP2B_595 7369 911 2697 4483 6269 784CIP2B_595 7372 912 2698 4484 6270 784CIP2B_599 7375 913 2699 4485 6271 784CIP2B_600 7381 914 2700 4486 6272 784CIP2B_600 7381 915 2701 4487 6273 784CIP2B_601 7383 915 2701 4487 6273 784CIP2B_602 7387 916 2702 4488 6274 784CIP2B_603 7391 917 2703 4489 6275 784CIP2B_604 7393 918 2704 4490 6276 784CIP2B_606 7397 920 2706 4492 6278 784CIP2B_606 7397 921 2707 4493 6279 784CIP2B_608 7405 922 2708 4494 6280 784CIP2B_609 7406 923 2709 4495 6281 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409 925 2711 4497 6283 784CIP2B_611 7409	903	2689	4475			L
905 2691 4477 6263 784CIP2B 590 7355 906 2692 4478 6264 784CIP2B 591 7363 907 2693 4479 6265 784CIP2B 592 7363 908 .2694 4480 6266 784CIP2B 593 7365 909 2695 4481 6267 784CIP2B 594 7368 910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 599 7375 913 2699 4485 6271 784CIP2B 599 7375 914 2700 4486 6272 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 606 7397 920 2706 4491 6277 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409	904	2690	4476	1		
906 2692 4478 6264 784CIP2B 591 7363 907 2693 4479 6265 784CIP2B 592 7363 908 2694 4480 6266 784CIP2B 593 7365 909 2695 4481 6267 784CIP2B 594 7368 910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 596 7372 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 601 7383 916 2702 4488 6274 784CIP2B 602 7387 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 606 7397 920 2706 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409	905	2691				<u></u>
907 2693 4479 6265 784CIP2B 592 7363 908 2694 4480 6266 784CIP2B 593 7365 909 2695 4481 6267 784CIP2B 594 7368 910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 599 7375 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 605 7395 919 2705 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 610 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7410	906	2692				
908         .2694         4480         6266         784CIP2B         593         7365           909         2695         4481         6267         784CIP2B         594         7368           910         2696         4482         6268         784CIP2B         595         7369           911         2697         4483         6269         784CIP2B         596         7372           912         2698         4484         6270         784CIP2B         599         7375           913         2699         4485         6271         784CIP2B         600         7381           914         2700         4486         6272         784CIP2B         601         7383           915         2701         4487         6273         784CIP2B         601         7387           916         2702         4488         6274         784CIP2B         603         7391           917         2703         4489         6275         784CIP2B         604         7393           918         2704         4490         6276         784CIP2B         605         7395           919         2705         4491         6277         784CIP2B </td <td>907</td> <td></td> <td></td> <td></td> <td></td> <td></td>	907					
909 2695 4481 6267 784CIP2B 594 7368 910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 599 7375 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6274 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 605 7395 919 2705 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409	908			L	-	
910 2696 4482 6268 784CIP2B 595 7369 911 2697 4483 6269 784CIP2B 596 7372 912 2698 4484 6270 784CIP2B 599 7375 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 605 7395 919 2705 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7410	909			L		
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912 2698 4484 6270 784CIP2B 599 7375 913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 605 7395 919 2705 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 606 7397 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 610 7409 925 2711 4497 6283 784CIP2B 611 7409 925 2712 4498 6284 784CIP2B 613 7411	911					
913 2699 4485 6271 784CIP2B 600 7381 914 2700 4486 6272 784CIP2B 601 7383 915 2701 4487 6273 784CIP2B 602 7387 916 2702 4488 6274 784CIP2B 603 7391 917 2703 4489 6275 784CIP2B 604 7393 918 2704 4490 6276 784CIP2B 605 7395 919 2705 4491 6277 784CIP2B 606 7397 920 2706 4492 6278 784CIP2B 607 7399 921 2707 4493 6279 784CIP2B 608 7405 922 2708 4494 6280 784CIP2B 609 7406 923 2709 4495 6281 784CIP2B 610 7406 924 2710 4496 6282 784CIP2B 611 7409 925 2711 4497 6283 784CIP2B 611 7410	912					
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947	2733	4519	6305	784CIP2B_634	7457
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1006	2792	4578	6364	784CIP2B 693	7664
1007	2793	4579	6365	784CIP2B 695	7674
1008	2794	4580	6366	784CIP2B 696	7675
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1056	2842	4628	6414	784CIP2B_745	7853
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1323	3109	4895	6681	784CIP2B 1013	8827
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1382	3168	4954	6740	784CIP2B_1071	9854
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1418	3204	4990	6776	784CIP2C 5	864
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1450	3236	5022	6808	784CIP2C_39	3463
1451	3237	5023	6809	784CIP2C_40	3466
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· 1497	3283	5069	6855	784CIP2C 86	4373
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1588         3374         5160         6946         784CIP2C_180         555           1589         3375         5161         6947         784CIP2C_181         565           1590         3376         5162         6948         784CIP2C_182         573           1591         3377         5163         6949         784CIP2C_183         576           1592         3378         5164         6950         784CIP2C_184         577           1593         3379         5165         6951         784CIP2C_185         577           1594         3380         5166         6952         784CIP2C_186         575           1595         3381         5167         6953         784CIP2C_186         575           1596         3382         5168         6954         784CIP2C_187         586           1597         3383         5169         6955         784CIP2C_189         585           1598         3384         5170         6956         784CIP2C_190         606           1599         3385         5171         6957         784CIP2C_191         606           1600         3386         5172         6958         784CIP2C_192         61						5590
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1616	3402	5188	6974	784CIP2C_207	6695
1617	3403	5189		784CIP2C_208	6746
1618	3404		6975	784CIP2C_209	6898
1619	3405	5190	6976	784CIP2C_210	6938
1620		5191	6977	784CIP2C_211	6943
	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C 217	7500
1626	3412	5198	6984	784CIP2C 218	7509
1627	3413	5199	6985	784CIP2C 219	7523
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1629	3415	5201	6987	784CIP2C 221	7564
1630	3416	5202	6988	784CIP2C 222	7568
1631	3417	5203	6989	784CIP2C 223	7631
1632	3418	5204	6990	784CIP2C 224	7813
1633	3419	5205	6991	784CIP2C 225	7831
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1635	3421	5207	6993	784CIP2C 227	7907
1636	3422	5208	6994	784CIP2C 228	7943
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1638	3424	5210	6996	784CIP2C 230	8216
1639	3425	5211	6997	784CIP2C 231	8225
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1643	3429	5215	7001	784CIP2C_234 784CIP2C_235	8503
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1646	3432	5218	7004	784CIP2C_237	
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1657		5228	7014	784CIP2D_4	3633
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	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
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1662	3448	5234	7020	784CIP2D_10	4774
1663	3449	5235	7021	784CIP2D_11	4894
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1666	3452	5238	7024	784CIP2D 14	7443
1667	3453	5239	7025	784CIP2D 15	8673
1668	3454	5240	7026	784CIP2D 16	8679
1669	3455	5241	7027	784CIP2D 17	8727
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1676	3462	5248	7034	784CIP2D 25	8918
1677	3463	5249	1	784CIP2D_25	8941
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1679	3465 3466	5251	7037	784CIP2D 28	8951
1680	1	5252		784CIP2D 29	8951
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1682	3468	5254	7040	784CIP2D_30 784CIP2D_31	9012
1683	3469	5255	7041	784CIP2D 32	9013
1684	3470	5256	7042	.L	9013
1685	3471	5257	7043		
1686	3472	5258	7044	784CIP2D_34	9053 9054
1687	3473	5259	7045	784CIP2D 35	9054
1688	3474	5260	7046	784CIP2D_36 784CIP2D_37	_
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1690	3476	5262	7048	784CIP2D_38	9134 9152
1691	3477	5263	7049	784CIP2D_39	
1692	3478	5264	7050	784CIP2D_40	9152
1693	3479	5265	7051	784CIP2D_41	9211 9223
1694	3480	5266	7052	784CIP2D_42	
1695	3481	5267	7053	784CIP2D_43	9223
1696	3482	5268	7054	784CIP2D_44	9231
1697	3483	5269	7055	784CIP2D_45	9236
1698	3484	5270	7056	784CIP2D_46	9236
1699	3485	5271	7057	784CIF2D_47	9303
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1701	3487	5273	7059	784CIP2D_49 784CIP2D_50	9326
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1721	3507	5293	7079	784CIP2D 69	9628
1722	3508	5294	7080	784CIP2D 70	9649
1723	3509	5295	7081	784CIP2D 71	9652
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1167		5302	7087	784CIP2D_78	9790
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nucleotide   length   sequence   peptide   sequence   sequence   sequence   sequence   sequence   sequence   seq	i ·			1	_	
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1735   3521   5307   7093   784CIP2D_83   10010	1734	<u> </u>	5306	7002	_1	
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1749 3535 5321 7107 784CIPZE \$ 4018 1750 3536 5322 7108 784CIPZE \$ 4018 1751 3536 5322 7108 784CIPZE \$ 4467 1751 3537 5323 7109 784CIPZE \$ 4467 1752 3538 5324 7110 784CIPZE \$ 4916 1753 3539 5325 7111 784CIPZE \$ 4916 1753 3539 5325 7111 784CIPZE \$ 4916 1755 3541 5327 7113 784CIPZE \$ 4926 1755 3541 5327 7113 784CIPZE \$ 4926 1756 3542 5328 7114 784CIPZE \$ 24963 1758 3544 5330 7116 784CIPZE \$ 12 4963 1758 3545 5331 7117 784CIPZE \$ 14 4988 1759 3545 5331 7117 784CIPZE \$ 15 5835 1760 3546 5332 7118 784CIPZE \$ 15 5835 1761 3547 5333 7119 784CIPZE \$ 17 7682 1762 3548 5334 7120 784CIPZE \$ 18 7699 1763 3549 5338 7121 788CIPZE \$ 19 7707 1764 3550 5336 7122 784CIPZE \$ 20 7707 1766 3551 5337 7123 784CIPZE \$ 356 1767 3553 5339 7125 784CIPZE \$ 39065 1769 3554 5340 7126 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1769 3555 5341 7127 784CIPZE \$ 39065 1770 3556 5342 7128 784CIPZE \$ 39065 1770 3556 5342 7128 784CIPZE \$ 39065 1771 3557 5343 7129 784CIPZE \$ 39065 1772 3558 534 7127 784CIPZE \$ 39065 1773 3559 5345 7131 784CIPZE \$ 39065 1774 3560 5346 7132 784CIPZE \$ 39065 1775 3561 5347 7133 784CIPZE \$ 4474 1773 3559 5345 7131 784CIPZE \$ 4474 1773 3559 5345 7131 784CIPZE \$ 4474 1773 3559 5345 7131 784CIPZE \$ 4470 1776 3562 5348 7132 784CIPZE \$ 5008 1778 3564 5350 7136 784CIPZE \$ 5008 1779 3565 5351 7137 784CIPZE \$ 5008 1778 3566 5352 7138 784CIPZE \$ 5008 1779 3566 5352 7138 784CIPZE \$ 10 5009 1779 3566 5352 7138 784CIPZE \$ 10 5009 1779 3566 5352 7138 784CIPZE \$ 10 5009 1779 3566 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 10 5009 1778 3569 5355 7131 784CIPZE \$ 1		I	5319	7105	784CIP2E 2	3628
1750 3536 5322 7108 784CP2E 6 4467 1751 3537 5323 7109 784CP2E 6 4467 1752 3538 5324 7110 784CP2E 7 4865 1753 3538 5324 7110 784CP2E 8 4916 1753 3539 5325 7111 784CP2E 9 4923 1754 3540 5326 7112 784CP2E 10 4926 1755 3541 5327 7113 784CP2E 11 4962 1756 3542 5328 7114 784CP2E 12 4963 1757 3543 5329 7115 784CP2E 12 4963 1758 3544 5330 7116 784CP2E 13 4964 1759 3545 5331 7117 784CP2E 14 4988 1759 3545 5331 7117 784CP2E 15 5835 1760 3546 5332 7118 784CP2E 14 4988 1760 3546 5332 7118 784CP2E 15 6862 1761 3547 5333 7119 784CP2E 15 7682 1762 3548 5334 7120 784CP2E 18 7699 1763 3549 5335 7121 784CP2E 19 7707 1764 3550 5336 7122 784CP2E 19 7707 1765 3551 5337 7123 784CP2E 19 7707 1766 3552 5338 7122 784CP2E 21 7752 1766 3552 5338 7124 784CP2E 21 7752 1766 3555 5336 7122 784CP2E 2 8357 1769 3555 5341 7127 784CP2E 2 8357 1769 3555 5341 7127 784CP2E 2 8357 1769 3555 5341 7127 784CP2E 2 8357 1769 3555 5341 7127 784CP2E 2 39065 1769 3555 5341 7127 784CP2E 2 3559 1770 3556 5342 7128 784CP2E 2 3559 1771 3557 5343 7129 784CP2E 2 3559 1772 3558 5344 7130 784CP2E 2 3559 1771 3557 5343 7129 784CP2E 2 3559 1772 3558 5346 7132 784CP2E 2 3559 1773 3559 5345 7131 784CP2E 2 3559 1774 3560 5346 7132 784CP2E 3 4021 1775 3563 5349 7135 784CP2E 3 5008 1779 3556 5342 7128 784CP2E 3 5008 1779 3556 5342 7128 784CP2E 3 5008 1779 3556 5342 7128 784CP2E 3 5008 1779 3563 5349 7135 784CP2E 3 5008 1779 3563 5349 7135 784CP2E 5 5008 1779 3563 5349 7135 784CP2E 5 5008 1779 3563 5349 7135 784CP2E 5 5008 1779 3563 5349 7135 784CP2E 5 5008 1779 3563 5349 7135 784CP2E 1 5009 1779 3563 5349 7135 784CP2E 1 5009 1779 3566 5352 7138 784CP2E 1 5009 1779 3566 5352 7138 784CP2E 1 5009 1779 3563 5349 7135 784CP2E 1 5009 1779 3566 5352 7138 784CP2E 1 5009 1779 3566 5352 7138 784CP2E 1 5009 1778 3569 5355 711 7137 784CP2E 1 5009 1778 3569 5355 711 7137 784CP2E 1 5009 1778 3566 5352 7138 784CP2E 1 5009 1779 3566 5352 7138 784CP2E 1 5009 1778 3569 5355 7114 784CP2E 1 5009 1778 3569 5355 7114 784CP2E 1 5009			5320	7106	784CIP2E 4	3673
1750		3535	5321	7107	784CIP2E 5	4018
1751		3536	5322	7108	784C_P2E 6	L
1752	1751	3537	5323	7109	,	
1753	1752	3538	5324	7110		
1754   3540   5326   7112   784CIP2E 10   4926     1755   3541   5327   7113   784CIP2E 11   4962     1756   3542   5328   7114   784CIP2E 12   4963     1757   3543   5329   7115   784CIP2E 13   4964     1758   3544   5330   7116   784CIP2E 14   4988     1759   3545   5331   7117   784CIP2E 15   5835     1760   3546   5332   7118   784CIP2E 15   5835     1761   3547   5333   7119   784CIP2E 16   7682     1761   3547   5333   7119   784CIP2E 18   7699     1762   3548   5334   7120   784CIP2E 18   7699     1763   3549   5335   7121   784CIP2E 19   7707     1764   3550   5336   7122   784CIP2E 20   7707     1765   3551   5337   7123   784CIP2E 21   7752     1766   3552   5338   7124   784CIP2E 22   8357     1767   3553   5339   7125   784CIP2E 23   9065     1768   3554   5340   7126   784CIP2E 24   9324     1769   3555   5341   7127   784CIP2E 24   9324     1769   3555   5341   7127   784CIP2E 24   9324     1769   3556   5342   7128   784CIP2E 2   3559     1771   3557   5343   7129   784CIP2F 2   3559     1771   3557   5343   7129   784CIP2F 3   4021     1773   3558   5344   7130   784CIP2F 3   4021     1774   3560   5346   7132   784CIP2F 6   4705     1775   3561   5347   7133   784CIP2F 8   4712     1776   3562   5348   7131   784CIP2F 8   4712     1777   3563   5349   7135   784CIP2F 8   4712     1778   3564   5359   7136   784CIP2F 1   5015     1779   3565   5351   7137   784CIP2F 1   5015     1778   3564   5359   7136   784CIP2F 1   5015     1778   3564   5359   7136   784CIP2F 1   5015     1780   3566   5357   7138   784CIP2F 1   5015     1781   3567   5353   7139   784CIP2F 1   5015     1781   3567   5353   7139   784CIP2F 1   5015     1781   3569   5355   7141   784CIP2F 16   8830     1785   3571   5357   7143   784CIP2F 16   8830     1786   3559   5355   7141   784CIP2F 16   8830     1786   3568   5354   7140   784CIP2F 16   8830     1786   3568   5357   7143   784CIP2F 16   8830     1786   3569   5355   7141   784CIP2F 16   8830     1786   3569   5355   7141   744CIP2F 16   8830     1786   3570   5356	1753	3539	5325		<u>·                                     </u>	
1755	1754	3540	5326			
1756	1755	3541	5327		L	
1757         3543         5329         7115         784CIP2E 13         4964           1758         3544         5330         7116         784CIP2E 14         4988           1759         3545         5331         7117         784CIP2E 15         5835           1760         3546         5332         7118         784CIP2E 16         7682           1761         3547         5333         7119         784CIP2E 17         7682           1762         3548         5334         7120         784CIP2E 18         7699           1763         3549         5335         7121         784CIP2E 19         7707           1764         3550         5336         7122         784CIP2E 19         7707           1765         3551         5337         7123         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 23         9065           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324	1756	3512	5328			
1758 3544 5330 7116 784CIP2E 14 4988 1759 3545 5331 7117 784CIP2E 15 5835 1760 3546 5332 7118 784CIP2E 16 7682 1761 3547 5333 7119 784CIP2E 17 7682 1762 3548 5334 7120 784CIP2E 17 7682 1763 3549 5335 7121 784CIP2E 19 7707 1764 3550 5351 5337 7123 784CIP2E 20 7707 1765 3551 5337 7123 784CIP2E 21 7752 1766 3552 5338 7124 784CIP2E 22 8357 1767 3553 5339 7125 784CIP2E 23 9065 1768 3551 5337 7123 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 24 9324 1769 3555 5341 7127 784CIP2E 24 9324 1769 3556 5342 7128 784CIP2E 2 3559 1771 3557 5343 7129 784CIP2E 3 3559 1771 3557 5343 7129 784CIP2E 3 3559 1771 3557 5343 7129 784CIP2E 3 4021 1772 3558 5344 7130 784CIP2E 4 4474 1773 3559 5345 7131 784CIP2E 4 4474 1773 3560 5346 7132 784CIP2E 6 4705 1776 3563 5349 7133 784CIP2E 7 4077 1776 3563 5349 7133 784CIP2E 7 5008 1776 3566 5342 7138 784CIP2E 8 4772 1777 3563 5349 7133 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1777 3563 5349 7135 784CIP2E 8 4772 1779 3566 5352 7138 784CIP2E 1 5008 1779 3566 5352 7138 784CIP2E 1 5008 1779 3566 5352 7138 784CIP2E 1 5008 1779 3566 5352 7138 784CIP2E 1 5008 1779 3566 5352 7138 784CIP2E 1 5005 1779 3568 5354 7140 784CIP2E 14 7725 1784 3569 5355 7141 784CIP2E 15 8828 1784 3570 5356 7142 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 16 8830 1786 3571 5357 7143 784CIP2E 17 9739	1757	3543	5329			
1759         3545         5331         7117         784CIPZE 15         5835           1760         3546         5332         7118         784CIPZE 16         7682           1761         3547         5333         7119         784CIPZE 17         7682           1762         3548         5334         7120         784CIPZE 18         7699           1763         3549         5335         7121         784CIPZE 19         7707           1764         3550         5336         7122         784CIPZE 20         7707           1765         3551         5337         7123         784CIPZE 21         7752           1766         3552         5338         7124         784CIPZE 21         7752           1767         3553         5339         7125         784CIPZE 23         8357           1767         3553         5340         7126         784CIPZE 24         9324           1769         3555         5341         7127         784CIPZE 24         9324           1770         3556         5342         7128         784CIPZE 1         2976           1771         3557         5343         7129         784CIPZE 2         3559	1758	3544	5330		_	
1760         3546         5332         7118         764CIP2E 16         7682           1761         3547         5333         7119         -784CIP2E 17         7682           1762         3548         5334         7120         784CIP2E 18         7699           1763         3549         5335         7121         784CIP2E 19         7707           1764         3550         5336         7122         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2E 1         2976           1770         3556         5342         7128         784CIP2F 2         3559           1771         3557         5343         7129         784CIP2F 3         4021	1759	3545	5331		· — ·	1
1761         3547         5333         7119         784CIP2E 17         7682           1762         3548         5334         7120         784CIP2E 18         7699           1763         3549         5335         7121         784CIP2E 19         7707           1764         3550         5336         7122         784CIP2E 20         7707           1765         3551         5337         7123         784CIP2E 21         7752           1766         3552         5338         7124         784CIP2E 22         8357           1767         3553         5339         7125         784CIP2E 23         9065           1768         3554         5340         7126         784CIP2E 24         9324           1769         3555         5341         7127         784CIP2F 1         2976           1770         3556         5342         7128         784CIP2F 1         2976           1771         3557         5343         7129         784CIP2F 2         3559           1771         3558         5344         7130         784CIP2F 3         4021           1772         3558         5344         7130         784CIP2F 5         4566     <	1760	3546				
1762         3548         5334         7120         784CIP2E_18         7699           1763         3549         5335         7121         784CIP2E_19         7707           1764         3550         5336         7122         784CIP2E_20         7707           1765         3551         5337         7123         784CIP2E_21         7752           1766         3552         5338         7124         784CIP2E_22         8357           1767         3553         5339         7125         784CIP2E_22         8357           1768         3554         5340         7126         784CIP2E_23         9065           1769         3555         5341         7127         784CIP2E_1         2976           1770         3556         5342         7128         784CIP2E_1         2976           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_3         4021           1773         3560         5345         7131         784CIP2F_3         4021 </td <td>1761</td> <td>3547</td> <td></td> <td></td> <td>_ ·</td> <td></td>	1761	3547			_ ·	
1763     3549     5335     7121     784CIP2E     19     7707       1764     3550     5336     7122     784CIP2E     20     7707       1765     3551     5337     7123     784CIP2E     21     7752       1766     3552     5338     7124     784CIP2E     22     8357       1767     3553     5339     7125     784CIP2E     23     9065       1768     3554     5340     7126     784CIP2E     24     9324       1769     3555     5341     7127     784CIP2F     1     2976       1770     3556     5342     7128     784CIP2F     2     3559       1771     3557     5343     7129     784CIP2F     3     4021       1772     3558     5344     7130     784CIP2F     3     4021       1773     3559     5345     7131     784CIP2F     4474       1773     3559     5345     7131     784CIP2F     4705       1774     3560     5346     7132     784CIP2F     4705       1775     3561     5347     7133     784CIP2F     4707       1776     3562     5348     7134     784CIP2F     9	1762	3548				
1764         3550         5336         7122         784CIPZE_20         7707           1765         3551         5337         7123         784CIPZE_21         7752           1766         3552         5338         7124         784CIPZE_22         8357           1767         3553         5339         7125         784CIPZE_23         9065           1768         3554         5340         7126         784CIPZE_24         9324           1769         3555         5341         7127         784CIPZE_1         2976           1770         3556         5342         7128         784CIPZE_1         2976           1771         3557         5343         7129         784CIPZE_1         2976           1771         3557         5343         7129         784CIPZE_2         3559           1771         3558         5344         7130         784CIPZE_3         4021           1772         3558         5344         7130         784CIPZE_4         4474           1773         3559         5345         7131         784CIPZE_5         4566           1774         3560         5346         7132         784CIPZE_6         4705 <td>1763</td> <td>3549</td> <td></td> <td></td> <td></td> <td>l</td>	1763	3549				l
1765         3551         5337         7123         784CIP2E         21         7752           1766         3552         5338         7124         784CIP2E         22         8357           1767         3553         5339         7125         784CIP2E         23         9065           1768         3554         5340         7126         784CIP2E         24         9324           1769         3555         5341         7127         784CIP2F         1         2976           1770         3556         5342         7128         784CIP2F         1         2976           1771         3557         5343         7129         784CIP2F         2         3559           1771         3557         5343         7129         784CIP2F         3         4021           1772         3558         5344         7130         784CIP2F         3         4021           1773         3559         5345         7131         784CIP2F         4474           1773         3560         5346         7132         784CIP2F         4705           1774         3560         5347         7133         784CIP2F         4707	1764	1				
1766         3552         5338         7124         784CIP2E_22         8357           1767         3553         5339         7125         784CIP2E_23         9065           1768         3554         5340         7126         784CIP2E_24         9324           1769         3555         5341         7127         784CIP2F_1         2976           1770         3556         5342         7128         784CIP2F_2         3559           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_3         4021           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_5         4566           1775         3561         5347         7133         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3563         5349         7134         784CIP2F_8         4712           1777         3563         5349         7136         784CIP2F_10         5008	1765	3551				
1767         3553         5339         7125         784CIP2E_23         9065           1768         3554         5340         7126         784CIP2E_24         9324           1769         3555         5341         7127         784CIP2F_1         2976           1770         3556         5342         7128         784CIP2F_2         3559           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_4         4474           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_6         4707           1776         3562         5348         7134         784CIP2F_9         5008           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015	1766					
1768         3554         5340         7126         784CIP2E_24         9324           1769         3555         5341         7127         784CIP2F_1         2976           1770         3556         5342         7128         784CIP2F_2         3559           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_3         4021           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_5         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_13         7724	1767					
1769         3555         5341         7127         784CIP2F_1         2976           1770         3556         5342         7128         784CIP2F_1         2976           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_4         4474           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_13         7724						
1770         3556         5342         7128         784CIP2F_2         3559           1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_4         4474           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_8         4712           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725 <td>1769</td> <td></td> <td></td> <td></td> <td></td> <td></td>	1769					
1771         3557         5343         7129         784CIP2F_3         4021           1772         3558         5344         7130         784CIP2F_4         4474           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828 <td>1770</td> <td></td> <td></td> <td></td> <td></td> <td></td>	1770					
1772         3558         5344         7130         784CIP2F_4         4474           1773         3559         5345         7131         784CIP2F_5         4566           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_7         4707           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>						
1773         3559         5345         7131         784CIP2F_5         44474           1774         3560         5346         7132         784CIP2F_6         4705           1775         3561         5347         7133         784CIP2F_6         4705           1776         3562         5348         7134         784CIP2F_8         4712           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_16         8830           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1774         3560         5346         7132         784CIP2F_6         4565           1775         3561         5347         7133         784CIP2F_6         4705           1776         3562         5348         7134         784CIP2F_7         4707           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1775         3561         5347         7132         784CIP2F_6         4705           1776         3562         5348         7134         784CIP2F_7         4707           1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1776         3562         5348         7134         784CIP2F_8         4707           1777         3563         5349         7135         784CIP2F_8         4712           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1777         3563         5349         7135         784CIP2F_9         5008           1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5015           1780         3566         5352         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1778         3564         5350         7136         784CIP2F_10         5009           1779         3565         5351         7137         784CIP2F_11         5009           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_12         5015           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1779         3565         5351         7137         784CIP2F_10         5009           1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7139         784CIP2F_12         5015           1782         3568         5354         7140         784CIP2F_13         7724           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						1
1780         3566         5352         7138         784CIP2F_11         5015           1781         3567         5353         7138         784CIP2F_12         5015           1781         3567         5353         7139         784CIP2F_13         7724           1782         3568         5354         7140         784CIP2F_14         7725           1783         3569         5355         7141         784CIP2F_15         8828           1784         3570         5356         7142         784CIP2F_16         8830           1785         3571         5357         7143         784CIP2F_17         9739						
1781     3567     5353     7139     784CIP2F_13     7724       1782     3568     5354     7140     784CIP2F_14     7725       1783     3569     5355     7141     784CIP2F_15     8828       1784     3570     5356     7142     784CIP2F_16     8830       1785     3571     5357     7143     784CIP2F_17     9739				,		
1782 3568 5354 7140 784CIP2F 14 7725 1783 3569 5355 7141 784CIP2F 15 8828 1784 3570 5356 7142 784CIP2F 16 8830 1785 3571 5357 7143 784CIP2F 17 9739						
1783 3569 5355 7141 784CIP2F 15 8828 1784 3570 5356 7142 784CIP2F 16 8830 1785 3571 5357 7143 784CIP2F 17 9739						
1784 3570 5356 7142 784CIP2F 16 8830 1785 3571 5357 7143 784CIP2F 17 9739						7725
1785 3571 5357 7143 784CIP2F 16 8830						8828
1786 2522 3337 7143 764CIP2F 17 9739				1		8830
1/86 3572 5358 7144 784CIP2F_18 9896						9739
	1/86	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%CS701!.DOC)

TARLE 7

TA	BLE 7		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
İ	location	corresponding	L=Leucine; M=Methionine, N=Asparagine,
J	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
5359	337	1131	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
ł		j	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	1		TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
	1		VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
\	}	1	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
}			KITQF
		1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
5360	2	1112	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
i			SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
1 .	1	į.	FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
1	l	1	VVI.PTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
			FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1	1	1.	GTLLLWLCOAOKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
-			AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
1	1		TPHTYTHPPPSCOLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
3301	_		SSKELWYMPEEYIROGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1			PKHIOLROLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
ļ	l	1	AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
1	1	į.	PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
-	ļ		SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
į	1		LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQXA
1	1		NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
	j		VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
1			FPSPADSGTNSVFSQLENNTNHYSSQLEGNTNSSFLKGGNGENA
1			VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1			EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
ļ		i	PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
1	ļ		ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
Ì	}	ļ	TVCHPNTLLTNONRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
l		}	GLCSSSFPNSGGPSONFTSNSSRVSVISGPQNTRSSHLNKKGNS
1		İ	ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
1	l.		SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
	l	1	VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
1		1	LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
		1	NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
	1	1	QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1	1		MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
		1	MILETKKNOLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
1			PALELRAETQNTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
1	1	1	PALELRAETQNTHSNVAVIPERQLIERKSPURIESSIGVITVIS EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
ı			SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
ŀ	ļ	]	HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD
	i	1	HENTPEETESMIASVDVGRFFCDGBECADSV HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
			KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
			DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
	1	}	TSOHRNILLIVFKRCCNSOVKETSEQEGAKNDVKDSDTCVSESND
	1	]	NSRTTATVSOKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
-	1	<b>\</b>	NTSSNUSNDFOEDNLCOSEROKASNLKRVNKEKNVSQNKKRKVE
- 1	1		KAEPASAAELSSVRKEEETAVAIOTIEEHPASFDWSSFKPMGFE
1			VSFLKFLEESAVKOKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
		İ	TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ	Predicted	Predicted end	1200
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid .	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
1	amino acid	secuence	Codon, /=possible nucleotide deletion,
	sequence	oogueee	\=possible nucleotide insertion)
<del> </del>			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		,,,,	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
-	ŀ		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
ł			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
	ì		CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMWVDCTCLGEGSGR
1	<b>!</b>		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
İ	ľ		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
(			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
	1		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
}			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDOW
1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	1	•	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
	ļ		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
ł	}	1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
Ì	-		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	i .		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
	1 1		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
i	1		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	1 1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\ABN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1	]		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	1		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1	1		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	1 1		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
ł			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
	}		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1 1		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	ļ .		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1	ĺ		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
ł	]		SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1		•	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1	'		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVTDVODNS
1			ISVKWLPSSSPVIGYRVTTT\PKNGPG\PTKTKTAGPDOTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
Į.	j i		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1	į J		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	! · · · · · · · · · · · · · · · · · · ·		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
	· [		NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	]		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1		•	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
ì	1		SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQB
	.	ĺ	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1		İ	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1	1		DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1	. 🖡		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
}	j	· ]	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
]			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
			ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		į	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
	<u> </u>		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
<b>\</b>	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	1	1	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
		<del> </del>	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
ŧ	i	1	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
l	}		
ŀ	1	l .	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
l			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
	1	i	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1		1	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
l	ł	1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
		i i	
ĺ		1	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
ì	i	i	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1	1	1	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1	1	{	DKOHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
}	ļ	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1		l	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1	1	1	
}		1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	1	1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
İ		1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
l	· ·	i	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1	i	i	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
	ì		POAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1	1	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
	1	1	
1	(		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
ı	1	1	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1	1	1	ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
ţ	ì	1	PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1	1	· ·	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	1	Į.	VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1	ı	i	
ı	1	ł	LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
į			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1	i	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1		<b>,</b>	GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
i		1	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1	I	l .	
1	i	i.	SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1	ł	1	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
j	i	<b>.</b>	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	1	1	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
ł		1	EGLOPTVEYVVSVYAONPSGESOPLVQTAVTNIDRPKGLAFTDV
1	Į	1	DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1		Į.	
1		1	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1		}	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	1	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1		t	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1	1	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1	1	1	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	1	1	
1		1	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
I	Ī	l .	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
ı	1	1	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1	1.		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	1		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1	1	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1	i		
1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
	1	1	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1	i		RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
i	1	ĺ	ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 2303	1 8088	1 '03	
1	1	į.	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
I		1	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
ł .		Ł	
Ì		1	QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
			QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
			QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK PEAEBTCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
			QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK

SEQ	Predicted	Predicted end	Amino acid compat
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
- [	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine.
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	scquence	sequence	Codon, /=possible nucleotide deletion,
<del> </del>	- Doquence	<del>                                     </del>	\=possible nucleotide insertion)
}			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
- (	ì		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
-		ľ	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
ļ		ļ	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
	į		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	·		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYOI
	1		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
i			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1			GHLNSYTIKGLXPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
}			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
- [			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
l			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
)			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLOFVN
ļ			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
į.			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
	1		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	· · ·		VSGLTPGVEYYYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1	1		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
]			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
ſ			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1	1		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
}	1		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTATPAPTDLKFT
	ļ j		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	i	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	1		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1	1		QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1			SCOOPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1	1		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
		Ì	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNOPT
		l	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
	1	į	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR RPGGEPSPFGTTGOSYNOYSORYHODTNTTRIAGELEGTMAN
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		.]	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
		1	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPOSPVAVS
1		1	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
]		1	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
		1	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
[ ]		ľ	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
		<del></del>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
.NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
<b>\</b>	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
ļ			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1	1		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
į.	(	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
<b>l</b> .	ļ	i .	GDSWEKYVHGVRYOCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
]	ł		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
	ı	ļ	
1		}	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	i	1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	Ī	1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1	1	1	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
}	ì		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
	1	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
l		İ	KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
ſ		1	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
ì			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
ł	1	į	PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1			TEVTETTIVITNTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
J		ļ	VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1	1	į.	LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
i	Į	1	HADOSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
	Į.		PPPTDLRFTN/ILGPDTMRVIW\APPPSIDLTNFLVRYSPVKNE
1		ł	GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
i	ì	}	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
ŀ	j	<b>J</b>	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
ı	1		SIVALNGREESPLLIGOOSTVSDVPRDLEVVAATPISLLI\SWD
1		1	
1	1	1	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
		ì	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
}	1	1	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
İ	1	1	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1	ļ	1	DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
	1	1	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
	I	1	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	ì	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1	1	1	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1	1	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
ĺ			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGS?PREVVPRP
i			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
}			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1		1	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1		1	ALSOTTISWAPFODTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
1		1	LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
ł			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
l			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1	1		HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1		1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1			ADREDSRE
F355	I	7.03	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
5367	235	3591	ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
- 1			
1	1		EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV
j			KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
1			GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
	1		SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
l l	i	1	LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
İ			LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
}		1	KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF
)	1	}	GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
1	1		FOVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
l			NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLBS
1	1.	1	ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEBEDNDEPLL
1	1	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
1	1	1	PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN
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Cortesponding   Coffred				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequen	NO:	1	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence  ### Se	1			H=H1Stidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence  SSETINE. T-Threcoline. V-Voline.  Amino acid sequence  Sequence  Sequence  NTFPADDYFROMERS. Wolfakown, *-Stop Codon, /-possible nucleotide deletion, \-possible nucleotide deletion NTFPADDYFROMERS.  NTRESENANCH.  NAMERS.	i			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence  #TTPPADARD. Y. Tyrus is a valuation, ". stop condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence condition and acid sequence conditions are conditional acid sequence conditions and acid sequence conditions are conditional acid sequence conditions and acid sequence conditions are conditional acid sequence conditions and acid sequence conditions are conditional acid sequence conditional acid sequence conditions are conditional acid sequence conditional acid sequence conditional acid sequence conditions are conditional acid sequence conditional acid sequence condition	j		5	P=Proline, Q=Glutamine, R=Arginine,
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				AVIIFFAIVVIIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	1	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		
<u> </u>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	ļ	\=possible nucleotide insertion)
ļ	<del></del>		TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF
i	1	ì	TOCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
	i		FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
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1	l .	1	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
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į	ł	1	TTLNMOTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
)	1	1	AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
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ı	1	j	EXSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
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1	-	1	QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1	1	1	TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
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ı	1	1	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1	l .	l .	KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1	{	1	IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
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RCQA/RGLPLPCECCRRFRIAPELALIMQVIAAAATDDWGFACH LCGGSFRGWAUALUHLARASAAKGPCKWARDAFWRRKAAS SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV SRRP PERGPPAKVFWGPRPRGPFIGTPRGFGGAVDRPPCQCC CCGKFRFRKYNINIASAAKGSGERPFQ/CSREGS\KFTNKPY LITS\RRRITHTARQPYPCKECGRFFRHKYNLISHSKIHKSEES AQAAFGGSCPQLPAGPGESAAEPTPAPUEKPAGEPPEGAPPEHP OPFIRAPPSLYSCDDGGRSFELEPFLRAHQRCHTGERPFTCASC GNFGKKTHLVAHSKYWSERPFELAGRUPGCRAPPEHP OPFIRAPPSLYSCDDGRSFELEPFLRAHQRCHTGERPFTCASC GNFGKKTHLVAHSKYWSERPFELAGRUPGCBAPPEHP OPFIRAPPSLYSCDDGRSFRHKPYLLAHIPPLAPAEKPYVCP DCRKAFSKSNIAVSHERITHTGERPACPDCDRSFSQKSNLITH RKSHIRDGAPCCAICGOTFDDEERLLAHQKKHDV  5376  4504  591  VSTFSLCLWPAGGGGRGRVSWMAQSKRHYSSTFSGSRMSAEAS ARPIRKVSSRVEVIGKRHRGTVAYVGATLFATCKRWGVILDEAGG KNDGTVQGRKYFTCDEGIGIFVRGSQTQVFEBDGATTSPETTDS SASKVLKREGTDTTAKTSKLRGLKFKAFTARKTTTERPFTEP ASTGVAGASSSLOPSGSASAGELSSSEPSTAGATLFATCKRWGVILDEAGG KNDGTVQGRKYFTCDEGIGIFVRGSQTQVFEBDGATTSPETTDS SASKVLKREGTDTTAKTSKLRGLKFKKAFTARKTTTERPFTEP ASTGVAGASSSLOPSGSASAGELSSSEPSTAGATLFATCKRWGVILDEAGG KNDGTVQGRKYFTCDEGIGIFVRGSQTQVFEBDGATTSPETTDS SASKVLKREGTDTTAKTSKLRGLKFKKAFTARKTTTERPFTEP ASTGVAGASSSLOPSGSASAGELSSSEPSTAGKUTLARAPTITAPT UTUSGGAVPPLPSPSEEBGLRAQVGTALFATCKRWGVILDEAGA KKLELEKKI QLEOVGEKKSKWGSQOQADLQRRLKRARKBAKEAL EAKERYMEEMADTAALEMATLTKEMAEERABSLOQFVEALKKRA KLKELEKKI QLEOVGEKKSKRWGSQOQADLQRRLKRARKBAKEAL EAKERYMEEMADTAALEMATLTKEMAEERABSLOQFVEALKKRA VDELITTOLEILKARLEEGESGGAASSTQLKCLGEENGARKKOALV RRRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRELQEELSQ AESTIDLEILKQUDAALGEENGAKTLANGLEVKRELRETUG DLEAMNEMDBULQENARSTSLEIRGLDMAGARVREQKRVEGAA OGTVADVQGTIKKYRGLERAUGHANGLEVVREQQREPLEESISC BAGGAGGOLFAALLKOLLAHARLEEQUDAGARVREQKRVEGAA OGTVADVQGTIKKYRGLERAUGHANGLEVVREQQOPPP ETFDFKKRFATKAKAKALEMELRQUEVAQANRHMSLLTAFMPD SELBAMBGGBOCTVALLUHPRLICKARLEKROQGENFELERGUNG SELRRGGGGBOCTVALLUHPRLICKARLEKROGQESTERGATCHATURVAVAUQEVAAAAQLI APALANGGOPTULADERSHIKKTTSTGSALCKSVG RLRAFLLGGGGBATDTALLLERLETGSQ\DAGARVARQATCHETGSVEVG RLRAFLLGGGGBATDTALLLERLETGSQ\DAGARVARQATCHETGSVEVG GAIGQAGSTOLAUALSELAFKASBQIVGTPSSEPYECLRGGCGIL INQUSTITTHVVDITTTSBAAKSBQIDTUVSGLAGERQUE SAKDALBRAGAGGU		1		RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
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SRPP-ERGPAKVFWGPRPRGPTGDTPPGGGDAVDRPP\QCA CGKRFRK\NPILSHAACTSERPJC\CSREG\RFTNKPY LTS\HRRITHTARGPYPCKECGRRFRHKPNLLSHSKIHKRSESS AQAAPGGSSQLPAGPGESAAEPTPAVPLKRAGEPPGAPPEHP OPPIEAPPSLYSCDOCRS-FILERAHQRGHTGERPPTCASC GKNFGKKTHLVAHSRVHSGERPFRLARKCGRFLPRASQSGGRN SAEPMAPPFGFPVCDCKAFFRHKYLAHRPILTAPEKPYVCP DCRKAFSQKSMI\VSHRRIHTGERPYACPDCDRS-FSGKSNLITH RSHIROBAFCCA-CGGTPDDERLIAHQKHTGERPFTCABCC ERGKTHLVAHSRVHSGGRFVSAMAGSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKCHRGTVANVGATLFAGKHVGVILDEAKG KNDGTVGGRKYFTLOEBCHI-FVRGSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP ARTGVAGASSSLAJESGSASAGELSSFSTAQTPLAPI-IPTP VLTSFGAVPPLPSPSKEEEGLRAQVRDLERKLETLRLKRAEDKA KLKELEKKKIQLEQVGMKSKMQEQOADLQRRLKEARKEALA EAKERYMEEMADTADALEMATLUKMBEERRESLOQEVEALKER VDELTTDLEILKAEIESKGSDGAASSYQLKOLECONARLKOALV RRDLSSEKQETWKLQEGVGMKSKMQELGVEVGGQRRCLQEELSQ AASTIDELKRQVDAALGAEEMWEMTJDRINLEEKVRELRETUG DLEAMMENNBELGENARETELELREGLDMAGARVERLQEETVG DLEAMMENNBELGENARETELELREGLDMAGARVERLQEETVG DLEAMMENNBELGENARETELELREGLDMAGARVERQKTVETAA OGTVADVQCTIKKYRGLTAHLQDVARGANTHMSLLTAFMPD SFLRRGGGBGBCVLVLLLHMFRLICKAELIRKQAGEKEELSENCSE REGLRGAAGSOLSFAALGLVY\SLMPAAGHTHRYY-CHALSQCR LD\VYKKVGSLYPBMSAHERSLDFILELLHKDQLDBTVAVEPLT KAIKYYGHLVSIHLARQPBEDTIELELHKDQLDTVAVEPLT KAIKYYGHLVSIHLARQPBEDTIELELHKDQLDTVAVEPLT KAIKYYGHLVSIHLARQPGETVAERPHSTY*CHALSQCR LDAGSTAALAFQOVSDTLLLCRGHLTWVAVLQEVAAAAQLI APLAENSGLLVAALEELAFKASEGIYGTPSSPYECLKGSCNIL STANKALVATAMGEGYDAATGLETGALLKKEKKEFEETMOLADALGALGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	i	i		LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
CCGKEFRIK/PNLIRSHAACTSGERPHO/CSREGG\RFTINKEY LTS\RRITHTHARGOPYPCKECGFREHKENLLSHSKIHKRSEGS AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP QDPIAPPSLYSCIDGCSRESTERFLERAHGRQHTGERFPTCAEC GNFGKKTHLVVAHSRVHSGERFFRLARKGGRFLPRASOGGGRI SAEPMAPRFGFFVCPDCGKAFRHKEYLAAHHPIATPAEKFYVCP DCRKAFSQKSNIL\VSHRRITHTGERFFYCPDCDGKAFRHKEYLAAHHPIATPAEKFYVCP DCRKAFSQKSNIL\VSHRRITHTGERFSGKSGNILTH RKSHIRDGAFCCAICGGTFDDEERLLAKCKKHDV  5376 4504 591 VSTFSLCLWPAGGGGGRGVSNNAGSRIVYSRFPSGSRMSAEAS ARPLAVGSRVEVIGKHRGTVAAVGATLFARGKNVGVILDEAKG KNDGTVGGRKYFTCDEGHGIFVRGSQIQVFEDGADTTSPETDS SASKVLKREGTDTTAKTSLIRGLKPKKAPTARKTTTRREKPTRP ASTGVAGASSSLGPSGSASAGELSSSEPSTAGTPLAAPIIPTP VLTSRGAVPPLPSPSKEEGGLARGVVRDLEERLETLELKRAEDKA KKELEKHKIQLEQVGDWSKKNGEQQADLGERLETLELKRAEDKA KKELEKHKIQLEQVGDWSKSNGEQGADLGERLETLELKRAEDKA KKELEKHKIQLEQVGDWSKSNGEQGADLGERLETLELKRAEDKA KKELEKHKIQLEGVGDWSKSNGELEVVRQORERLQEELSQ AESTIDELKEQVDAALGAEEMVENLETVRQCABERGUESCYEALKER VDELTTDLEILKAEIEKSGDGAASSYQLKGLEGONARLKDALV RRDLSSSEKGEHVK\LQKLMEKVELGVURGEREVGGPPP ETFDFXIKFAETKAHAKALEEKEKGDGAASSYQLKGLEGVRAKKEAA GETVADVQQTIKKYRQLATHLQQUVARELTVRQGEREVGQPPP ETFDFXIKFAETKAHAKALEMELRQMEVAGARRHMSLLTAFMPD SFLRREGGHDCVLVLLLMFRLLCKAELIRKQAGDKEFLSENCSE RRGLRGAAGGOLSFAAIGLVY\SIMPAGRHYRRY*CHALSQCR LD\VYKKYGSLYPBMSAHERSLIDFIILELHKDOLDETVAVEPLIT KAIKYYOHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGBATDTALLLRDLETGS\DITRGFCKKIRRRMGFT DAPGIPAALAFGGVGSTDLEDFGALLKRYGCHAAAAAQLI APLAENSGLLVAALEELAFKASEGIYGTPSSSPYECLRGSCNIL ISTNIK\LVTANGEGEYDAERPFSALFRAEEGHPVVALAAAAAQLI APLAENSGLLVAALEELAFKASEGIYGTPSSSPYECLRGSCNIL ISTNIK\LVTANGEGEYDAERPFSALFRAEEGHPVALARREITDA GGLGLKLEDRETVIKRLKKSKIKIGEELSENNTHILLEKKLDS AAKDADBRIEKVGTRLEFFGALLKRKEKEFEFTMALQADHIVELI KGAQMKASLASLPPLATVALLEHEGFGSELBAGALTVRKTSQLLET LNQLSTHTHVVDITTRISPAAKSPSAQLMEQVAQLKSLSDTVEKL KGEVLIPAEAGEKGQVITLEFGGSELFGAFARKTSQLLET LNQLSTHTHVVDITTRISPAAKSPSAQLMEQVAQLKSLSDTVEKL KGEVLIPAEAGEKGQVITLETGGGSEGEG\F*YHEVRQAEGES*X KWESCALGFGGRHKLVLTGGCGGEGEG\F*YHEVRQAEGES*X SWPGYDGWNGGQVIFIFROMREBGP  5378 2009 664 ODFCATTRELDEDLDGLGKERETSSRNRALKERGRLVILMTSCLPAL	}	<b>)</b>		SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV
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OPPIRAPPSLYSCHOORSFALERPLRAHORQHTGERPPTCABE GKNFGKKTHLVAHSRVHSGERPFRLARKCGRFLPRASQSGGRN SAEPMAPRGFPVCPDCCKAFRHKYYLAARIRPIATPAGERYYVCP DCRKAFSQKSNIA/VSHRRIHTGERPYACPDCDRSFSQKSNLTTH RSHITDGAFCCA ICGOTPDERLIAHOKKHDV  5376 4504 591 VSTFSLCUMPAGGGGRGVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGHRGTVAYVGATLFATKKNVGVILDEAKG KNDGTVQGRKYTTCDEGHGITVRQSQTQVEBOGDDTTSPETPDS SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRKPTPTRP ASTGVAGASSSLGPSGSASAGESSESPETPADTPLAAPIIPTP VUTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA KLKELEKHKIQLEQVQSWKSKMGEQQADLQRRLKEARKEAKEAL EAKREYMEMADTADAISMITLDKEMMEERAESLOQEVEALKEAR VDELITTDLEILKABIEEKGSDGAASSYOLKOLEGONARLKOALV HRNDLSSEKQEHVKALQALKEKQDELVVRQORERLQEELJQ ORTVADYQQTIKKYRQLTAHLQNEELJOQEVEALKOQEVERPA ORTVADYQQTIKKYRQLTAHLQNEELJOQEVEALKORGVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOQEVEALKORGVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOAGRAVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOAGRAVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOAGRAVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQLTAHLQNEELJOKAGARVREAQKRVEADA ORTVADYQQTIKKYRQTAHLAURALLARDEALGEROAGRAVREACKREADA SELIPAGAGGOLFALLERURLARDEALGEROAGRAVREACKREADA ORTVADYQQTIKKRYRQLTAHLQNEELLKOQLDETVANSPLIT KAIKYYOHLVSIHLAEQPEDETOMALADHIKTYCALLCKRYSEVYG RIARALGGGRATDIALLRDLETGSC)DIRGPCKXIRRRMPGT DAPGIPAALAFGPQVSDTLLLRDLETGSC)DIRGPCKXIRRRMPGT DAPGIPAALAFGPQVSDTLLLRRKEKEELSEADARAAQLI ISTINKALVTAMGEGETAGARDIYGTSSAPYECLRGSCONIL ISTINKALVTAMGEGETAGARDIYGTKSGLISGEGGGAAAAQLI GAIPGQAPGSVPGTYKKRESSAPLILQGISAMKHILSQLOHENSIL KGAQMKASLASLPPLHVAKLSHEGGGEEDAGAALYRKTSQLLET LIQUISTHHVVDITTRTSPAAKSPSAQLMDOVAGLKSLSDTVYKG KORGNARALASLPPLHVAKLSHEGGGGDAGAATRKTSQLLET LIQUISTHHTVDITTRTSPAAKSPSAGLMDOVAGLKSLSDTVYKG KORGNARALASLPPLHVAKLSHEGGGGEEGOFTYHEVROAGEGS* VEGQDAVRLUHTQLKTKKRPSGTLKAKFYLHTGSKFFAARISCTX SS*WPGYDGWGGQYIFIFRGMRMEEQD  5378 2009 664 OASGTTLRFLE	1			
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				RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
'	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	1	<del>                                     </del>	SFSFRNSKQTYSGVP11AANMDTVGTFEMAKVLCKS*VPGSFWD
	1		VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
	Į.		
ļ	Ì	1	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
	(	İ	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
		10	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	ĺ	ĺ	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
	i	į.	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
	1	Į.	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
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5379	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
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(	1		SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
ļ	1		VPOMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
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ļ	ļ	1	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
ì		1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
	l		EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	İ		HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
}	1	1	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
	ļ	1	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
İ	<b>,</b>	1	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
	<u> </u>	1	VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
{	1		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1	1		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
ł	1		SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
j.	1		RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
Ì	1	·	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
i	1		
1	1		RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
(			F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
ł	}	1	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1	1	1	FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
ì		ļ.	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
J	}	1	KLHPWYTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
i	1	I	
Ì	ì		ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
ł	i	1	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
1	1	1	*PEPPRTDEALCPXETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1	ł	}	PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
1 -553	1 ~	1	SOPSSNRAAPODELGGRGSSSSESQKPCEALRGLSSLSIHLGME
}	l .		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1 .	1		
1	1	1	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1	1	1	RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1	1	[	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
l	ł	ł	RGPI/EQVYQEIA/ILKKLDHPNVV/KLVEVL/DDPNEDHLYMV
ì	1	1	F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
l	1	1	
1	1	]	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1	1	1	FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
ì	1	1	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
ì	1	1	KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
1	1	1	ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
Į.	1	1	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
1	1	1	
I	1	1	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1		}	PDLVGAPGSHFCFLNIALLRYNSHTM.
5382	1536	203	GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS
I	1		VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
I	l	}	LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG
l	ı	1	
1	ł	}	YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
1	l	1	DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
1	1	1 .	RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
1	1	1	KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV
1	1		RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
1	1	}	WROVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP
ı			

SEQ	Predicted	T Dungal and T	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
7.0.	location	1	Glutamic Acid, F=Phenylalarine, G=Glycine,
}	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
- [		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	į.	\=possible nucleotide insertion)
} _			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
L	Į.	}	ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
1	1	ł	VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
1 .		l	CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
1		İ	HILLOO BY EVEN ON THE PROPERTY OF THE PROPERTY
1	ŀ	ł	HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
ł	1	ı	EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
1		į	PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
	Į.	į	IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
			PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
1	1		IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSFLSTLPGQ
ı	}		SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIROILEKKE
- 1	1		GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKI.TYP
			QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
1	1		QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNROPTLH
1			RPSIQAHRAR LPEEKVLRLHYANCKAYNADFDGDEMNAHFPOS
ļ			ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
1	1		CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
			TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
1	<b>J</b>		ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
	į i		LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
ĺ	1		CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
1			KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
1	j l		MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
	İ		PRITCI V PDE E E EUCMA CRECI ADMANGMENT CON CONTROL CO
<b>i</b> 1	·		RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
1			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
	i		RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
	! · · · · · · · · · · · · · · · · · · ·		ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD
1			YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
i l			LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
			ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
1 1			ESFCMEEKQNKFQVYQLRFQFLPHAYYOOEKCLRPEDIIRFMET
1 1	ļ		RFFKLLMESIKKKNNKASAFRNVNTRRATORDLDNAGELGRSRG
j	l l		EQEGDEEEEGHIVDAEAEEGDADASDAKRKEKOEEEVDYESEER
1 1			EEREGEENDDEDMQEERNPHREGARKTOEODEEVGL/GH*GGPV
1 1	1		PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYOYD
1	l		TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
) i			LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
] [	{		AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
] [	ļ		EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR
ļ	·		SPSACLVVGKVVRGGTGLFELKOPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI
1 1	ĺ		TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
1			APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
1 1	ļ		GQFAAPLRGIYPFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
1 1			ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
1 1	· 1	i	SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
1		1-7	SPTERPRET *I PROPERTY ALTERNATION NAMED AND ASSESSED ASSE
1 1	1		SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
} I	1		VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
5386	326	700	SDGERKAYVRLAPDYDALVVATKIGIT
		799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
, ,	. 1	ļ	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
	1	ľ	VKKIENNSLLVFTVDVKANKHOIKOAVKK/LCDIDVAKVNTT.TO
			SDGERKAYVRLAPDYDALVVATKIGIT
5387	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA
1		í	SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
[ ]		. [	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
1 1		į.	ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA
1	}	ł	TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ			S=Serine, T=Threonine, V=Valine,
i	amino acid	residue of	S=Seline, l=Intendice, v=varine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *≈Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	] <sup>-</sup>	\=possible nucleotide insertion)
ļ	sequence	ļ	SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
1	(	ĺ	IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
ì	ł	1	
1	ì	ļ.	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
1	i .		VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
i	1	1	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
i	i	1 .	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
}	Į.	1	
		1	ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
i .	ì	(	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
i		l .	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
	1		DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1	1	1	FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV
l .	1	İ	1 "
	1		DVA
5388	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
1	1	1	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1	I	1	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSV9EAQSALDST
}	1	}	THOMAS A CHAMINATION OF THE LANGUAGE AND AND AND AND AND AND AND AND AND AND
ł	ļ	1	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
I	1		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
1	ł		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
l .	1	1	ILEHLQTKN
		753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
5389	1569	/23	WHEN A WOMEN'S CHOLD DAMN OF THE COURT COT CCEVCNOD
1	1	l	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1	}	ł	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
	<b>.</b>	1	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	1	1	DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
1	1	· ·	TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
1	1	1	
		<u> </u>	ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
1	i	1	EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
1	1	Í	SAPICIAPTGPHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
ļ	j	1	LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
1	1	1	LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
1	i	i	
1	1		TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
1.	ì	1	ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
j	1	}	LTGCRSVAEINRNLVQFSRL
<u> </u>		1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
5391	1	1292	QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
1	i	1	GERACINCHINOROPY AND AGRICULTURE CONTACT TO THE CON
1	Į.	1	VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
1	ł	l	RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
1	1	1	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
1.	1	1	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
1	1	1	VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
1	i i	1	A TANDOLUNIA CONTRACTOR TO THE TOTAL OF THE
1	1	1	DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
i	1	1	YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
1	1	1	PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
F303	<del></del>	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
5392	1	1 1043.	CAAPCPLPALSRCRGAGSRGSRGSRGAAGSGDAAAAAEWIRKGS
	1	1	CAMPCPLPALORCROAGORGORGORGAAGOGDAAAAAAENIRROS
1	l	i	FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
J	1	ł	RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1	1	l	GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
		Ì	YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
ı	1	i	I AUT AUVOE THÄNUNCUT HENNENDOT EIBINANIS I DUNE HÄT
1	1	l	LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
1	1	1	GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
-	ŀ	ì	PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
i	1	(	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
]	1	1	T DODDWITCOMODD A COME DA DODOT TODOWNDOOVIA TOME
- <b>i</b> .	l	1	LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH
1	1	1	AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
1	ı		SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
1 33,73	1	1	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
	1	ſ	EVM TUTTE E LITHARD / COO A TRICOOM AT A DISCOURAGE AND AND A STATE OF THE PROPERTY OF THE PRO

SEQ	Predicted	T 12 T 17 T 1	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H-Histidine, I-Isoleucine, K-Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ŀ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
Ì	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	sequence	sequence	Codon, /=possible nucleotide deletion,
<b></b>	- Jodgaenee		\=possible nucleotide insertion)
1	İ		\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
ì	1	l	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
1			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1	Î	1	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1			STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
5394	<del> </del>		RAPTDDDKNIYLTLPPNDHVNSNN
3394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
i		ł	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
1 .		į	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
1		,	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
1	(		SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1	1	i	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
J	j		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
5395	<del></del>		RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
			KPTETPPVKETQQEPDERSLVPSGENLASETKTESAKTEGPSPA
		,	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
f	[		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
1			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
i	<b>(</b>		PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
}	]		ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
1			YPQPSDLSTFVNETKFSSPTEELDYRNSYBIEYMEKIGSSLPQD
			DDAPKKOALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
)			ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
1			SEATETTAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
1			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1	i		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	·		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
			YQALKVHA\EEKLDRANAB\IAQVRGKAQQEQAAHQASLAERSS
5396	3135		CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
1 3330	3133	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1 1	1		SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1 1			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
1. I			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
j <b>í</b>	<u> </u>		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1 1	ļ		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPAS?
1	1		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
<u> </u>	1		ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
j j	ļ		TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
] [	ſ		YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1 1	i		DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
[ ]	1		ALVNTAAKNOHPVPRGLAFNOESHLOVPEKSSOKELEAMGLGTP
j			SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
1 !		İ	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1 1	ł	ļ	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
] ]	Į.		YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
[ [	I		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
F 5307			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	l		SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
] }	}	ļ	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
ļ į			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	1	l	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
	1	1	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
<u> </u>		l	PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 20.		1	
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	1	\=possible nucleotide insertion)
			POCSYNFOPOTCOESVOPFKTSSKTPSSPSKSPASFEIPASAME
1			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1	Į.	l	TPAATPETPPVISAVVHATDEEKLAVTNOKWTCMTVDLEADKOD
	1	ŀ	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
	<b>{</b>	1	!
ĺ		1	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
l	t	1	ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
}	ľ	ł	SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
1	1	1	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1	(	1	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1	1	1	YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
l	1	1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
l	I	1	YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
l	1	1	CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
1	}	3320	HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
1	l	Į.	<b>-</b>
{	1	1	ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFFPGFLGPAT
1	]	1	TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE
ł	l		ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYLRLSSEQEK
1	l .	1	EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
	1		DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK
1		[	MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT
1			KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSER
1			TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP
i	•		FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
1			AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
I		i	ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK
Ì	ļ	1	TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
I			EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
1	-	ì	KCDTREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL
			I and the second
1		1	IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ
l	Į	I	KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
1	1	<u>l</u>	PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK
i			SEEVRPNIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE
1		1	LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
1		}	SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
l		1	DSVSQISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQV
Ī	1		KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ
		1	QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE
<b>}</b>	1		LOEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
I	1	1	TOKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT
ł	Į.		KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK
)	J		LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV
Į.			QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
1	}	1	, · · · · · · · · · · · · · · · · · · ·
Į.			EQLINQKVEEAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQV
1	1	1	EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
)	Į.		NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA
ł	1		ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE
1	1	1	ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI
1		· ·	MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
1	1		STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK
Į	1	1	ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ
1			KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
i		1	PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE
1			ISSPIDISGOVILMDOKMKESDHQIIKRRLRTKTAK
5399	705	220	
1 3333	,,,,	530	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
1			ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE
l			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
			\ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK
ł	1	1	QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE
L		1	TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN
<u> </u>	1	<del></del>	1

WO 01/53312 PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence.	Codon, /=possible nucleotide deletion,
	sequence	ļ	\≈possible nucleotide insertion)
ŀ			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIQTVKQV
			QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
			RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
1		1	QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
1	1	1	KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
1			SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
1		İ	HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\BE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
ļ			DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
ì		l	FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
1	1	ł	NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
1	1		LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
J	1	1	PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDTL
		1	TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
1		1	PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
ł	i	1	PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
ì	1		ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDL1YINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
	•		PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
1			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
ŀ			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
ł			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
į			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
1			PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL
1			TVEASCHDGDETIETIBAAEALLNMDSPGPMLDEKRINNNIFSS
1			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLNRKHKNKP\D
1			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
1			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
1 .	ļ		PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
(			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
5404	187	1111	QVAMKQNELLEPNSF
"""	10,	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT
			DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
j i			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
			SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
	Į		KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF
			CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIOPTA
			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
]	1		PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
1 [	1		NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS
[	1		LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
j	1		SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
1 1	į		YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
			NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWOCLDTAQONLYRNVMLENY

Predicted   Predicted   Predicted   Predicted   Procession   Process				
No:   nucleotide   location   corresponding   to first   maino acid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortion   Corresponding   to first   amino acid   amino acid   casiduc of   amino acid   casiduc of   amino acid   casiduc of   amino acid   casiduc of   casid			1	
to first amino acid residue of amino acid residue of amino acid sequence  Percline, Q-Goltumanine, R-Arginine, S-Serine, T-Threonine, V-Valine, amino acid sequence  Requence  REMUNEATING AND THE STATEMENT OF TH	NO:			
to first amino acid residue of amino acid amino acid residue of amino acid sequence  #Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \text{Voposible nucleotide deletion,} \text{Voposible nucleotide deletion,} \text{Voposible nucleotide deletion,} \text{Voposible nucleotide deletion,} \text{Voposible nucleotide deletion,} \text{Voposible nucleotide insection,} Voposi				
amino acid residue of amino acid sequence  sequence    Sequence	1			,
remidue of amino acid sequence (amino acid sequence) white properties and acid sequence (amino acid sequence) white sequence (amino acid sequence) acid sequence (amino acid sequence) acid sequence (amino acid sequence) acid sequence			II.	
amino acid sequence    Coden, /=possible nucleotide deletion, /  -possible nucleotide insertion		amino acid	residue of	
Sequence    Appossible nucleotide insertion	ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
RINJELGY 11 TANSERDLITCLEGGEREPREPRIENDAKPEPUNG SHPTODEW PROMISPINGCHAPTISCHEMINHSVORE SHPTODEW PROMISPINGCHAPTISCHEMINHSVORE CKYHROGYMOFNOCH PATOSEK FELPTISCUKAPFIKERSINSHELLS HTERKILFRCERCOKEP FOLLSHLADHI LITHTOWFECKERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERGORYMISSELTTHKKRUTTER KLYKCECGGARPORPSILTTHKILFRCERTYKCERGORYMISSELTHK KRITHKILFRCERCYKCERGORAFINDSTLTHKKILFRCERCYKCER KOCKARNOPSILTHKINENINGERYTICEGGCKYPROSTLTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINGSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINGSELTHKKILFRCERCYKCERGORAFINGSELTHK YKCERGGGAFKWSSILTHKKILFRCERCYKCERGORAFINGSELT		amino acid	sequence	Codon, /=possible nucleotide deletion,
RINJELGY 11 TANSERDLITCLEGGEREPREPRIENDAKPEPUNG SHPTODEW PROMISPINGCHAPTISCHEMINHSVORE SHPTODEW PROMISPINGCHAPTISCHEMINHSVORE CKYHROGYMOFNOCH PATOSEK FELPTISCUKAPFIKERSINSHELLS HTERKILFRCERCOKEP FOLLSHLADHI LITHTOWFECKERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERKOGKAF NCPS LITHKILFRCERCYKCERGORYMISSELTTHKKRUTTER KLYKCECGGARPORPSILTTHKILFRCERTYKCERGORYMISSELTHK KRITHKILFRCERCYKCERGORAFINDSTLTHKKILFRCERCYKCER KOCKARNOPSILTHKINENINGERYTICEGGCKYPROSTLTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINSSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINGSELTHKKILFRCERCYKCERGORAFINSSELTHK KRITHKILFRCERCYKCERGORAFINGSELTHKKILFRCERCYKCERGORAFINGSELTHK YKCERGGGAFKWSSILTHKKILFRCERCYKCERGORAFINGSELT	İ	sequence	1	\=possible nucleotide insertion)
CXVHRGGYNGFNGCLPATOSKTFLFDKCVKAFFIKESNSNEHLS HTEKKLFKCKEGGKSFCMSHLAGNKL HITMOFFICEKGKGKAF NCPSIITHKHRINTGEKFYTCERGGKYFMSSELTHKKNYTRY KIYKCEGGKAFMSSESLTHKKNYTRY KIYKCEGGKAFMSSELTHKKNYTRY KIYKCEGGKAFMSSELTHKKRYTRY KIYKCEGGKAFMSSELTHKKLHTGEKFYKCEGGKAFMSSELTHKKRYTRY CECGGAFMOPSIITHKRHTHGEKFYKCEGGKAFMSSELTHKKRYTRY CECGGAFMOPSIITHKRHTHGEKFYKCEGGKAFKSSELTHKK KNYTRYKLYKCEEGGKAFMSSELTHKKHHTGEKFYKCEGGKAFK KORARNOPSIITHKRHTHGKFYKCEEGGKAFMSSELTHK KNYTRYKLYKCEEGGKAFMSSELTHKKHHTGEKFYKCEEGGKAF AFMASSKLTHKKHTTGEKFYKCEEGGAFMOPSILTHKKHHTGEFYKCEEGGKAFM SSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHKKHHTGEFYKCEEGGKAFT SSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKCEEGGKAFT SSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHK HORITTGELKYKKFYCECKGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHK HNIHTGELKYKKFYCKECKGKAFMOSSILTHKHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTHK HORITTGELKYKKMILGSNAKDPROMYCCKGSONKSKELOVY YMCMOSTELBAFTTGETTATTTGETAFT KORMIGHT BOLKKWMILGSNAKDPROMYCCKGSONKSKELOVY YMCMOSTELBAFTTGETAFTTGETAFT OS PERROGSCCTGGAGMAGMACHATATTGETAFT KORMIGHT BOLKKWMILGSNAKDPROMYCCKGSONKSKELOWY YMCMOSTELBAFTTGETAFTTGATTGAFT ARABOTTTLAGTAFTATTGATTGAFT ARABOTTTLAGTAFTATTGATTGATTGATTGATTGATTATTGATTGATT	<del></del>	<del> </del>	<del> </del>	
CXVHRGGYNGFNGCLPATOSKTFLFDKCVKAFFIKESNSNEHLS HTEKKLFKCKEGGKSFCMSHLAGNKL HITMOFFICEKGKGKAF NCPSIITHKHRINTGEKFYTCERGGKYFMSSELTHKKNYTRY KIYKCEGGKAFMSSESLTHKKNYTRY KIYKCEGGKAFMSSELTHKKNYTRY KIYKCEGGKAFMSSELTHKKRYTRY KIYKCEGGKAFMSSELTHKKLHTGEKFYKCEGGKAFMSSELTHKKRYTRY CECGGAFMOPSIITHKRHTHGEKFYKCEGGKAFMSSELTHKKRYTRY CECGGAFMOPSIITHKRHTHGEKFYKCEGGKAFKSSELTHKK KNYTRYKLYKCEEGGKAFMSSELTHKKHHTGEKFYKCEGGKAFK KORARNOPSIITHKRHTHGKFYKCEEGGKAFMSSELTHK KNYTRYKLYKCEEGGKAFMSSELTHKKHHTGEKFYKCEEGGKAF AFMASSKLTHKKHTTGEKFYKCEEGGAFMOPSILTHKKHHTGEFYKCEEGGKAFM SSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHKKHHTGEFYKCEEGGKAFT SSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKCEEGGKAFT SSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHTHGEKFYKCEEGGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHK HORITTGELKYKKFYCECKGKAFMOSSILTHKKHHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKFYKCEEGGKAFMOSSILTHK HNIHTGELKYKKFYCKECKGKAFMOSSILTHKHTGEPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTH NIHTGELKYKKFYCKCECKAFMOSSHTOMEOPYKC ECGKAFMYSSHLTHKKHHTGEKPYKCEEGGKAFMOSSILTHK HORITTGELKYKKMILGSNAKDPROMYCCKGSONKSKELOVY YMCMOSTELBAFTTGETTATTTGETAFT KORMIGHT BOLKKWMILGSNAKDPROMYCCKGSONKSKELOVY YMCMOSTELBAFTTGETAFTTGETAFT OS PERROGSCCTGGAGMAGMACHATATTGETAFT KORMIGHT BOLKKWMILGSNAKDPROMYCCKGSONKSKELOWY YMCMOSTELBAFTTGETAFTTGATTGAFT ARABOTTTLAGTAFTATTGATTGAFT ARABOTTTLAGTAFTATTGATTGATTGATTGATTGATTATTGATTGATT		ł	<b>}</b>	1 · · · · · · · · · · · · · · · · · · ·
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LSTHKI IHTGER PYKCEKCKARNIPSSALIEHKKI HTGEOPYKE GECKARNIPSSALITH RICHKENDY KEGEKARNOYSNITTH NIKHTGEKLY KYEDVTYLITTPQTFSIN IK  8787878585CTTGWLÄGWLLRAAPRFCRRTETDMEGGKGLAVLIL ALILLGGTLAGSI KRINHEVKY YNY QUEDOSVLITCDAERKINTWF KOGMIGFLTEDKKKWILGSIAKDRAPRFCRRTETDMEGGKGLAVLIL ALILLGGTLAGSI KRINHEVKY YNY QUEDOSVLITCDAERKINTWF KOGMIGFLTEDKKKWILGSIAKDRGMYQCKSQMKSKPLQVY YRMCQNICIELNAATISGFLPAETUST FDLAWGYYF LAGTMEFF GS VARMONGELNAATISGFLPAETUST FDLAWGYYF LAGTMEFF GS VARMONGELNAATISGFLPAETUST FDLAWGYYF LAGTMEFF GS SANDON GUERRH GS VARMONGELSAAP FTOLAGGSOPPTHYPORLPH HAROHTPLPLGSADYRRVUSWPDGPHRDPKDSSDAAKREGGSL ARPEVPASRGKTLLKGWROAPROPPORDER LCSAS PPWASRF STPCFGGAVREDTYPUGTOGYPSLALAGGGPOGSWRFLEWKSWP RLPTDLDIGGPWFPHYDFERSCWRAI SQEDQLATCWOARHCGE VENNKOMSWPEEMSF TANSSKIDCHKYPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFI SGRHLYELMRTNIPICHKGHMAKCYGD LUQGELWSGTCKWAPLKURWT LAKAPRENGFQQODS GELLAFL LLGHEDLNRVILEKPYVELKDSDGRPDWEVAAEAMDHHLRRWRS I VVVDLFBGGLRSQVKKYCGHI SVRPFRISS,PLPMDSYMHL EITVIKLDGTTPVRYGLKURWT LAKAPRENGFQQODS GELLAFL LAEVHGROLKSPOTLY BENGKOM KORNON KVRLSVSGFTPHISS,PLPMDSYMHL EITVIKLDGTTPVRYGLKIMDEKYTGLKKQLSDLGCLANSQOLL LAEVHGROLKSPOTLY BY STANDSYNTEL LAEVHGROLKSPOTLY BY STANDSYNTEL EITVIKLDGTTPVRYGLKIMTHRYMFTLTYPLSSGNRR PSLEGMPLIVPDGTYSTAND FOR STANDSYNTEL STANDSYNTEL EITVIKLDGTTPVRYGLKIMTHRYMFTLTYPLSSGNRR PSLEGMPLIVPDGTYSTAND FOR STANDSYNTEL S	1	1	1	
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AILLOGTLAGS IKGNILVKVTDYØDEDSVLITCDAERANTTWE KOGKNIGFLTEDKKKWALGSANADPRGMYCKSGONKSKPLOVY YRMCQNCIELNAATISGFLPAEIVSIFDLAVGVYFIAGTGMEPR OS\RASDKQTLLP\NDDAPTQPLKDPRKMTYSHLQGA\QURRIN 5408  2745 6128  GGSKGTCHFQAQQWBGSWQGSEPSFYMFQRL\QURRINGSKARGGSL ARREVPASRGGKTLCKGYRQAPEPAQFORFICSASPPMASG ARREVPASRGGKTLCKGYRQAPEPAQFORFICSASPPMASG INFOLIGIG PWFPHYDFERSCWVRAISQGEQGSWEFLEWKSMP RIPTDLDIGG PWFPHYDFERSCWVRAISQGEQGSWEFLEWKSMP RIPTDLDIGG PWFPHYDFERSCWVRAISQGEQLATCWQAEHCGE VENKOMSWBEEMSFIANSSKIDRHKVPTEKGATGLSNIGANTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSCTQKNVAPLKLRWTLAYAPRENGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRNRS; IVVDLFHGQLRSQVKCTTCGHEXPPFPMFLSLPLPMBSYMHL EITVIKLDGTTPVRYGLRLMMDEKYTGLKKQLSDLCGLNSBQIL LAEVHGSNIKNFPQDNKVRLSVGFLCAFEIPVEVSTISASSP TOTIDFSSSPSTNEMFTLITINGDLPRIFIFIDHMEN-VVPCGTEX NFTNGMVNGHMPSLPDSPFTGYIIAVHR KMMRTELYFLSQKIRR PSLEGMFLIVDCTVHTRKKDLVMIVQVSGLASFLPPDGASNH AQDCDDSMGYQYPFTLRVQKDGNSCAWCDWKFCRGCKLDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHSSVEGSRAQ VEPINLDSCLRAFTSEELERMYVCSKCKTHCLATKKLDLWR LPPILLIHLKRPQFVNGRWIKSQKIVKFPRESFDESAFLVFRDB ALCOMKPLTPQGDELSEPFILLSKKVDAQSSAGEDVLLSKS PSSLSANIISSSFKGSPSGSPSSRSSSSPNSSPNSTDRIGRS KGRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRAD VLGGSQPELVTFQDHEVALANGFLYBEHEACGNGCGNGYSNGOLG MISEEDSTDQREDTRIKPITNIVAISIGSILIGGGHYVTYAKN PNCKWYCNDSSCKSLHPDEIDTDSAYILFFEQGIDVAQFLFK TDGKKMADTISSMDEPFSDYYEKYCVQPSSAGEDPULLSKS STCCGGAVREDTTYPOTGCYPSLALAQGGPQSWFFLEWKSMP PNCKWYCYNDSSCKSLHPDEIDTDSAYILFFEQGIDVAQFLFK TDGKKMADTISSMDEPFSDYYEKYCVQPSSAGSPOLLSAFL STCCGGAVREDTTYPOTGCYPSLALAQGGPQSWFFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVALAGSDQDLATCWQAEHCGE VANKMSWPEEMSFIANSSK LARKVYTEKGAGLSINLGNTCFM NSSIQCVSNTOPLTYPTGGCPYSLALAQGGPQSWFFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVALAGSDLATCWAEHCGE VANKMSWPEEMSFIANSSK LARKVYTEKGAGLSINLGNTCFM NSSIQCVSNTOPLTYPTGTGGYPSLALAQGGPQSWFFLEWKSMP RLPTDLDIGGBWFPHYDFERSCWVALAGSDLATCWAEHCGE VANKMSWPEEMSFIANSSK LARKKYTEKGAGLSINLGNTCFM NSSIQCVSNTOPLTYPTGTGGYPSLALAAGGBLAARTCTCH NSSIGCVSNTOPLTYTGTARYPTGLKKQLSDLCLANSGELLAFL LDGLEWSGTGVANPLKLRWTIAKYAPFENFGQODSQELLAFL LDGLE	5407	<del>  1</del>	659	
KIGKMIGFLTEDKKKWNILGSNANDPREMYCKGSONKSKPLOVY YRMCONCIELNARTISGFLPAFLVSITPDLAVOVYPIAGTGMEPR OS\RASNKQTLLP\NDPAPTQPLKDPKKMTQYSHLQGN\QLRN OSKGTCHPQAQQFWDEGWQEAPSGSEPFGGSGSPPTMFQRLP HARQHTPLPLGSADYTRVVSVRPQGPHRDPKDSRDAKREGGSL APRPVPASRGKTLCKGYRQAPPGPPAQFQRFICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWFFLEWKSN RILPTOLDIGGPWFPHYDFERSCWRAISQEDQLATCWQAEHCGE VENKOMSWBEEMSFIANSSKIDEHKVPTEKGATGLSNIGNYCFW NSSIQCVSNTQPLTQYFISGRLFWEENTRYTGKKGHAKKYGF LVGLEWSGTOKNVAPLKLRWFISQEDQLATCWQAEHCGE LVGLEWSGTOKNVAPLKLRWFISQEDQLATCWQAEHCGE LVGLEWSGTOKNVAPLKLRWFISQEDQLATCWQAEHCGE LVGLEWSGTOKNVAPLKLRWFISQEDQLATCWQAEHCGE LLGGLHEDLNRVHERPYVELKDSRPDWEVAAEAMDINHLRRNS LVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGGLRLWMDEKYTGLKKQLGBLCGLNSEQIL LAEVWIGSNIKNFPODNGKVRLSVGFLCAFEIFVVVSPISASSP TOTDFSSSPSTNEMFTLITMSDLPRIFIFINGMPN-VVPCGTEK NFTNGMVGGHMPFDADHFYDALFRYLTSLYFLSGKGLASEQIL LAEVWIGNIKNFPODNGKVRLSVGGELCAFEIFVFVSPISASSP TOTDFSSSPSTNEMFTLITMSDLPRIFIFINGFRCGKINGGE NFRIGMAYIAVDMPTPALHERYTSTSCERVWDEHESVEQSRRAQ VSPINLDSCLRAFTSEELGENEMYCSKCKTHCLATKKLDLWR PSLFGMPLIVPCTVHTRKKDLYDAWIQVSRLASPLPPQEASMH AQDCDDSMGYQYPFTLRVVQKGGNSCAWCFWRFFCRGCKINGGE DRAFIGMAYIAVDMPTPALHERYTSGCERVWDEHESVEQSRRAQ VSPINLDSCLRAFTSEELGENEMYCSKCKTHCLATKKLDLWR LIPHLIIHLKRPGFVONGRIKSKOKIVAFFRESEDSAFLVPRDD ALCQHKPLTPQGDELSEPRILAREVKXVDAQSSAGEEDVLLSKS PSSLSANIISSSFKGFSCSSSSKNSSPNSSPRTLGRS KGRLRPQTGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFILYBLEAGGNCCCMYSNOQLG MISEEDSTDORGENTIK HYLATASCHSGLIGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTISSMDEBDFSDYLKSYCULGGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTISSMDEBDFSDYLKSYCULGGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTDSAYILFYEQGGIDYAQFLPK TDGKKMADTISSMDEBDFSDYLKSYCULGGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTGSAYILGGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTGSAYILGGGHYVYTAKN PNCKNYCYNDSSCKELHPDEIDTGAYILFYEQGGIDYAQFLPK TDGGAVREDTYPVGTQGVPBECWGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3207	1	1	
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GS\RASDKQTLLP\NDPAPTQPLKDPRMTQYSHLQCN\QLRRN   5408   2745   6128   GSKGTCHPQAQQFWDEGVWQAPSQSEPWGQSQEPTMPQR\LP     HARQHTLPLGSADYRRVVSVRPQGPHRDPKDSRDAKREGGSL     APRPYPASRGCKTLCKGYRQAPPGPPAQFQRPICASSPPWASRF     STPCPGGAVREDTYPYGTGYSLALAQGGPGGSWRFLEWKSMP     RIPTDLDIGGPMFPHYDFERSCWVRAISQEDQLATCWQAEHGGE     VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM     NSSIQCVSNTQPLTQYFISGRHLYSLDRTNPIGKGMAKCYGD     LVQELWSGTQKNVAPLKLRWTIAKYAPFFNGFQQQDSQELLAFL     LGGLHEDLINFVHERPYVELKDSDGRPDWEVAAEAMDHLHRNRS     LVVDLFHGQLRSQVKCKTGGHISVRPDFNFILSLPHDSYMHL     EITVIKLDGTTPVRYGGLRINMDEKYTGLKKQLSDLCGLNSBQIL     LAEWIGSNIKMFPQDNQKVRLSVSGFLCAFEIPVPVSFISASSP     TQTDPSSSPSTNEMFTLTTNGDLPRFIFIPVPVSFISASSP     TQTDPSSSPSTNEMFTLTTNGDLPRFIFIPVPVSFISASSP     TQTDPSSSPSTNEMFTLTTNGDLPRFIFIPVPVSFISASSP     AQDCDDSMGYQYPFTLRVQKQDGNSCAWCPWYRFCRGCKLDCGE     DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSKRAQ     VSPINLDSCLRAFTSEEELGEMEMYCSKCKTHCLATKKLDLWR     LPPILIHLKRPGFVNGRN IKSGKTVKFFRESFDPSAFLVPRDP     ALCQHKPLTPQCDELSEPRILAREVKVDAQSSAGEEDVLLSKS     PSLSANIISSPKGSPSSSRKGSTSCPSSKNSSPNSSPKTLGRS     KCRLRLPQIGSKNKLSSSKENLDASKENGAGGICELADALERGH     VLGGSQPELVTPQDHEVALANGFILKHEACGNGCCNGYSNGQLG     MISEEDSTDDOREDTRIKPLEBACGNGCCNGYSNGQLG     MISEEDSTDOREDFETNY LYRIVALSCHEGGHGVYTYAKN     PNCKWYCYNDSSCKSLHPDEIDTDSAYILFYEQQGIDYAQFLPK     TDGKKMADTSSMDEDFEDDY LSKTCLGGGGPPTMPQRLP     HARQHTPLPLGSADVRRVVSVRPQGPRDFNDSRDAKREQGSL     APRPYDASRGGRYLLCKGYRQAPPGPPAGFRICASSP PWASRF     STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWFFLEWKSMP     RLFTDLDIGGPWFPHYDFERSCWRAISGEDQLATCWQAEHGE     VKRKMSWPBEEMSFIANSK INRHKYPTEKGATGLSNLGNTCFM     NSSIQCVSNTQPLTGYFISGRHLKGKGTGGGGCLAPL     LDGLEBDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS     LVQLLWSGTQKNVAPLKLRWTIAKKPGTPGQGDSGSLAPL     LDGLEBDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS     LVVDLFHGGLRSQVKCKTCCHISVRPDPFNFLSLELPHDSYMHL     LTVIKLDGTTPVYYGLIKMPDEKYTGLKKQLSDLCGLMSGULL     LTVIKLDGTTPVYYGLIKMPDEKYTGLKKQLSDLCGLMSGULL     LTVIKLDGTTPVYYGLIKMPDEKYTGLKKQLSDLCGLMSGULL     LTVIKLDGTTPVYYGLIKLMPDEKYTGLKKQLSDLCGLMSGULL     LTVIKLDGTTPVYYGLIKLM	}	1	l	
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HAROHTPLEJGSADYRRVYSVRPOGPHRDPKDSRDAAKREGGSL APRYVPASRGKTLCKGYRQAPFGPPAGFORPICSASPPWASRF STPCPGGAVREDTYPVGTGGVPSLALAQGGPQGSWRFLEWKSMP RIPTDLDIGGPWFPHYDFERSCWYRAISQEDQLATCWQABRICGE VRNKDMSWPEEMSFIANSSKIDRHKVYPTEKGATGLSKLIGNTCFM MSSIQCVSNTOPLTQYFISGRHLYELMRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWIIAKYAPRFNGFQQDSGELLAFL LDGLHEDLMRVIEKPYVELKDSDGRPWEVABEAWDHALRRWIS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSIPLPMDSYMHL EITVIKLDGTTPVRYGLRLMMDEKYTGLKKQLEDLGCLNSBQIL LAEVHGSNIKNFPQDMDKVWLSVSGFLCAFEIPVPVSFISASSP TOTDFSSSFSTNEMFTLTTMGDLPRFIFIPNGMPNTVVPCGTEX NFTMGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYPLSSQKNR PSLFGMPLLVPCTVHYRKKDLYDAVHIQVSRLASFLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPDAHLRVYTSGERVVDEHESVEOSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPFILIIHLKRPGFVNGRWIKSGKIVKFPRESFDFSAFLVPRDP ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSRKSGTSCPSKMSSNSSSPRTLGRS KGRLRLPQIGSNKKLSSSKBNLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVYALANGFLYEHEACGNGCGNGYSNGQLAG NISEEDSTDDQRSDTRIKPIYNLXISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYFQQGIDYAQFLPK TDGKKMADTSSMDEDTESDY\EKYCVLO  5409 2745 6128 6128 6128 GSKGTCHPQACQPWGEAPSGSBPWGGSPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHDPDKDSRDAAKREQGSL APRYPDASRGGKTLCKSYRQAPPGPPAQFGRFICSASPPMASRF STPCFGGAVREDTYPVGTOGUPSLALAQGGPOGSWFFLEWKSMP RLPPTDLDIGGPWFPHYDFSCWAMALAGGDOLGLATCOACHEGGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLITQYFISGRHLYLELNRTNFIGMGHMAKCYGD LVQELMGGTQKNAPALKLRWFIAKFAPRIGFQQQDSGELLAFL LDGLHEDLNRVHEKPYVELKGDSGRPDWEVAARAMDNHLRRNRS IVVDLFHGGLRSQVKCKTCCHIISKFPDFFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLGGLMSEGLI	L		<u> </u>	
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LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVARAMDNHLRRNRS TVVDLFHGQLRSQVKCKTGHISVRPDFFNFISLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVIGSNIKNFPQDNQKVLSVGGFLCAFEIPVPVYSPISASSP TOTDFSSSPSTNEMFTLTTNGDLDFRPIFIPVPRYSPISASSP TOTDFSSSPSTNEMFTLTTNGDLDFRPIFIPVPRYSPISASSP TOTDFSSSPSTNEMFTLTTNGDLDFRPIFIPVPRYSPISASSP TOTDFSSSPSTNEMFTLTTNGDLDFRPIFIPVPRYSPCASNH AQDCDDSMGYQYPFTLRKVDLYDAWIQVSRLASFIPPQEASNH AQDCDDSMGYQYPFTLRKVDLYDAWIQVSRLASFIPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVUMPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRMIKSQKIVKFPRESFDPSAFLVPRDD ALCOHKPLTTQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSKNSSPNSSPRTLGRS KCRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGSSQDELVTPQDDEVALANGFLYEHBACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQGGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ GSKGTCHPQAQCOPUDEGWAGEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSURPQGPHRDPKDSRDAAKREQGSL APRPVPARSRGKTLCKGYRQAPPGPPAQFGRPICSASPPWASFF STPCPGGAVREDTYPYGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSRIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGFMAKCYGD LVQELMSGTOKNVAPLKLRWTIARYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAFAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLMNDEKYTGLKKQLSDLCGLNSEQIL	1	1	ł	
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DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEDVLLSKS PSSLSANIISSFKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCCNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ  5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPFGPPAQFQPPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFLANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLFLPMDSYMHL EITYIKLDGTTPVRYGLRIMMDEXTTGLKKQLSDLCGLNSEQIL	1		1	
VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPOFVNGRWIKSOKIVKFPRESFDFSAFLVPRDP ALCOHKPLTPQCDELSEPRILAREVKKVDAQSSAGEDVLLSK PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLVAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLO  5409 2745 6128 QGSKGTCHPQAQCPWDEGVWQEAPSGSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQPRICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFILANSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKVAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITYIKLDGTTPVRYGLRIMMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
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ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGGSKNKLSSSKENLDASKENGAGQICELAADALSGGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLVAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ  5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSURPQGPHRDPKDSRDAAKREQSSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPMASRF, STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSVRFLEWKSMP RLPTDLDIGGPWFFHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKCHMAKCYGD LVGELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEXTTGLKKQLSDLCGLNSEQIL		1	1	
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PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ  5409  2745  6128  QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPYGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELMRTNPIGMKCHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLFLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	ł	j	J	
TDGKKMADTSSMDEDFESDY\EKYCVLQ  5409  2745  6128  QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP  HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL  APPPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF  STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP  RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE  VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM  NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKCHMAKCYGD  LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL  LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS  IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLFLPMDSYMHL  EITVIKLDGTTPVRYGLRLNMDEXTTGLKKQLSDLCGLNSEQIL	1		1	
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HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFILANSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
APRPVPASRGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	
APRPVPASRGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	ł	I		HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDFFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFN NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKCHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDFFNFLSLFLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFN NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKCHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDFPNFLSLFLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	
NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLÆWTIAKVAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLFLPMDSYMHL EITVLKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
LVQELWSGTQKNVAPDKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL				
LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAFAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		
IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	ŀ	j	1	I DOLINOLINGUENDALEI MEDUDUEMY ILYANDIEN ILYANDEN ILYANDE
EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1		TIME BUONT DOMINONTORUS CONDENSES, CT.DI. DMDCVMII.
LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP	ı		i	
LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP	ł			EITATKTDGLLAKAGTKTWWDEKALGPKKÖPPDFCGTWREGTP
	L			LAEVHGSMIKNFPQDNQKVKLSVSGFLCAFEIFVPVSPISASSP

CEO	T & T 37	,	<u> </u>
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
	location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amine acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
•	l		TOTOFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
ì			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
1	1	] '	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1	!		DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
j			VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
]			ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGOLG
			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
5410	2	710	TDGKKMADTSSMDEDFESDY\EKYCVLQ
5.20		710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
į į	ļ		VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
			NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
1 1			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
	·		GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEOTLONHOOEN
! !			GGEFFLIGVSGGTASGKSSVCAKIVQLLGONEVDYROKOVVILS
'			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
]			KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
1 (			DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALENSLMASPNN
1	Į.		KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1 1	1		NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
1 1			KRRYSALEVDEEAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
1 1	1		IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
1			KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
1			HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV GLDDETPQLLGPTHKKKSKKKKKKKSNHQEFESLAMPEGSQVGS
1 1	į		EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
1			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1 1		. i	SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
			VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
1 1	1	}	LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1		ſ	LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
			KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
j .			SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK
1 1	1		EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
( . /	1		KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDINEI
	1		DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYI.
	ļ	J	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
5413	3753		SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
	3/33	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
1	. [	· · · ·	TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
1	}	1	HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
1	}	1	KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
1		. 1	IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
1		j	SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAG
· }	J		VSAAFGAPVGGVLPSLEEGASFWNOFLTWRIFFASMISTFTLNF
J			VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
		ſ	GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
			FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

C 220	D. 27		
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
,	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
ļ	seddence		17
}	1		SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
1	1		SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV
	i		RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
1	†	ļ	HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
ĺ			DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
1	1	i i	FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
[	Í		LSEFMNPSPYTVPQEASLPRVFKLFRALGLRHLVVVDNRNQVVG
	<u> </u>		LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
1			QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
1	1		AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP
l	1		RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINILNYMDRFTV
]	1	<b>!</b>	AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
1	1		RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
į	į		STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD
ł	1		MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
			NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
	1		RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
ı		f	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
ł		Ì	IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
į	ļ		AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG
		Ì	AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL
	1	1	IISPLRCLFEEKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF
ļ	Į.		RLDMLKNKAKRSLTESLESILSRGNKARGLQEHSISVDLDSSLS
	ŧ		STLSNTSKEPSVCEKEALPISESSPKLLGSSEDLSSDSESHLPE
i	1	1	EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
1	1	1	RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL
I	1		RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEOGPFGPPPE
ł			EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
[	1	[	LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
1	1	1	GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
	i		SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
Ì	1		VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM
1	(		IILQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSLYAAPWFLTMF
Į.	1		ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN
ļ	1	<b>{</b>	LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH
	1	1	VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
1			RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
<u></u>	L	<u>                                      </u>	AKPSDREPECTQPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
ł	}	· ·	YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
)			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1			ENROLPPPSPOLPKHNLHVTKTLMETRRRLEQERATMOMTPGEF
ł	1		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
1	j		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
	1	Ì	AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
l	1	1	SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
1.		l	TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
l .	]		RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
I	1	1	AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
I	1		KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1	1		MDLVDTCVGTSVETNSVGISCOPECKNKVVGPELPMNWWIVKER
l	1		VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1	1		NLNLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
l	1		MAVPRIADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
ł			TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
1	}		PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR
I	1		RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
l			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
1	]		EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPB
	l	<u> </u>	T

SEO	Predicted	Y	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
(	sequence	Doguenoc	\=possible nucleotide insertion)
<b> </b>		<del> </del>	QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1	ł		ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
Į.	(		ESSSESDDECDVIEYPLEBEEEEEDBDTRGMAEGHHAVNIEGL
į.	ł		KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
J	Ì		PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
		j	SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLIDADVCNVD
-	1	l	HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASOAG
ı	Ĭ	1	QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
į		1	HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
1	1		HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK
		/-	YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
1	1	1	LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1	}		ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
]			RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
1	l	}	SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
	j		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
1	1		SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
1			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
1	1		RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
}		· ·	AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
1			KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1	1		MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
1.			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
1	ł		MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ
J	<b>]</b>		TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
l			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQI:TVGLTASR
l	1		RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIOKLLAEOO
j		ı.	TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
	1	•	EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSOTSOPE
ł	}		QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDOIAAGLYACTNN
1	[ ]		ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1	i l		ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL
1	1.	•	KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
1 .	}		PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
		•	SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD
1	{		HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG
1			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
]	.		HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
5418	24		HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
	24	1133	SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
j l			KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR
			RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
[	}		DGHQEVEKVQPPGPVKEMAHGSQRAEAPGAVAGAAEVPR\EPPI
j	· }	:	LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
1 1	[		GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL
į į			EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE
] ]			EEQAVLDRLTPDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR
5419	1395	259	GQRFDPAMFNISPGAVQF
	1333	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG
] [	ļ	• }	SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA
1 1	į		KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL
1 1	[	. }	PORIQOWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH
j	ļ		ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR
l i	İ		VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT
, ,	1		YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK
l l			
	)		RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN
5420	117	7723	RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	RAGLLALMLHOTIQHDPLTTDLRSSADR NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHBRIR

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<b>]</b>	\=possible nucleotide insertion)
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
		[	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
	1		LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
1	}	1	YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
)		1	YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
Į.	1		QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
i			EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
}	Ì	l	YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
1	ļ.		TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5421	117	1733	RAELIRAFGERE NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
		1 1/33	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
1	1	[	ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	l .	1	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIOWLNGS
l	1	ļ	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
1			YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1		ì	YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	<b>{</b>	Ì	QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
1			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
j	Į.	1	EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
1		1	YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
İ			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5422	3	1263	RAELIRAFGERE
3122	1	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
l			KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
1			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQIJ.YAKKLYDSAF
		i	HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
ĺ			NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
	<b>{</b>		LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
(			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
			FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
L			EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
Í	[		PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
1			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
}			LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQBRAEPRG GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
1	l		GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
1			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
1	[		TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
l			SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPOL
1			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
]	]		LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1			PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1			EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
			SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
I	]		NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
5424			DKKPMAAMEHPCEGV
2424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
			PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
			LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
			GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
	1		TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
	<u> </u>		TAMESTALLE SCENE STONE OF THE S

SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	
No:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine
- (	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
*	amino acid	sequence	Codon, /=possible nucleotide deletion
L	sequence		\=possible nucleotide insertion)
1			SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
ŀ	1		RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
	ļ	Ì	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
ĺ	1		PASFPSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
	{	ł	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
	i	İ	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1		<u>.</u>	SMITCING CONTROL AND CONTROL AND CONTROL OF THE CON
	İ	l	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
	1	ļ	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
5425	1086	115	DKKPMAAMEHPCEGV
	2000	113	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
1		1	NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1	j		ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
}			AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
Ì			KYELGPALYLGNSASLISILGGLCLCSACCCGSDEDPAASARRP
l	j i		YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
		*	PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
5426	<u> </u>		NCSWEVAYLPSEAGSLIF
3426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1	!		GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAAROLLDDEEDI.
l .	j j		TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGOYMEK
1	j		LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGOR
1	1		KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMOLHGVLRVIL
ı	1		EPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
1	1		TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1	l J	,	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
	! !		POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1	i l		LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
1	l i		VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
	1		MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
	Į l	:	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1	ľ		KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
i			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1	1		VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
	· }		ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
	Ì		LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
1			PKPUTPCLELOVPCPCPCVA COLON PLANTANTANTANTANTANTANTANTANTANTANTANTANTA
[ .	1		RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
	}		SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
]			GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
, 1			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
·			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5427	42	3425	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
{	1	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
j [	}		PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
j	]	•	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
	1		TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
1	į		LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
	ł		KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
, (	i		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
j <b>i</b>	į.		TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
	1		LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEBLN
[	}	·	POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1	1	ł	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEOVLOWNVIG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1		1	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
. 1	Ţ		PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
i		l	VKLKLAGRSFRSHVUREDLNPRWNEVFEVIVTSVPGQELEVEVF
l		. 1	DKDLDKDDPI CECKATA I MINIT NOCES PRINT NO CEST PRINT NO CE
	<u></u>	<u></u> L	DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	- Sequence	Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
		J	ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
		l	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ì	ì	<b>{</b>	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
- }	I	j .	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
1		ľ	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1	1	}	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5428	3	1839	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
1 3120	,	1839	SSRSERLSACATAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
1	1	1	LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
1		I	LAASIPYFHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG
1	1	1	NLAIDQONVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
1		l	RQFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
1	1		VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
-	1	Ī	FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
l l	1	Į.	AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
1	j	1	CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
1		1	WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
i i	1	ł	TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
	<u> </u>		YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
· I		ĺ	AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
		ł	TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429	828		I
1 3.23	020	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
1			AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ
1	ļ		LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS
1			GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
5430	441	1500	LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
3.30	447	1507	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALC_FQGVPVRS
			GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
1			GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
			HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
1			TVTWRHISPKAVGFVSEDBYLEIQGITREQSGDYECSASNDV\A
			APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
1			EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
			CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
5431	2	1246	HLLLKF
	- 1	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
] ]			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1 !	ľ		GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1 1			SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
]			YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1 . [			FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
1 1	]		DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
1			AMAIFELLDYIVNBPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
5432		1220	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
	*	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
1	İ		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLELELDEQQ
	Į.	į	KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
1 1	1		GLIMARKLIHLEIKPAIRNQIIRELOVLHECNSPYIVGFYGAFY
} I	1		SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
l l		ĺ	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
}	1		FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
] ]	į		DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
1	i		AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
5433	360		DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
333	360	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
<b>!</b> !		1	LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGOADCKAODERF
L			SLIFTLGSFMNNFMTFPTGYIFDRFXTTVARLIAIFFYTTATLI

SEQ	Predicted	I Dyndiana and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide deletion,
	<del>                                     </del>	<del> </del> -	IAFTSAGSAVLLFLAMPMLTIGGILFLITHLQIGHLFGQHRSTI
{	,	-	ITLYNGAFDSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
}	1	<b>!</b>	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
			GSYSOPSSEOPPRUDOCOCREDICA DOCUMENTA CORRECTION CONTRACTOR CONTRACT
1			GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
	Į	ì	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
1			CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
	}	}	LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
	1	ł	SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
5434	66	652	MLAILLTFFHPFLVYRECRTWKESPSAIA
1	1	052	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
İ	1		HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
í		[	LRQGRFGMFIGCINYPECEHTBLIDKPDETAITCPQCRTGHLVQ
1 .	ļ		RRSRYGKTPHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
5435	4704	1597	AQGVKHFCASKQCGKPVSAE
1	1 .,,,	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
1	ļ		HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
	i		GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
ſ	ĺ	0	TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
1			VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
<b>.</b>			RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
1 1			LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
	1		KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
			IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
1	i		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
1	l		RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
İ		•	DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
1 1			KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
]			TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
1 1			TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
1 1			SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
}			YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
			RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1 1	· ·		PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
1 1	ļ		PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
[ [	i		KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1 1			HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
1 1			RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDS I PWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
1 1	·		RARELRVALAA ECDA VYITTIDA ALT CA DESCRIPTION OF THE CONTROL OF THE
	]		RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
(	1		LVYCVRPCCDI ACDOVACANENDODANIONO DE ANDRES
[ ]	ļ		LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1	ļ		SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
1 . 1	ŀ		EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
] ]			QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
1		1	QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
j l		/	PBBADGGGENGGGDADGY DELMEDIAGING ANGERIKA BAKA BAKA BAKA BAKA BAKA BAKA BAKA B
} [	ľ		PRRVDSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
1 1	1		PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1	j		WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
1	1	I	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
]. [	}	. ]	AALDTIGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1 1	1	I	CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG KGL
5438	2443	1252	
]		1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
	[	1	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
1		i	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
, ,	1	.	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
[ ]	ĺ		DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
L I			NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

Deginning Deginning Corresponding to first amino acid residue of smino acid sequence    Corresponding to first amino acid residue of smino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence    Corresponding to first amino acid sequence   Corresponding to first amino acid sequence   Corresponding to first amino acid sequence   Corresponding to first sequence   Corresponding			r	
No: nuclectide corresponding to first amino acid amino acid corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to the corr	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid residue of amino acid residue of amino acid amino acid sequence residue of amino acid sequence sequence sequence residue of amino acid sequence sequence sequence residue of amino acid sequence sequence sequence residue of amino acid sequence sequence sequence residue of amino acid sequence sequence residue of amino acid sequence sequence residue of amino acid sequence residue of amino acid sequence residue re	J.			
to first amino acid residue of amino acid residue of amino acid sequence  Peptoline, Oscilutamine, Re-Appiange, sequence  Sequence  Codon, Paposible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide for the sequence  FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELYMCTYLIAPGDYNCFHEPTDWTVSHRHFFGSLMSVNP FERNELWCHAPAGNERGERGARANHFFGLAURGKGREENKGSDRVS MSPEALCLASBULTVLTTLAPGALARGEGREENKANHFFGLAURGKGREENKGSDRVS MSPEALCLASBULTVLTTLAPGALARGEGREENKANHFFGLAURGKGREENKGSDRVS MSPEALCLASBULTVLTTLAPGALARGEGREENKANHFFGLAURGKGREENKANHFFGLA	NO:			1
to first smino acid residue of smino acid residue of smino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence  REGNESURCYTIADDA INCIDENT SUBSTITUTE SUB	1	1		
smino acid ceid sequence sidue of samino acid sequence (%TTPLYCOPIEN, X-MUNICOWN, *Stop samino acid sequence (%TTPLYCOPIEN, X-MUNICOWN, *Stop Codon, %Popsible nucleotide deletion, %Popsible nucleotide sequence (%TTPLYCOPIEN, X-MUNICOWN, *Stop (MARNIKE) COMPANIA (MARNIKE) COMPANI	1		3	L=Leucine, M=Methionine, N=Asparagine,
##TYPYDODRAD, Y=TYTOSIRE, K=UNKNOWN, *Stop amino acid sequence  ##TYPYDODRAD, Y=Dossible nucleotide deletion, 'possible nucleotide deletion,' 'possible nucleotide deletion,'  ##TYPYDODRAD, rucleotide deletion,'  ##TYPYDODRAD, Y=DOSSIDE nucleotide deletion,'  ##TYPYDOR nucleotide deletion,'  ##T	[	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine, .
sequence   Sequence	ļ.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
sequence    codon, /=possible nucleotide deletion,    -possible nucleotide insertion    EEGNELYHCUTYLAFGDVHCHEPTDMTVSIRRHFPGSIMSVNP     EEGNELYHCUTYLAFGDVHCHEPTDMTVSIRRHFPGSIMSVNP     FORDIHITSSRINKGSTMPSSVTHTNREGVPHALRGEHLG/OS     FRIGSTYLUIFEARMORPHOLATGGKH RGGEALGS    STAFFRREGORDHARAKHEPGLARRGERGENEAN     SA39	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
### SEQUENCE    SEONELYHCVITLANGONYACHSETPUTVOSHRHEPGSLMSVNP   GRARNIKELPCINRRVVLTGONKIGFFSLTAVGAT\mcstrrfy   FORDILITISPRINGSVNTPSTVTTNREGVPHALGSELLG/G   FORDITTSPRINGSVNTPSCATTURGEVPHALGSELLG/G   FORDITTSPRINGSVNTPSCATTURGEVPHALGSELLG/G   FORDITTSPRINGSVNTPSCATTURGEVPHALGSELLG/G   FORDITTSPRINGSVNTPSCATTURGEVPHALGSELLG   SEPARATE   STATE	)	amino acid	sequence	
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FIAFAYSYKSRORKMYGDVTGAQAYASTAKCINIWALIGIFMT ILIII ITVIJVJOQQR  5441  2 2054 CRDGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFPSFIN NSDLWVANITETGERRRITFCHQCLSNVLDDEKSAGVATFVIQEE FORFTGYWCPTASKBEGSEGLKILISEDDESSEVEIVEPSP ALBERKTDSYRYPRTGSKINPKIALKLAFFQTDSQCKIVSTQEKE LVQPFSSLFPKVEYIARAGWTGSAWAMFLDRPGONLGLVLIL PPALFIPSTENEEQNILARAGWTGAWAMFLDRPGONLGLVLIL PPALFIPSTENEEQNILASAGVTROVEYVVEEVTIVVINVIR DIFYPPPOSEGBELG-TRANBEKTGFCHINFUTAVLKSQGYDW SEPPSPGGGGGSL-TWALHVNBETKLUVPGGTKOTFLEIHHLVVUS YEAAGEIVRLTTPGFSISCSMSQNFDMFVSHYSSVSTPPCVHVY KLSGPDDDPLHKQPRFWASMEBAKITHFHTRSDVRLYGHIYKD HAALQPGKKHPTULFVYGGPQQLVMNSFKGIKJKRLHNTLASLGY AVVVIDGRGSCQRGLRFFSGALKNOMGQVEIEDQVGELQFVAEKY GFIDLSRVAIHGWSYGGFLSIMGLIHKPQVFKVAIAGAPVTVMN AYDIGTTESYMDVPSNNOHGYBASALHVELLPBENFRILLIK GFLDENVHFFHTNFLUSGLIRAGKPYQLQVALPPUSPQIYPNR HSIRCPESGEHVEYTLLHFLQEYI  5442  1 3474 CGQRSRRRSPDMPEAKPAAKKAPKGKOAPKGAPKEAPPKEAPAE APKEAPPEDQSPTAEEPTGYVELKFDSVSVETGKDAVVXAKVOK KELPDKPTIKWFKKMLELGSKSGARFSFKSHNSASNVTVEL HIGKVULGDRGYYRLEVKAKUTCDSGSFNIDVAPRQDASGGL ESFKRTSEKKSUTAGELDFSGLLKKVEVEEKKKKHODDLG IPPEIWELLKGAKKSEYEKIAFQYGITDLRGHKRLKKAKVUV KXAAFYKKLDPAYQDVRGNKTLADDAAYEVAKNOEKCHTELFV KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEGGAQVMMMKDGVEL TREDSFKARYRFKDGKRHLITINKCTLADDAAYEVAKNECHTELFV KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEGGAQVMMMKDGVEL TREDSFKARYRFKKDGKRHLITISPDVQEBRGRYQUTINGGQCI ABLIVEEKGLEVIQDIADLIVWASEQAVFKCEVSDEKVTKMYK NGVEVPSKRITISTSVGFHLAUIDDVRFDEDGDVTFVPDGYAL GSLSAKINFLEIKVEYVPKQQEPPKIPLGFASGGTSENAD/IV VAGNKLRILDVS,TIGAPASPFATIKGSQDEFTFUKRYK NGVEVPSKRITISTSVGFHCHUDDVRFDEDGDVTFVFDGYAL GSLSAKINFLEIKVEYVPKQQEPKIPLKGGDGFTYCKAV NGVEVPSKRITISTSPFHLBGILEFMKURGGGGIDGY LVSTGLEGSEEWVFANTEPVBRCGFTVKAVE NGVEVPSKRITISTSPFHLBGILEFMEURAGGGIDGY LVSTGLEGSEEWVFANTEPVBRCGFTVKAVE RWKLKRPEVPTSTTVESTKHIEGILFEMEURALFRAVEGORM TKFPMFLAFTSSPHLLIVEGSEEWVFANTEPVBRCGGGIDGY LVSTGLEGSEEWVFANTEPVBRCGFTVKAVERPRNVTERGRITTGK NALVEMOAPKDOMSE HON TYTKRUGFTVKAVERPRNTUTERNTETE FRESSPHATAGOPTTTRAVERPRNTUTENTETTERTTE FRESSPHATAGOPTVCAVE VMKNOKVMENTEDDEFELLITNYGGVLTLINIRRSPFFDAGFTYCAV VMKNOKVMENTEDDEFELLITNYGGVLTLINIRRSPFFDAGFTYCAV	5440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
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LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIEMMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTWEMFNVYERNHTSC TVSDLJVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1		İ	IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV		1		
NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV		1		1 · · · · · · · · · · · · · · · · · · ·
TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1	1		1
PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1	1	1	
VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	I	1		
	1	1		
NEIGEALARCKDEVROPQ	İ	Ī		
	L	L	<u> </u>	METGENTHECKTEAKANA

C SEC	I prodict - 3	T-5	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid R-
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
l l		corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSSSSSSRRSRSAAEPA
	i	j	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
1	1	ļ	LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
1	1	į.	NKIEEFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
1		ł	RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
1			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
1			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
	1	f	FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
		J	RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
<b>(</b>			TRUE A DIMARA WALL CONCERN DA DEDUK DA DE DE DE DE
1			IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG
}	]		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
i			QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
	i		SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
1			SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
1			LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
	Į į		*PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP
1			RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH
5445	2364	486	QGGGCGYGQSQGPSGRPRGGAGSRH
1	2504	400	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT
1			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
1	1		EEESEPPAPNIRMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
1	]		QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
1			ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
1		•	QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
1			DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
[			ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG
1	ĺ		LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
]			PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
1	. [		NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
1		•	DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLF
}			PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
5446	972		LPTLQVVPL
3110	372	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
į l			TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP
1 1			VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
j	· 1		MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
[	1		GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
5447	207		KGGGRR
344/	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
1	i	i	PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
1 1	ì	•	GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
<u> </u>	. [		RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFOKKKCEDCVVPY
[ [		i	TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
1 1	ŀ		IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
į į			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
[ ]	İ	[	SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
1 1			GFSSEMKAWDIRTGKVMRSYKATIOOTLDILFLREGSEFLSSTD
			ASTRDSADRTIIANDFRTSAKISNOIFHERFTCPSLALHPREPV
] [			FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
1	1		GDLLVTGSADGRVLMYSFRTASRACTLOGHTQACVGTTYHPVLP
1	1		SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
		1	KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
	1	- 1	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
ļ. <b>I</b>	1	)	RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
	i	!	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKLRKAAHLEV
	į	j	HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
<u> </u>	Į.		GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
		<del></del>	TOTAL ASPROACE ASPROACE AND AND AND ASPRESS OF THE PROPERTY OF

SEO	Predicted	Treastages and	Tame and a second and a second as a second
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	i	
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion) IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
		[	
	j		RRHVDRTSEGVLRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSSR
j	1	ļ	QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
	1		VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
		ſ	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
l	1		TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
	1	l	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
	1		SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
(			SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
1		1	LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
5449	194	1833	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
1 2222	1 224	1033	MASKYTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
1	.}	ļ	1
1			RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
[		[	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPOCET
1	j	j	IRPEETAWNTGTLRNGPSKDTORTITNVSDEVSSEEGPETGYSL
1			RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1		ì	QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
1	1		VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
	1	1	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
Į	Į.	f	TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
ł		]	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDA>K
Į	1	)	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
1	1		SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
	<b>[</b>		VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
ì			LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
į.			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
1			PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
1		ł	LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
ļ	1	}	YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
1			VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
		·	RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
1	1	l	HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
1		1	HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA
1	1		AGCRLEEEEYEDDAYGHYEAFSTLAPEAWPAMELPEPCVPEPGL
1	1	-	PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK
1	1	[	SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
1	1		GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
	Į.	ĺ	HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
I	1	l	SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
1		}	VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
1			LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
1			AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL
1	<u>}</u>	<b>!</b>	SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS
1	1		PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYGA
	1		TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
1	1		LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
1	1		TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE
1	1	J	SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
1	1		TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
1 .	1	!	TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
l .		)	YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
			AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
i	1		SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
ì	1		RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
1			LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
,			GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT

SEQ	Predicted	Predicted end	I Amino polid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
		<del></del>	LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1	Į.	1	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
1	j	<b>}</b>	TNTGLQMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV
1			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
1			TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
	į .		SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
1	1	·	GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
1		•	AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
İ			RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV
{			YAHGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
j			ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
	1		RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
1	(	!	QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
1	]		SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
	1		DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
ł	!		WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
1			VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
	;		AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
ł	1 1		ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
			IIPMCLVLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
	[ [		GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
	l 1		ALKNGOYWV
5451	ī	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
1	į į		KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
1	]		TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
l .			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
I	ľ		PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
1			IISELACYTYSMVAVPLYDTLGPEAIVHLVNKADIAMVICDTPQ
1			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
1	1		YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHON
ļ			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
1			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVONE
	}		AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIODSL
}	]	•	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
i i			FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
1 1	- 1		TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
	. [		KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
	1		VVPDTDVLPSFAAKLGVKGSFEELCONOVVREAILEDLOKIGKE
	1		SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
<u> </u>			IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
[			LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
, ,	1	•	HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
[	1		VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAOLIOG
			DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
			RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
j l		İ	AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
, ,		į	PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
Į	1	]	KGLDTETTVEVANCELQDRKLTKSERQRFKEEAEMLKGLOHPNI
, ,	ļ		VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
( 1	I		RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
]	İ		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
į į	1		LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1	1	]	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI
ļ	1	1	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAOEMVESG
		1	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
	1		AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
. (	1	ł	PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
		ļ	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
		<del></del> ,(,	THE TOTAL PROPERTY OF THE PARTY

	1 5 - 31 - 3		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
}	amiro acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ì	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	Sequence		\=possible nucleotide insertion)
1	1	}	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
1			RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
{	l .		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1			LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1	1		EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
]	}	ļ	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
5455	1359		YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
3433	1339	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
ì	ì	i	WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
l .	1		GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
	1		QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1	1		KALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
1			DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
1	1		TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
EAEC	<u> </u>		LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
l .	1		TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
ŧ			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
<b>1</b> .	{		QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
1	}		KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
			DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
}	ì	ŀ	EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
}	ĺ		ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
ł	ì		QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
1	ļ		SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
ĺ			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
ł	} .		ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
	1		QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
1			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1	1		SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
İ			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
5457	2	1540	MSMYRVRGGRVAGGCFIGWRAPCPRAIX
1 3.37	1 ~	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
			LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
ł	{		TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
1	)		
1			RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
l .	}		
1			PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER PLTECHOGLSNVLDDPKSAGVATEVIOEFEDPETCVMVCDTAGW
ł	}		RLTFCHQGLSNVLDDPKSAGVATFV1QEEFDRFTGYWWCPTASW EGSEGLKTLR1LYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
1			GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
(			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
J			
5458	6642	4022	ASLCQSCPQECPAVCGVRGGHQRLDQCS
	4.50	4042	FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV
			KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
1			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
			VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI
į į			QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
1			VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
[	[		LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
]	}		EPNNDAEALVNGPEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
1			DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
l i			SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
<b>j</b>			DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
[			HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
[	[		DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
<b>j</b>	<b>\</b>		DYYREGOGGAGRTSPEGGRTSPEARGRRSPILLPKGLLAPEAGRA
]			DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
L			AAVDRTTELSRQRIASQELGPAVDKDKEALMEEILKLKSLLSTK

SEO	Predicted	I Decellated	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ſ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			REQITTLRTV:KANKQTAEVALANLKSKYENEKAMVTETMMKLR
1			NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
i			KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
		<u> </u>	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
1		1	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
1	Ĭ		GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
-	1	ĺ	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
ſ	1	1	DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
l l	}		QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
l.			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
1			GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
1			GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1			ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1			CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
1	1		KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLROOAE
1			VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
1	·		QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
1			AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
ļ			VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
Ì			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
1			NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
			LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
}	}		IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
			SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
	}		SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
1	1		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1	1 1		NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1	1		ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
1			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
			EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
1	· .		QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
Ł			TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
			RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
ł			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1			CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
			VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
			WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
1 1			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
}	·		NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
[ ]			SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
	]		RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
			WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
[ ]		,	NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
[ · ]		l	RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
[ [	1	i	LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
			DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
<u> </u>		j	LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
1 1	1		QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
1 1	į.	1	WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
5463	237	1010	KHFIMAPNPDDMEEDP
		1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
	<u>-</u>		YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEQ	Predicted	Predicted end	Amino agid cogment containing gignel negtide
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
t	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	\=possible nucleotide insertion)
<b> </b>	Dequence		
1	1		LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
1 .	Í		PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
1	ł .	l	DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
5464	195	677	RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
3404	1	6//	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
ł			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
Ì	}	Ì	LAFDVTDLESPEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
5465	5278		DRKYQSILENHLTESIKLSPDQSRSRCC
3463	32/8	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
l .			VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
į	Ì		PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
Į.	<b>{</b>	1	KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1	j		RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
1	1	i	VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1	i	١.	DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
j	]	}	IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
	l .		HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
1	1		DEDSSDSEADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
}	i	Ì	TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
1			HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHFA
l	ĺ		EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
ļ	ļ		GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
-			SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
ł			LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
1	<b>{</b>		RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
{	[	[	YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
l	ļ	İ	LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
	ļ		AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
[			FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
5467	27.02	<u> </u>	QLACHPNLDKLGYSQKMRFTY
3407	2103	4	GEALRYGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
			RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
1			YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS
1			RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
			FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT
i i		İ	HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
1			IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
1			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
1		Ì	QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
1			CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
1			IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
[			FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
}			DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
1			LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF
1 1	!		ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
F450	20-		RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
[			CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
1 1			RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
j	ļ•		RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
]			DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
			ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
,			SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
( l			VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
[ [			KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
			KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
( i			QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
			AVAQMFSTNSFNEQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
1			ENIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ

		· · · · · · · · · · · · · · · · · · ·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, F=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
i	amino acid	residue of	S=Serine, TaThreonine, V=Valine,
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
<b> </b>	sequence		\=possible nucleotide insertion)
ŀ	1		FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDOVYALKLKG
ŀ	1		ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALOTFIKLLLSI
			PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
	ł		ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ
	1		ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
			LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
	L		TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
į.			EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
1	i	l	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
1		ì	EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
1			IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
-{	•		CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
1	1	\$	CYVSITKIKKENWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
	J	j	EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
	1	ł	SAWCPVEISKTVLWPESISVVRCVELPEAPVECEEEEEVEEEKG
1	1	ł	SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
1			MGESCLLPPSGSTSAHMPNDEFPSAGPKEAPPWGKEQPLHLEPS
İ			PPASPTQSPDNLTCTETPLVLAGNPAYRSFSNSLSQSPCPRELG
	í		PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
1	j l		LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
i	Į į		YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
	i i		PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1	i l		KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
1			OTDIMASPORCECCORPA CEDETTE DA PERCENCIA DE LA CONTRA CEDETTE DA PERCENCIA CEDETTE DE PERCENCIA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDETA CEDET
İ	· [		QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
f i	i i		SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM RVS
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF
Į			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
1			INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1 1	ļ		SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
	i		LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
1 (			LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1 1	1		YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
} ]	i j		LSLTLCFVMFWTPNVSEXILIDIIGVDFAFAELCVVPLRIFSFF
1 1			DUDUTUDALI TUMI MTI VVEENI ADCOM DATITA TA CAMPANI
1 1	•		PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
1			EGEDSAMTDMPPTEEVTDIVEMREENE
5471	1868	658	DECADECTORANA AND AND AND CONTROL OF THE PROPERTY OF THE PROPE
1	1	9.56	RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV
<u> </u>			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
1 1	ļ		KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
ļ [	[		ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
1 1	j.		GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
1 1			HTGFLTEYVATRWYRAPEINLNSKGYTKSIDIWSVGCILAEMLS
		Į	NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
1	1	1	PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
, ,	!	j	YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ
5472	1469	753	PGVLEAP
	2203	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
	i	j	DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
[	Į.	[	GSDKMPGRVVTLLEDHEGCTWGVAYOVOGEOVSKALKYLNVRRA
1	- [	į	VLGGYDTKEVTFYPQDAPDQPLKALAYVATPONPGYLGPAPERA
1			IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
5473			VGTMLPCFCPTEQALALV
27.3	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
1		į	KEMFATMSKLKEQLTKVKECYSPLLYESOOLLIPLRELEKOMTS
J	ł	]	FYDSLGKINEIITVLEREAQSSALFKOKHOELLACOENCKKTLT
į		· [	LIEKGSQSVQKFVTLSNVLKHFDOTRLOROIADIHVAFOSMVKK
1	1	.	TGDWKKHVETNSRLMKKFEESRAELEKVLRIAOEGLEEKGDPEE
}	ļ		LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEOEOGGLOEAUR
			KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	ļ	\=possible nucleotide insertion)
1 .	i		KLMPQEGSEKIIKEHRVFFSDKGPHHLCEKRLQLIEELCVKLPV
			RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS
1	•	Ì	EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG
			ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTLLS
		1	EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQAEKILDTE
1	·	i	NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
1	J	j	HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR
1		1	YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQAEN
ſ	[		LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYVIDK
	ļ		S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
1	1	1	LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
í	1		QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT
1			LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAJAPEVGRTLS
1			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ
EARE	<b> </b>		PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
5475	2	506	ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF
1	1		VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
1	}		STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
6476	<del> </del>		GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR
5476	192	1457	SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR
	1		PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPTGTL
	1		VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG
1	1		SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNIDFGAVRGLN
1			YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
Į	1		AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL
			ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ
1			SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC
i	<b>.</b>		LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI
5477	3	1044	SLPPVLPWTEPECDFPDEKDSYWEF
1 34,77	, ,	1044	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI
1			VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV
i		1	PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE
l	1		LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE
1			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ
1	1		EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA
1	1		GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE
5478	2	835	EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
1	] "	0.55	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
l	]		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
ı			LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
1			MEGRILYTLHCHQCPATTVAFSRTGEYFASGGSDEQVMVWKSNF
I			
	[		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
1	]		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
]			LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
j	·		DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
}			MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF
			DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
[	į į		DIGDAGEVIRVERPAILASSMGNLTVSILEQRLTLEEDKLKQC     LENQQLIMQRATP
5480	444	1952	
		2006	LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI
l i			
			LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV
i			EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR
			KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH
			EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
			HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR
	1		THE TENEDRAL TO THE PORT OF THE PROPERTY OF TH

r <del></del>	T		
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R-
]	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
-	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	_	\=possible nucleotide insertion)
]			LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
	[	1	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYOOAEDSEEDKKFI.T
ı		1	GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
F403-			TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLLLLHESPQPPALRV
1		•	VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTI.V
ļ	j		QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
	1		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
i			YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
)			ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
1	1		LDXRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
Ì	İ		KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
1		i	QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
			AKGKSVFLDQMKKFVEWLQNAEEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
ľ			EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
j	ļ		CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDROLPSFOTFFAPA
1			LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAOCNVTLEVSTGP
1			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
j			IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
	1		TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSGLSRMGAVP
5483	1	788	VMVPAQSQAGSLV FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
			ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
1			FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
			FIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILEHOR
5484			KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
2484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS
	1		ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
			SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
1	•		AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
1 1	ì		LQNSDDDEKMONTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1 1	<u> </u>		SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
1	İ		NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
1. 1	İ		PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
1 1	}		DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
]	•		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLOGOA
1 1			VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD
1 1	1		PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
}			PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
			EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
5485	161	1074	AGTN KPKILSSMMDSEAUEVEDDELMEGVODA (1911-1911-1911-1911-1911-1911-1911-191
, ,	-	m-/1	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
1 1			RGILPPLMQKTTTLALMFGLYEDLSCLLHKHVSAPEFATSGVAA
(			VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
} [	. 1		GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
] [	1		DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFOKI
<u> </u>		i	WLERDRKLINLFRGAHLMYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
1	1	ŀ	PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
ļ į	1	i	GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
		ļ	IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
		ļ	FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
			LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
	ŀ	ł	DSRAILCRYNEBSQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
			DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SEO   Predicted   nucleotide   nucleotide   nucleotide   location   nucleotide   location   corresponding   to first   amino acid   residue of   amino acid   residue of   amino acid   amino acid   amino acid   amino acid   sequence   sequence   sequence   Secure, Paper   No.   Secure	DDP  AAC  TIH  IEN  LLL  KTL  AGE  AVD
No: nuclectide location corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequenc	AAC TA SGK TIH LLL KTL AGE AVD
location   corresponding   to first   amino acid   residue of   residue of   residue of   amino acid   residue of   amino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   sequence   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, manino acid   S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Threonine, V=Valline, S=Serine, T=Univolen, V=Valline, V=	AAC TA SGK TIH IEN LLL KTL AGE AVD
Corresponding to first amino acid amino acid residue of amino acid amino acid sequence   S-Serine, T-Threonine, V-Valine, x-Indinown, *-St. Codon, /-possible nucleotide deletion, \	TA SGK FIH IEN LLL KTL AGE AVD
to first amino acid residue of residue of amino acid residue of amino acid sequence  8-Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=St- Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  ACDGLFKVFTPEEAVNFILSCLEDERIQTREGKSAADARYE NRLANKAVQRSSADNVTWWVRIGH  5487  535  182  AVSLEQIRGLQFTPAVPLPSLQFCPSNCOMERVTLALLLLAG LERNDPFANKDDPFYYDWKNLOLSGLGCGLLAIAGIAAVL CKCKSQKQHSPVPEKAIPLITGGSLTCT  6HKFFIGFGGKGANQCVQAARLGAMTSMVCKVCKOSPGNDY LKQNDISTSFTYTYRDAATTC  5488  1072  259  AMAASGEPQRQWGEVAAVVVGSCWTDLVSLTSRLPKTGE GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVCKOSPGNDY LKQNDISTSFTYTYRDAATTC  6HKFFIGFGGKGANQCVQAARLGAMTSMVCKVCKOSPGNDY LKQNDISTSFTYTYRDAATTCSIIVNNEGONIIVVJAGAN NTEDLRAAANVISRAKVMVCQLEITFATSLEALTMARRSGV FFPAPAIADLDPGFYTLSDVFCCNESEAEILTGLTVGSAAD AALVLLKRGCQVVITITGASGCVVLSQTEPEPKHIPTEKVK TVVSFKI  S489  81  893  GKGPVAAFIDQSNIFLITDPXIPLGQWREEPKMPLLLLGETT LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LEFTVEWVIKVFVATSSGSTAIRKKQQEVVGFLEANKIDFF FAKEENIIYSFIGLAPPPDSKGSEKAEGGGETEAQKEGSE NLPPAQEKNEEEGETATEETSEIAMEGAEGAEEEEETAEC GEDEDS  S490  81  893  GKGPVAAFIDQSNIFLITDPXIFLGQWREEPKMPLLLLGETT LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFFTVEWVIKVFVATSGSSTAIRKKQQEVVGFLEANKIDFF FSKKEENIIYSFIGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPPAQEKNEEEGETATEETSEIAMEGAEGAEEEEETAEC GEDEDS  S490  81  893  GKGPVAAFIDQSNIFLITDPXIFLTDPXIFLDQURSECFPRDFUEQ LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFFTVEWVIKVFVATSGSSTAIRKKQQEVVGFLEANKIDFF FSKKEENIIYSFIGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPPAQEKNEEEGETATEETSEIAMEGAEGAEEEEETAEC GEDEDS  GGGPDAS  GKGPVAAFIDQSNIFLITDPXIFLTDPXIFLTDPXIFLTDEPXIFTNEGQVCGDH FSKKEENIIYSFIGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPPAQEKNEEEGGTTATEETSEIAMEGAEGAEEEEETAEC GEDEDS  GKGPVAAFIDQSNIFLITDPXIFLTDPXIFTNEGQVCGDH FSKKEENIIYSFIGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPPAQEKNEEEGGTTATEETSEIAMEGAEGAEEEEETAEC GEDEDS  GKGPVAAFIDQSNIFLITDPXIFTNEGAECELSGDDSGEVEFPHSPEIEI LEALFECKAAPHAGLGLIQVASREQLLYLYARKKQVKVGNCN SFFPPFECKQKKSANTATGGGPVISATWETTIREEDNNIFTYCREN ITKAIKSKNVDVNVVKDEEGGRALLHWACDRGHKELVTVLLQI INCQDBRGQTRALHYASACEFLDIVELLLQGA	TA SGK FIH IEN LLL KTL AGE AVD
amino acid residue of amino acid sequence sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion)  ACDGLFKVFTPEEAVBFILGCLEDEKIQTEEKSAADARYE NRLANKAVQRSSADNVTVMVVRIGH  5487 535 182 AVSLEGIRGLQTPEPVPLEQCEPERICMERVTLALLLIAG LERNDFANKAVDPFYYDWNVLOLSGLICGGLLAIAGIAAVL CKCKSSQKQHSPVPEKAIPLITPGSATTC  5488 1072 259 AMASSEEPCRQWGEEVAAVVVVGSCOTTDLVSLTSRLPKTGE GHKFTIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGONIIVTVAQAN NTEDLRAAANVISTARKVMVCQLEITPATSLEALTMARRSGV LKQNDISTEFTYQTKDAATGTASIIVNNEGONIIVTVAQAN NTEDLRAAANVISTARKVMVCQLEITPATSLEALTMARRSGV TYVSFKI LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGAIRKKQQEVVGFLEANNIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQVGDB FSAKENIIVSFLGLAPPPDSKGSEKAEGGETEAQKEGSE NLPEAQEKNEEGETTAETETETAMGAAGEGEAEEEETTAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEFWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANNIDFF IAGDEDNRRWMRENVPGEKKPQNSIPLPPQIFNEEQVGDB FSAKEENIIVSFLGLAPPPDSKGSEKAEGGETEAQKEGSE NLPEAQEKNEEGEGTTETETETAMGAAGEGEAEEEETTAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEFWAAASPDLALACLCHCQDLSSGAFPNRGVI LFFTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANNIDFF IAGDEDNRRWMRENVPGEKKPQNSIPLPPQIFNEEQVGDB FSAKEENIIVSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAGENGENMEENVGFKYNGNIPLPPQIFNEEQVGDG FSAKEENIIVSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAGENGENMEENVGFKYNGNIPLPPQIFNEEQVGDG FSAKEENIIVSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAGENGENGENGENGENGENGENGENGENGENGENGENGENG	TA SGK FIH IEN LLL KTL AGE AVD
residue of amino acid sequence	TA SGK FIH IEN LLL KTL AGE AVD
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion)  ACDGLFKVFTPEEAVWFLLGCEDERIQTREGKSAADARYE NRLANKAVQRGSADNTVMVVRIGH  5487 535 182 AVSLEQIRGLQTPAFVPDFLQPCPSNCDMERVTLALLLAG LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVL CKCKSQKQHSPVPEKAIPLITPGSATTC  5488 1072 259 AMAASGEPGRQWGEVAAVVVGSCWTDLVSLTSRLPKTGE GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVCKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGONIIVTVAGAN NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGV FMPPAPAIADLDPGFYTLSDVFCCNEESAEILTGLITVGSAAD ALAVLLKRGCQVVITILGASECVVLSQTEPEPKHIPTEKVK TTVSFKI  5489 81 893 GKGPVAAFIDQSNIFLTDPKIPLGGWREEPKMPLLLGETE LEEDCRSPVEPWAAASPDLAIACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMENVPGEKKPQKGIPLPPQIFREQVCGDF FSAKENIIVSFLGLAPPDSKGSEKAEGGETEAQKEGSF NLPPAQEKNEEBGETTAQKEGSF NLPPAQEKNEEBGETTAQKEGSF NLPPAQEKNEEBGETTAGKTGGBDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LEEDCRSPVEPWAAASPDLAIACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFREGVCGDF FSAKEENIIVSFLGLAPPPDSKGSEKAEGGETEAQKEGSF NLPPAQEKNEEBGETTAQKEGSF NLPPAQEKNEEBGETTAQKEGSF NLPPAQEKNEEBGETTAGKTGGNUSPPGTSCKGF FSAKEENIIVSFLGLAPPPDSKGSEKAEGGETEAQKEGSF NLPPAQEKNEEBGFTATEETEIAMEGAEGEAEEEETAGK GEDEDS  5491 204 1194 GSAPRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPYTQSKEDRPDTEK GEDEDS  SAFRILSGFTGAQARDPDWARPFSRPPTTQSKEDRPDTEK GEDEN ITTYCKEN ITKALKSKNUDVNVKDEEGGRALLHWACDRGKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTGCKTVSLVLQPHTTGKA	TA SGK FIH IEN LLL KTL AGE AVD
amino acid sequence   Codom, /=possible nucleotide deletion,   =possible nucleotide insertion)	TA SGK FIH IEN LLL KTL AGE AVD
Sequence   Seposible nucleotide insertion	TTA SGK TIH IEN LLL KTL AGE AVD
ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYE NRLANKAVQRGSADNVTWWVIGH AVSLEQIGRIQTPEPPPUBLQPCPSNCDMERVTLALLLIAG LEANDPFANKDDPFYYDWKNLQLSGLICGGLIAIAGIAAVL CKCKSSQKQHSPVEKAIPLITTGSATTC CKKSSQKQHSPVEKAIPLITTGSATTC GHKFFIGFGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVANGEGONIIVIVAGAN NTEDLRAAANVISRAKVMVQQLEITPATSLEALTMARRSGV FPPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPBPKHIPTEKVK TTVSFKI  S489 81 893 GKGPVAAFIDQSNIFLTDPXIPLGQWREEPKMPLLLIGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGBKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETSEIAMEGAEGEAEEEETAEC GEDEDS  S490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGGWREEPKMPLLLIGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMENVPGEKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETTATEETSEIAMEGAEGEAEEEETAEC GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWARPPSRPYTQSKEDRPDTEC GGDMASSFLPAGAITGDSGGELSSCDDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLVARYKQVKVONCN: SFFDFEGKQKWBAWKALGDSSPSQAMQEYIAVVKKLDPGWI PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCREM ITKAIKSKNVUNVNKDEEGRALLHWACDRGHKELVTULIQI INCQDNEGGTALHYASACEFLDIVELLLGGSADPTLROQDK	TTA SGK TIH IEN LLL KTL AGE AVD
NRLANKAVQRGSADNYTWWVRIGH	TTA SGK TIH IEN LLL KTL AGE AVD
5487 535 182 AVSLEQIRGLQTPAPVPLPLQFCPSNCDMERVTLALLLAG LEANDPFANKDDPFYTDWKNLQLSGLICGGLLATAGIAAVL CKCKSSQKQHSPYPEKAIPLITPGSATTC  5486 1072 259 AMAASGEPQRQWEEVAAVVVVGSCMTDLVSLTSRLPKTGE GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGRDY LKQNDISTEFTYQTKDAATGTASIIVNNEGONIIVVAGAN NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGV FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489 81 893 GKGPVAAPIDQSNIFLTDPXIPLGQWREEPKMPLLLIGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGBKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDGKGSEKAEGGETEAQKEGSE NLPEAQEKNEEEGETATETETEIAMEGAEGEAEEEETAEC GEDEDS  5490 81 893 GKGPVAAPIDQSNIFLTDPKIFLGQWREEPKMPLLLIGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGBKKPQNGIPLPPQIFNEGYCGDF FSAKEENIIYSFLGAPPPDKSGEKGEGETEAQKEGSE NLPEAQEKNEEBGETATETETEIAMEGAEGEAEEEETAEC GEDEDS  5490 81 893 GKGPVAAPIDGSNIFLTDPKIFLGQWREEPKMPLLLIGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEGYCGDF FSAKEENIIYSFLAPPPDKSGEKAEEGGETEAQKEGSF NLPEAQERNEEBGETATETETEIAMEGAEGEAEEEETAEC GEDEDS  5491 204 1194 GSAPRLSJGFTGAQARDPDWWARPPSRPYTQSKEDRPDTEK GGMASSFLPAGAITGDSGGELSSGDDSGVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLIYLYARYKQVKVGNCN: SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENI ITKAIKSKNVDVNVKDEEGGRALLHWACDRGHKELVTVILLQI INCQDNEGQTTALHYASACEFLDIVELLLQSGADPTLRDQX EEVTIGCKTYSLVYQRATCHCH	FIH IEN LLL KTL AGE AVD
LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVL CKCKSSQKQHSPVPERAIPLTPGSATTC  AMAASGEPQRQWQEEVAAVVVVQSCMTDLUSLTSRLPKTGE GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGAN NTEDLRAAANVISRAKVMVQQLEITPATSLEALTMARRSGV FNPAPAIADLDPGFYTLSDVFCCNESEAEILTGLTVGSAAD AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  S489  81  893  GKGPVAAPIDQSNIFLTDPKIPLGQWREEPKMPLLLLGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRWMRENVPGBKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEETAEG GEEDDS  S490  81  893  GKGPVAAPIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFT IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  S490  10  GSAPRLSLGAFTGAQARDPDWWARPPSRPYTOSKEDRPDTEX GCDEDS  S491  204  1194  GSAPRLSLGFTGAQARDPDWWARPPSRPYTOSKEDRPDTEX GCDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKGNCN: SFPDFEGKQKEMAKLGDSSPSQAMGEYIAVVKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCREN ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTIGCKTYSLVLQRHTTGKA	FIH IEN LLL KTL AGE AVD
LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVL CKCKSSQKQHSPVPERAIPLTPGSATTC  AMAASGEPQRQWQEEVAAVVVVQSCMTDLUSLTSRLPKTGE GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGAN NTEDLRAAANVISRAKVMVQQLEITPATSLEALTMARRSGV FNPAPAIADLDPGFYTLSDVFCCNESEAEILTGLTVGSAAD AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  S489  81  893  GKGPVAAPIDQSNIFLTDPKIPLGQWREEPKMPLLLLGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRWMRENVPGBKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEETAEG GEEDDS  S490  81  893  GKGPVAAPIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETF LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFT IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  S490  10  GSAPRLSLGAFTGAQARDPDWWARPPSRPYTOSKEDRPDTEX GCDEDS  S491  204  1194  GSAPRLSLGFTGAQARDPDWWARPPSRPYTOSKEDRPDTEX GCDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKGNCN: SFPDFEGKQKEMAKLGDSSPSQAMGEYIAVVKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCREN ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTIGCKTYSLVLQRHTTGKA	FIH IEN LLL KTL AGE AVD
CKCKSSQKQHSPVFEKAIPLITPGSATTC  5486  1072  259  AMASGEPQRQGEVAAVVVVGSCMTDLVSLTSRLPKTGE GHKFFIGFGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGAN NTEDLRAAANVISRAKVMVCQLEITPATSLEALIMARRGSV FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489  81  893  GKGPVAAFIDQSNIFLTDPXIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDINRWMRENVPGEKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEIAMEGAEGAEEACEEEACAC GEDEDS  5490  81  893  GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTYMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFY IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEIAMEGAEGAEEACEEETAGC GEDEDS  5491  204  1194  GSAPRLSLGFTGAQARDPDWWARPPSRPYTGSKEDRPDTEK GGDEDS  GGDEDS  5491  204  1194  GSAPRLSLGFTGAQARDPDWWARPSRPYTGSKEDRPDTEK GGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEI LAELFEKAAAHLQGIJQVASREQLLYLYARVKQVKVGNCN: SFFDPEGKQKWARWALGGDSS PSQAMQEYIAVVKKLDPGWF PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENI ITKAIKSKNUDUNVKDEEGRALLHWACDGGKKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTIGCKTVSLVLQRHTTGKA	PIH IEN LLL KTL AGE AVD
5488  1072  259  AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGE GHKFFIGFGKGANQCVQAARLGAMTSMVCKVGKDSFGNDY LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGAN NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGV FNPAPAIADLDPQFYTLSDVFCCMESEAEILTGLTVGSAAD AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489  81  893  GKGPVAAFIDQSNIFLTDPXIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEGGETEAQKEGSE NLPEAQEKNEEEGFTATEETEEIAMEGAEGEAEEEEETAEG GEDEDS  5490  81  893  GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDE FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEG GEDEDS  5491  204  1194  GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEG GGDEDS  5491  204  1194  GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEG GGDMASSFLPAGAITGDSGGELSSGDSGEVEFPHSPEITEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGRON SFFDPEGKQKWAWKALGDSSPSQAMQEYIAVYKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCREN ITKAIKSKNVDVNVKDEGGRALLHWACDGGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDG EEVTIGCKTVSLVLQRHTTGKA	IEN LLL KTL AGE AVD
GHKFFIGFGKGANQCVQAARLGAMTSMVCKVGKDS FGNDY LKQNDISTE FTYQTKDAATGTAS I IVNNEGQNI IVIVAGAN NTEDLRAAANVI SRAKVMVCQLEITPATSLEALTMARRSGV FNPAPAIADLDPQFYTLSDVFCCNESEAE ILTGLTVGSAAD AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTV3FKI  5489 81 893 GKGPVAAFIDQSNIFLTDPKIPLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWNRENVPGEKKPQNGI PLPPQI FNEEQYCODF FSAKEENI IYSFLGLAPPPDSKGSEKAEGGETEAQKEGSE NLPEAQEKNEEEGETATEETEIAMEGAEGEAEEEETAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKI FLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGI PLPPQI FNEEQYCGDE FSAKEENI IYSFLGLAPPDSKGSEKAEGGETEAQKEGSI NLPEAQEKNEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWARPPSR PYTQSKEDRPDTEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWARPPSR PYTQSKEDRPDTEG LAELFEKAAAHLGGLIQVASREQLLYLYARYKQVKVGNCN: SFFDPEGKGKWEAWKALGDSSPSQAMQEY IAVVKKLDPGWI PEKKGKEANTGFGGPVISSLYHEETIREEDKNI FDYCRENI ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INQQDNEGQTALHYASACEFLDI VELLLQSGADPTLRDQDC EEVTGCKTVSLVIQRHTTGKA	IEN LLL KTL AGE AVD
LKQNDISTEFTYQTKDAATGTASIIVANEGQNIIVIVAGAN NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGV FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  S489 81 893 GKGPVAAFIDQSNIFLTDPKIPLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEGQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEGGETEAVEGGEDES NLPEAQEKNEEEGETATEETEIAMEGAEGEAEEEETAEG GEDEDS  S490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEFWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAVKGGSF NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEG GEDENS SFFDFEGKGKWEAWKALGDSSPSQAMQEVIAVVKUNGNCN SFFDFEGKGKWEAWKALGDSSPSQAMQEVIAVVKUNGNCN PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCREN ITKAIKSKNVDVNVKDEGGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDG	LLL KTL AGE AVD
NTEDLRAANVISRAKVMVCQLEITPATSLEALTMARRSGV FNPAPAIADLDPGYTLSDVFCCRESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  S489 81 893 GKGFVAAFIDQSNIFLTDPKIPLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEEGETATEETEIAMEGAEGEAEEEEETAEG GEDEDS  S490 81 893 GKGFVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDE FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSF NLPEAQEKNEEEGETATEETEIAMEGAEGEAEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTOSKEDRPDTEK GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTOSKEDRPDTEK CGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNT SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWF PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFPYCRENI ITKAIKSKNVDVNVKDEEGGRALLHWACDRGHKELVTVLLQI INCQDMEGQTALHYASACEFLDIVELLLQSGADPTLRDQDG EEVTGCKTVSLVLQRHTTGKA	KTL AGE AVD PLK
FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489 81 893 GKGPVAAFIDQSNIFLTDPXIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIATRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAZEGGETEAQKEGSE NLPEAQEKNEEBEGTATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEK QGDMASSFLPAGAITGDSGGELSSGDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCN: SFFDFECKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENN ITKAIKSKNVVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTGCKTVSLVLQRHTTGKA	AGE AVD PLK
FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAAD AALVILKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489 81 893 GKGPVAAFIDQSNIFLTDPXIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIATRKKQQEVVGFLEANKIDFK IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAZEGGETEAQKEGSE NLPEAQEKNEEBEGTATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEGETATEETEEIAMEGAEGEAEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEK QGDMASSFLPAGAITGDSGGELSSGDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCN: SFFDFECKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGW PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENN ITKAIKSKNVVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC EEVTGCKTVSLVLQRHTTGKA	AGE AVD PLK
AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVK TTVSFKI  5489 81 893 GKGPVAAFIDQSNIFLTDPXIPLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFK IAGDEDNRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEG GEDEDS  5490 81 893 GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETE LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVI LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFF IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDF FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSE NLPEAQEKNEEGETATEETEEIAMEGAEGEAEEEEETAEG GEDEDS  5491 204 1194 GSAPRLSLGFTGAQARDPDWWARPPSRPYTQSKEDRPDTEG GGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEI LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCN: SFFDPEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWF PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENI ITKAIKSKNVVDVNVKDEEGRALLHWACDRGHKELVTVLLQI INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDC	PLK
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SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRP	
PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLd	
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VLETRVMERRGMETCAMETRGMEARGNDARGLEMRGPVPS	
MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQG	
GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGASKQ	
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5493 1 1876 RAPMMTKAVPEEPRKPGRLTQALMSPLTWEHVWICVPGGT	GSQ RQSI
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	GSQ QSI
VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFV	GSQ QSI PDCL CSLH
EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKT	GSQ QSI PDCL CSLH RTLA
EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKR	GSQ QSI PDCL CSLH CTLA TNLE
GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQG	GSQ QSI PDCL CSLH CTLA PNLE QKKM
SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLAS	GSQ QSI PDCL CSLH CTLA PNLE QKKM
SAFREDRAL VEIDEARD VIDESGAMENT ARMY LANDY ENGLAND	GGSQ QSI PDCL CSLH CTLA PNLE PKKM
HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEV	GGSQ QSI PDCL CSLH CTLA TNLE DKKM VVEW SSAL
QAKADLEKELECAREGEERREREEVLREEIQTLTSKLQE	PDCL CSLH CSLH CTLA TNLE DKKM VVEW SSAL KQLL
KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEG	PDCL CSLH CSLH CTLA TNLE DKKM VVEW SSAL KQLL LQEM
RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQ	PDCL CSLH CSLH CTLA TNLE DKKM VVEW SSAL KQLL LQEM LPRP

SEO	Predicted	1 Bar 32 - 1 - 1	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Î	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valing,
- (	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<del></del>	sequence	<u> </u>	\=possible nucleotide insertion)
- [		İ	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
- }		i	PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
-		}	HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
5494	71	536	SLPTKNFPV
[		1 330	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
1	ł	l ·	RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
}		j	GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
į.	ľ	ł	ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
			QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
			GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
İ			LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
ł		]	SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
1	]		CTVMTDLKDAKAPPGCLTPERIPEVHHISODPLHYSIASVSASO
I	[		KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
1	1		GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
1			LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
1			PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
[	ĺ		IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
j	1		WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
L	)		AEMIQKLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
1	<b>{</b>		MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
1			SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGOKPSSSDTFFR
1			PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
1			NLRKDVEAVTGSPASOTSICIGILLRSAELALLLHPVDOANTLK
1			SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
			MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
			LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
i l			MKRSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
1			TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
			VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
	İ		NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLO
1 1	1		CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIOVSNTKINI.
]	ł		KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
]	<b>!</b>		GNDLKENVKSDSVLLTSGKYDLKKQRSVTOATOTSPGVPWPSOS
1	ĺ	i	ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
5497	1821	3308	HHIKKMTVE
		2200	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
] [			CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFFVCFQLSN GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
1 1	• 1		YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
1 /	ļ	ŀ	PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
] ]	}		LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSOVS
1 1		ĺ	DYDYFSVSGDQEADQQEFDKSSTIPRNSDISOSYRRMFOAKRPA
1 1	1	Į.	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
1 1		j	TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPOG
1 1		į	VTSMPSSMWSGQASVNPPLPGPKPSIPEEHROAIPESEAEDOER
(	٠. ا	i	EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
5498	2434		TTNDRSAPRFS
]	4424	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
1	ſ		KVFSHKSNLTEHEHFHTREKPFECNECGKAFSOKOYVIKHONTH
			TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
			QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
			PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
			LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
<u> </u>	Bequence	<del></del>	QKIHTH
5499	324	926	
34.23	324	326	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
1		ł.	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
	ļ	i	WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
1	1	1	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
	<u> </u>	<b></b> _	PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
		1	VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
1	}	<b>,</b>	DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
1	ł	1	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
}	1	1	YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
l	Į.	1	DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
1		1	AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
1			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
ì	1	1	CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
1			NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
1		ŀ	LOWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
1		1	GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIO
i	ľ	1	REIALAKKHGTQNKRAALQALKRKKRFEKOLTQIDGTLSTIEFO
1		1	REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
I			EQODIAQEISEAFSORVGFGDDFDEDELMAELEELEOEELNKKM
Į.		1	
1	1	<u> </u>	TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT
5503	216	<del></del>	
2202	216.	654	KGVRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
1	1	1	EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
{	1		AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
5504	58		SPAGTLGEKPVNS
3504	28	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
1	l	1	GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
į.			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1	I	1	LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
j	}		IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
1			DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
1	1	(	EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
1		Į.	SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
1			QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
ł		Į.	GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
1			· ·
1	l .	ŀ	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
1		ļ	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
1			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETTVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILED VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSTYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFMAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBUSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETLVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSTYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL
5505	3312	1219	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLWELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIVRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVCVPJISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBUSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGGIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
5505	3312	1219	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATHLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMENNRNNKLPSNLPQLQNLIKRDPPAYIEEFLQ QYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF
5505	3312	1219	CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHBUSKAHRLCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN DFEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILBD VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGGIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ

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Ocation   Ocat		1	1	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid F=
Corresponding   Correspondin	NO:	nucleotide		Glutamic Acid. F=Phenylalanine G=Glycine
Coffred   Samon acid   Sequence			corresponding	H=Histidine, I=Isoleucine, K=Lysine.
amino acid residue of amino acid residue of amino acid sequence    Poproline, Q-Glutamine, R-Arginine,   Sequence			to first	L=Leucine, M=Methionine, N=Asparagine.
maino acid maino acid sequence    M-Tryptoplan, Y-Tyrcsine, X-Juknown, *-Stop   Codon, /-possible nucleotide deletion,   Y-possible nucleotide nucleotide deletion,   Y-possible nucleotide nucleot	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence  Codon. / Apossible nucleotide insertion  Vapossible nucleotide insertion  Vapossible nucleotide insertion  VAPOSSIBLE nucleotide insertion  VAPOSSIBLE nucleotide insertion  VAPOSSIBLE Nucleotide insertion  KISSKNIKKIEDNIKUTENTENTENTALTAVITACESK  KISSKNIKKIEDNIKUTENTENTENTENTENTENTENTENTENTENTENTENTENT	ł			S=Serine, T=Threonine, V=Valine,
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LAAPPSIGAGGSTPEAPPESWTQLWFFRFVNANGYASPWUGGY LLVQYFFRKNYLETGRIGCPPLVKACVGNBPKASDEVPLAPRT EAARTTPMGALKLLFCATGLQVSYLTNGVQLQRWTRSYGATA TSPGERFTDSQFILVINNRVLALIVAGCVLCKOPPHGAPWTRY SFASLSNVLSSWGVEALKFVSFPTOVLAKASKVIPVMLMGKLV SRSYSTEMBEVLTATLI SIGVSWPLLSSGPPRSSPATTLSCLIL LAGYLAFDSFTSNWQDALFAYRMSSVQMWFGVWFFSCLFTVGSL LEQGALLEGTRFWGHSEFAAHALLSICSAGGLFIFYTIGGP GAAVPTITMTLRQAFAHALLSICSAGGLFIFYTIGGP FRGTRRGCRFAGASRARRRFPCFGPAAPGSLEIGGFGTAAGKK VAVADVQFGPMFFHQDOLQVLLVFTKEDNQCNGGCFGRCEKAGFK VAVADVQFGPMFHQDOLQVLLVFTKEDNQCNGGCRCEKAGFK KISSNTVIVGVVVRRVDESELSVMPFISAGFTRRVVENNNINACY NELLQLEFGEVSGLKKARANSYFTASBADFITASCLIST GKEWGGI YVAKKKNGDHOLQMVKLIPGGGGIRHVVSILRVC NGNNKAEKISECVQSDTHTDNOTGHKXRADLDTINSCLRI GKEWGGI YVAKKKNGDHOLQMVKLIPGGGGIRHVVSILRVC NGNNKAEKISECVQSDTHTDNOTGHKXRADLDTINSCLRI LDRVLEILRTTELYSPQFGAKODPHANDLVGGGISRRSWFIRA EVSSQRRASSARINSTISADVLHATAYFLSKERIKETLDPIDEVAAL LAATHINDVHORTINSTICAGGELLLYNDTAVLSSHRALAF GLATHINDVHORTINSTICAGGELLLYNDTAVLSSHRALAF QLATGGDKCNIFKMMERNDYRTLRGGI IDMVLATEMTHHFEHNU KCADVSNPCRFLQVCIEWAAR ISEEYFSGTDEBGOGGJPVMVNF FORNTICS IPKSGISFIDYFITTMFEHADAFVOLPDLMMHLDNNF KYMKGLDEMKRINRPPPB  S508  1151  691  LSSVSGRSRASMFANGGTOKNGEVTYNGTENGTHAMPTENTHITIKRMLI KCADVSNPCRFLQVCIEWAAR ISEEYFSGTDEBGGGGDFPW VLKKVLVDQLVAS PLLCVWFFIGRCTITIKDTTLTKMLI KCADVSNPCRFLQVCIEWAAR ISEEYFSGTDEBGCGGGPPW VLKKVLVDQLVAS PLLCVWFFIGRCTITIKDTTLTKMLI KCADVSNPCRFLQVCIEWAAR ISEEYFSGTDEBGUGGDFPW VLKKVLVDQLVAS PLLCVWFFIGRCTITIKDTTLKFENTL KRML KCADVSNPCRFLQVCIEWAAR ISEEYFSGTDEBGUGGLPVWDP FORNTICS IPKSGISFIDYFITTMFEHADAFVOLPDLMMHCHNNF KYMKGLDEMKRRNRPPPB  ESSPERASMFAVGCGWGFFIHWWYLSLDEDFPAGGLGGFPP VLKKVLVDQLVAS PLLCVWFFIGRCTITIKDTTLKFULT KRML THE THE THE TOTT TO THE				CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
EAACTTPMWOALKLLECATGLQVSTLTMGVLORWTRSYGATA TSPEGEFTDSGPLVLWARVLALIVAGLSCVLCKOPHGAPMYRY SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVI FVMLMGKLV SRSYEPHMYLTATILS IGVSMPTLSGOPERSPATTLSGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVWFPSCLFTVGSL LEQGALLEGTRFWGRISEFAHALLLSICSAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFYTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTLRQAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP GAAVFTIIMTRAGAFAILLSCLISAGGUFIFTTIGGP AVADAVGFGPRSPROVALVERACKSUPTRAGETACHACKAGE VAVADAVGFGPRSPROVALURACKSUPTRAGETACHACKAGE KISENTYLSTVAKKANGENICHTURKAGALLDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGALLDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGALDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGALDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGALDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGALDTINSCLIST GKEWGGIYYAKKANGENICHTURKAGAUSAVASAAT EVSSQRHSSMARIHSMTIEAPTIKVINIINAAGESSPMPVTER EVSSQRHSSMARIHSMTIEAPTIKVINIINAAGESSPMPVTER EVSSQRHSSMARIHSMTIEAPTIKVINIINAAGESSPMPVTER EVSSQRHSSMARIHSMTIEAPTIKVINIINAAGESSPMPVTER EVSSQRHSSMARIHSMTIEAPTIKVINIINAAGESSFMPVTER EVSTAMANAATATAGATATAGATAGATAGATAGATAGATAGATAGA	1			LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY
TSPEERFIDSOFLVLMNRVLALIVAGISCYLCKOPRHGAPHYRY SFASLSINVLSSWOCYRALKFSFTOVLAKASKUT PVMLMGKLV SRRSYEMWFUTATILISIGVSMPILSSGPEPRSPATTISGIIL LAGYIAFDSFTSNWQDALFAYKMSSVQMWFGVFFSCLFTVGSL LEQCALLEGTRFMGRISFRAHALLSIGSACGUPIFYTIGGS GAAVFTIIMIRQAFAILLSCILYGHTVTVGGLGVAVVFAALL LRVYARGREKQRGKKAPVESPGVG GAAVFTIIMIRQAFAILLSCILYGHTVTVGGLGVAVVFAALL LRVYARGREKQRGKKAPVESPGVG GAAVFTIIMIRQAFAILLSCILYGHTVTVGGLGVAVVFAALL LRVYARGREKQRGKKAPVESPGVG FFGTRAGEKAGKKAPVESPGVAF VAVAUVOFGPMR PHODOLOVLLUVTKSDNOCNGFCRAGEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAZALCRSIRSS KISENTVIUGVVRRVDREELSVMPFISAGFTRRYVENNNIMACY NELLQLEFGEVRSGUKLRACKSVYTALENSEDALISTEDDRFIQ YANDAFFTTMGYGGGELIGKELGBVFINEKABALLDTINSCIRI GKEMGGIYYAKKNOENIQOWATIPVIGGGKIRHVSIIRVC NGNKABKISECVGSDTHTDMCYTGKHKADALLDTINSCIRI GKEMGGIYYAKKNOENIQOWATIPVIGGGKIRHVSIIRVC NGNKABKISECVGSDTHTDMCYTGKHKADALLDTINSCIRI GKEMGGIYYAKKNOENIQOWATIPVIGGGKIRHVSIIRVS NEVLSTRAYIQWVSSNIITPISLDDVPPALAMENSEYMPDFI FELEAATHNRPLIYILGLMFARFGICFHLCSESTLASMLQIIE ANNHSSNPYHNSTHSADVLHATAYFISKERIKETLDPIDBVAAL LANTIHDVDHGGTRSFLCNAGSELALLVNDTAVLESHAALAP GLITGDDKCNIFKNMERRDVRTLRQGIIDMCTAFMTKHRSHVM KPNSINKPLATLEENGETDKNQEVINTMLRTFENTILIKRMLI KCADVSNPCRPLQYCIEMARISETYSGTDEEKGOGLPVVMPV FDRNTCSIPKSGISFIDYFITDMFDAMDAFVULPDLMCHLDNNF KYNKGLDEMKLANLRPPB  5508  1151 691 LSSVFSRRSASNFAVGCSMGFFLHYWYLLDRIPABGLRGFN VIKKVLVDQLVASPLUGWYPLGIGLGEGOTVGSECQLHERFW EFYKADWCWPRAQPVNELFVPPGFVTYINGLTLGMDTYLSYL KYNKGLDEMKLANLRPPB  5509 1238 619 RKSRGCQNALSASGFRAARARINVRKLKPHECKLLKQVDFLNWE VTOHNLHELRVLRRYRLQREDTTRYNQLSRAYELARRIRDLP EPOLFVYDSKIKKRYFULTSREDTDFDLEA AEGEROPPDSSEEAPPATONFIIPKSELLCDPVTASSFCRR LPYVLLKLENAGHLQAAVAFVEGGHWRVDPUVTDPAFLVTRSM LDFVTUVDSKIKKRYFULTSREEDTDFDLEA AEGEROPPDSSEEAPPATONFIIPKKEGELCDPVTASSFCRR LPYVLLKLEVNOSKIKRRYLEYNEERDDFDLEA AEGEROPPDSSEEAPPATONFIIPKKEGELCDPVTASSFCRR LPYVLKESVONSTRIDVGKKLTFFFRYSGATEKLVALLINTLDRWID EFPDPUDPSRFCNKAYRTWAKLDERERILVAVTVPPHLAAAVP EVAVLKESVONSTRIDVGKKLTFFFRYSGATEKLVALLINTLDRWID EFPDPUDPSRFCNKAYRTWAKLDERERSLOGVWGLDDFOFLPFI WGSSGLIDHPYLEPRHFVDEKAVNERENDENDHDYWHECTLFFTLEKT GFFABBSOCLNINISAGUSKANVENE	1	1		LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
SFASISNIJSSWCYFEALKPUSFPTOLKARSKUTPVMLMCKLU  SRRSYEHWFULTALTISIGSWEPPSSPATTLSCLIL LAGYIAFDSFTSNWODALFAYMSSVOMMFGVNFSCLFTVGSL LEQGALEGTFMCRHSEFAHALLISICSACGQLFIFYTIGGE GAAVFTIIMTIRQAFAILLSCLLYGHTVTVVQGLGVAVVFFALL LRVVARGRIKQRGKKAVPUSPVQKV  PRGTRCCFFAGRASRRARREPFGFGAAPGSLEIGGFGTAAGKK VAVADVQFGPMFFHODOLQVLLVFTKENNOCMGFGRACEKAGFK VAVADVQFGPMFFHODOLQVLLVFTKENNOCMGFGRACEKAGFK CTVTKEAQAVLAGFLDKHHOI IDHRNPROLDAFALCRSTRSS KISENTVIVGVVRRVDREELSVMPPISAGFTRRYVENPNIMACY NELLOLEFGEWFGSOLKIRACNSTALENSBOAIZITSEDRFIQ VANPAFETTMGYQSGELIGKELGBVPINEKKADLLDTINSCIRI GKEWGGIYYAKKNGDNIQONVKIIFVIGGGKIRHVVSIIRVC MSNNKARKISSCVGSDTHTNDTGKHKNRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITRVINININAGESSPMVTEA LDRVLEFILRTTELYSPOFGAKDDPHANDLVVGGINSOLKRLGS NEYVLSTKNTQNVSSNIITPISLDDVPPTARAMENEEYNDPDI FELEATHNPRLYILGLMPPARFGICEFLHCGSSTLRSWIOIIE ANNYSSNPYINSTHSADVLHATAYPLSKERIKETLDPIDEVAAL LAATIHDVDHPGRTNSFLCNAGSELALLYNDTAVLESHHAALAF QLITGDDKKNIFEMMGRNDYRTGHID IDMUNTAVLESHHAALAF KCADVSSNPCRFLQYCIEWAARISESYFSQTDEBERGQGLPVVMPV FORNTCSIPKSQISFIDYFITMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMIKINIRPPPB  5508  1151 691 LSSVFSRESASMBAVGGSWGPFLHWYLSLORLPPASGLRGPPN VLKKVLVDQLVASPLLGVWFPLGGIVGESCGEREKFW EFYKADWCWPBAQFVNTLFYPPGGTVETNIGHLTGMDTLSSL KYRSPVPLTPPGCVALDTHAD  SKYNEGCONALSASGPAAAAAAIMWKKLKFHEOKILKQVDFLNE LPTVLLKLRMAQHLQAAVAFVEQHVRVQGDVVTDAFAFLVTRSM LPTVLLKLRMAQHLQAAVAFVEQHVRVGDDVVTDAFAFLVTRSM LPTVLLKLRMAQHLQAAVAFVEQHVRVGDDVVTDAFAFLVTRSM EPPVTWDSSKIKRRIVLEVNERDDFFDLEA  5510 96 1195 PAGAHLSSGSSEPLEVEFGGRGVKGERGLQAGSGAPGRSKM AEGEROPPPDSSEAPPATONFIIPKKEIHTVPDMKWKRSQAY ADTIGFILTINERSVKSKLITFYREPAGSGGWMSLDDFGFLFFI WGSSCLIDBYLEFRHFVDERAWRLDKTYRPLACLCLKGVTRVDDQ IAIVFKVFNRYLEVWRKLQKTYRPEARSGGGWMSLDDFGFLFFI WGSSCLIDBYLEFRHFVDERAWRLDKTYRPEARGSGGVMSLDDFGFLFFI WGSSCLIDBYLEFRHFVDERAWRELGKKFYTUCHF		)		EAALTTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
SRRSYEHHEYLTATLISIGYSMFLLSSGEPRSSPATISCLILL LAGYLAFDSFTSMODALFAFWSOMMFSCHPTYGSL LEQGALLEGTFFMCRHSEPAHALLSICSACGQLFIFYTIGGF GANVFIIMTHRAPAFILLSCLLYGHTYVVGGLGVAVVFAALL LRVVARGRIKQRGKKAVPVSPVQKV  5507 3704 1271 PRGTRCCFAGRASRRARRRFPCFGFAAPGSLEIGGFGTAAGKK VAVADVQFGPMFRFGOOLOGVLUFTKENDOCOGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDHRYPROLDAZALCRSIRSS KISENTVIVGVRVDEDELSWAPPISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDALZITSEDRFIQ YANDAFFTTMYQGGGELSWAPPISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDALZITSEDRFIQ YANDAFFTTMYQGGELSICKELGEVPINEKKADLLDTINSCIRI GKEMGGIYYAKKNGDNIQONVKIIFVIGGGGKTRHVSIIRVC NENNKABKISECVQSDIHTDNOTGKKKSRKSLDVKNVASRAT EVSSGRHSSMARIHSMTIERJKVINIINAAGESSFMPVTER LURVLEILRTTELYSPOPGGKODDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQNVSSNIITPISIADHVARGREKETHVDFIDEVAAL ANYHSSNPYHNSTHSADVLHATAYPISKERIKETLDPIDEVAAL IAATIHDVDHPGETNSFLCINAGSELAILYNDTAVLSEHHAALAP QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMKHHEHNN KPNNSINFLINLEENGETDKNGGELAILYNDTAVLSEHHAALAP QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMKHHEHNN KPNNSINFLINLEENGETDKNGGELAILYNDTAVLSEHHAALAP QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMKHHEHNN KPNNSINFLINLEENGETDKNGGENITMLKTPERRTLIKRMLI KCADVSNPCRPLQYCIEWARISEEYFSQTDEBKQGGLPVWMPV FDRNTCSIPKSQISFIDTPITTMPDAMDAFVDLPDLMQHLDNNF KYWKGLDEMKLNNLRPPB  5508 1151 691 LSSVFSRSSASMPAVGCSMGPFLHYWYLLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGWVFLFLGLGCLBGQTVCESCQELRERFW EFYKADWCWPAAQFVNTLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPUPLTPPGCVALDTRAD  **KYRSPUPLTPPGCVALDTRAD** **KYRSPUPLTPPGCVALDTRAD** **KYRSPUPLTPPGCVALDTRAD** **EFYKADWCWPAAQFVNTLFVPPQFRVTYINGLTLGWDTYLSFCRRF LPTVLLKLEMAGNLORAVFVEQCHVRYGPDVATDPAFLVTRSM EPFYTWDSSKIKRHVLEXTNEENDDFLEA  **TOPHVUDSSFRENKAYRTWYAKLDEREPDTLEA **DPGVPATSSFCRRF LPTVLLKLEMAGNLORAVFVEQCHVRYGPDVATDPAFLVTRSM EPFYTWDSSKIKRHVLEXTNEENDDFLEA **AGEERGPPPDSSEEAPPATONFIIPKENLIKTVPDMCKMKRSQAY ADVIGFIILTINGRVKKLKTYFRYRSAEIRKLULAUNTLORMID ETPPUDQPSFFFRNAYRTWYAKLDERENDLVATVVPTHLAAAP EVAPVLKESVGNSTRIDVSTGHAAPAFLCCLCKUGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSGGWGLDDFQFLPFI WGSSGLIDBYLEPRHFUDERAVMENIKUTWFLEGLIFITEMET **GERPAGHSTON** **GERPAGHSTO	1	•		TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
LAGYIAFDSFTSNWQDALFXMSSVQWMFGVNFSCLPTVGSU LEQGALLEGTFMGRHSEFAAHALLSCLSAGQDFIFYTTGQF GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLQVAVVFAALL LRVYARGRIKQRGKKAVAVPUSSPVQKV VAVADVQFGRRFRGDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDDLQVLLVFTKEDNOCMGFGRAGEKAGKK VAVADVQFGPRFHQDQLQVLLVFTKENDOCMGFGRAGEKAGK VAVADVQFGPRFHQDQLQVLLVFTKENDOCMGFGRAGETSPS KISENTVIVGVVRRVDREELSVMPPISAGFTRRVENPINMACY NELLQLEFGEVRSQLKRAGKNSVFTALEBOFFTQ VANPAFFTTMCYQSGELIGKELGBVFINENSEDATLSTEDRFTQ VANPAFFTTMCYQSGELIGKELGBVFINENSEDATLSTEDRFTQ VANPAFFTTMCYQSGELIGKELGBVFINENSEDATLSTEDRFTQ VANPAFFTTMCYQSGELIGKELGBVFINENSEDATLSTEDRFTQ VANPAFFTTMCYQSGELIGKELGBVFINENSEDATLSTENSEDVANASRAT EVSSQRRHSSMARIHSMTTEPITTVIIII INAAQESSPMPVTEA LDRVLEILRTTELYSPOGRAKDDPRILAGRENENENGPITI EVSSQRRHSSMARIHSMLTFPTRILAGRENGTETHAGESTLASBUQIIE ANYHSSNPYHNSTHSADVLHATUSKERKIKETLDPIDEVANL IAATIHDVDHPGRTNSFLCNAGSELALLYNDTAULSHHAALAP QLTTGDBKCNIFKMENDYRTSADVLHATUSKERKIKETLDPIDEVANL KFONSINKPLATLEENGBTDKAGEVINTMLATFERNTLIKRMLI KCADVSNPCRPLQYCIEMARISESFSGTDEBEQQGLPVMPV FORNTCSIPKSGISFTDYSTENDAMATSENGTSEDQLDWMPHACHLDNNF KYMKGLDEMKLRNLRPPPB  LSVFSRRSASMFAVGCSMGFFLHYWYLSLDRLFPASGLRGPPN VLKKVLVDQLVASPLLGWWFJLGLGCLGGQTVGESCGELRERFW EFFKADWCVMPAAQFVNTIFVPPQFRVTYINGLTLGMDTTLSYL KYNSPVPLTPPGCVALDTRAD  5509  1238  619  RSSRGCONALSASGPAAAAALMVKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNGLERAVENLARRINDLP ERDQFFVRASAALLDKLAVFTGSELLCDFVTASSFCRR LPTVLLKLENAQHLQAAVFVEQGHVWRQPDVTDPAFLYTRSM EPFVTWDSSKIKKHVLEXNEREDDFDLEA  BEPFVTWDSSKIKKHVLEXNEREDDFDLEA  ADVIGG ILTILBECKTOWKGKKITTEFWSSELIKGLUALINTLDRWTD ETPPUQPSFRFCNKAYFNWYAKLDEBERDLVATVVPTHLAAAVP EXPVLYKLESVGNSTRIDVGTGHERAPAFLCCLCCLGCURVDDQ IALVFKVFRYLEVMRKLQKTYRMPAGSQGWMGLDDFGFLPFI WGSSCLI DHPVLERRHFVDEKAWENKK	1	1		SPASISNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV
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VAVADVĢROPMEPHODOLQVILIVPTKEDNOCNOFORRCEKAĢEK CTVTKEAQAVLACFIDKHHOI II IDHRNPRQLDAEALCRSIRSS KISENTVI VGVVRRVDREELSVMPITSAGFTRRYVENPRIMACY MELLQLEFGEVESQLKLRACNSVFTALENSEDALITISEDRFIQ VANAPAFETIMGYGGGELKELGEVVEINEKKADLLDTINSCIRI GKEMGGIYYAKKKNGDNIQQNVKI IPVIQQGKIRHYVSIIRVC MGNNKAEKISECVQSDTHTDNOTGRKKORLDTINSCIRI EVSSQRRHSSMARHSMTIEAPITTVINIINAQGESPMPVTEA LDRVLE ILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTOMYSSNI ITPISLDDVPPRIARAMENEEYWDPDI FELEAATHNRPLIYLGLKMFARFGICEFTHCSESTLRSNLQIIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVAAL IAATHHVDHBGRTNSFICNAGSELAILVNDTAVLESHIAALAP QLTTGDDKCNIFKMERRDYRTLRGGI IDMVLATEMTKHPEHVN KPVNS INKPLATLEENGETDKNQEVINTMLRTPERRTLIKRMLI KCADVSNPCRFLQVCIEWAARISESYFSGTDEBKQQGLEVVMPV FDRNTCS IPKSQISFIDVFITMFDAWDAFVDLPDLMQHLDNNF KYMKGLDEMKURNLRPPPB  5508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGWYYFLGICLEGGTVGESCQELREKFW EFFKADMCVWPAAQFVNFLFVPPQFRVTYINGLITLGWDTYLSTL KYRSPVPLTPPGCVALDTRAD  75509 1238 619 RKSRGCQNALSASGPAAAAANANWKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRRDYTRYNGLSRAVREIARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDAPLVTRSM EDFVTWVDSKKKRHVLEYNEERDDFDLEA AEGEROPPPDSSEAPPANDFI I PKKR IHTVPDMKKMRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTIDRNID ETPPVVDPSSEAPPATQMFI I PKKR IHTVPDMKKMRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTIDRNID ETPPVVDPSSEARPARGNAYRTWYAKLEEAENLVALLVTVPTHLAAAVP EVAVYLKESVONSTRIDVPSSKYNGGLLRMYKGCGGLOASGAPGRSKM AEGEROPPPDPDSSEAPPATQCCLCKIGVLRVDDQ IALVFKVFNRYLEFWRKLQKTYRWEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVMENHCDYMFLECILFITEMKT GPFABHSDQLWNISAVPSWKNNGGLIRMYKAGCLEKFPVJCHF GFFABHSDQLWNISAVPSWKNNGGLIRMYKAGCLEKFPVJCHF	5507	. 3704	1271	
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				KFGSLLPIHPVTSG

1 000	Dwadiata	T 5 - 3	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
70:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
)	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ļ <u>-</u>	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND
1	1	1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
		1	TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG
		1	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
}		l	FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
	Ì		LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
1			SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
1			SLYATRDLAAAIDRMDKYNFDEMIYVTDKGQKKHFQQVFQMLKI
		ĺ	MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
1			MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
1	ļ		VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
ł		·	VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
5512	120	1015	QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
1 33.2	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
l			IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
1			RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK IGETIFFRGPRGRLFYNGPGNLGIRPDQTSEPKKTLADHLGMIA
1		ĺ	GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
			BIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
	1		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
j			PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
{	ĺ		FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
}			GKMLDKYIYGAQGVLLVYDITKYQSFENLEDWYTVVKKVSEESE
1			TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
i			DSVFLCFQKVAAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS
<u> </u>	ļ		RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
}	1		CYLGSKTLFYRLEILEGITIVGMALTGMAGEQFIPGCPHLMLYD
1			YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
i			MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
1			EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPANDLM
İ	<b>'</b>	•	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKNAEREOESEEEM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAP
	1	200	TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEBLYSYL
	ì		KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY
•			FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
			VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG
ł			SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
1			NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
1	(		IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
1			KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
L			YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
5516	3	735	NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
[ '			IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG
1	[		KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
1			DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
į l			YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
5517	246	400	PLEEPTTEPPVNLTYSANSPVGR
	220	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
5518	3	1375	TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
		13/3	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
			FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
[			EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
]			IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY
] [			NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
[	}		GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
	1		SFWNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK
		<del></del>	THE TANK THE TANK THE TANK TO THE TANK TO THE TANK THE TA

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence se	=Stop  TIPEKS DHSAAT  VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ	=Stop TIPEKS TOHSAAT VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
location corresponding to first amino acid residue of amino acid amino acid sequence	=Stop  IIPEKS  DHSAAT  VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
corresponding to first amino acid residue of amino acid residue of amino acid sequence  87  87  477  18520  117  943  PTEGROKVLKTFTVPRSALAMTKTSTCIYHFULSHVLLQSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLQTIYYEVSTYLLAFWILLGLAFWILLSTYLLAFWIL	=Stop  TIPEKS DHSAAT  VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
to first amino acid residue of amino acid residue of amino acid sequence Se	=Stop  TIPEKS DHSAAT  VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
amino acid residue of amino acid sequence    Seserine, Tethreonine, Vevaline, method sequence   Seserine, Tethreonine, Vevaline, wetryptophan, Yetyrosine, Xeunknown, sequence   Sequence	TIPEKS DHSAAT VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
residue of amino acid sequence    Sequence	TIPEKS DHSAAT VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)  HICPYRTNKYGEYYLLLPGSYIINVTVPGHDPHITKV QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLI KPSLFLFLVSLLHIFFK  5519 87 477 IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAM GVAVAGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIM AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSI PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYT SQEGKDEVKPKILANGARWKYMTLLNLLQTIFYGVTC RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFRILE IYPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWYPVFAKLSLLGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFG PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG GVSQEAEGNPRGGPNQPGGGFKEDTPVRHLDPEEMIRG LREEIRRVNNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	TIPEKS DHSAAT VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
Sequence   Sepurate   Sepurate   Sepurate   Sequence   Sepurate	VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
HICPYRTNKYGEYYLLLPGSYIINVTVPGHDPHITK\	VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
ONFSALKKDI LLPFQGQLDS I PVSNPSCPMI PLYRNLI KPSLFLFLVSLLHIFFK  1 KSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAF GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIR AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSF SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTC RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFMILE I YPKVLDTVI PVWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWYPVFAKLSLLGLAF YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFC PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQFKEDTPVRHLDPEMIRG LREEIRRVNKFVMMHWKQRHSRSRPYPVCFRP LREEIRRVNKFVMMHWKQRHSRSRPYPVCFRP 5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT	VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
KPSLFLFLVSLLHIFFK	VAAVVG NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
S519   87   IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAM GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIA AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSI AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSI SQEGKDEVKPKILANGARWKYMTLLLILLLQTIFYGUTG RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILE IYPKVLDTVIPWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFG PAKHQLVKNIR S121   S46   911   KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP GSPLGGRSEEKMWVFGYGSLIWKDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
5520 117 943 PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYT SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTC RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILE IYPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWYPVFAKLSLLGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFC PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQFKEDTPVRHLDPEEMIRG LREEIRVRNKFVMMHWKQRHSRSRPYPVCFRP 5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	NGGGVA PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
5520 117 943 PTEGROKVUKTFTVPRSALAMTKTSTCIYHFLVLSWYT SQEGKDEVKRYLLANGARWKYMTLLLILLLQTIFYGUTC RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILE 1YPKVLDTVI) PWLNHAMHTFIFPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGWVYPVFAKLSLIGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFC PAKHQLVKNIR 5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSCPAEGNPRGGPNQPGQSFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP 5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	PSS FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYT SQEGKDEVLKYLLANGARWKYMTLLINLLLQTIFYGUTG RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILE IYPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWYPVFAKLSLLGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFG PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRVNNKFVMMHWKQRHSRSRPYPVCFRP LREEIRVNKFVMMHWKQRHSRSRPYPVCFRP WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	FLNYYI LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
SQEGKOVBKT TVPKSALAMTKTSTCIYHFLVLSWYT SQEGKDVKPKILANGARWKYMTLINLLLQTIFYGVTC RTKKGGKDIKFLTAFROLLFTTLAFPVSTFVFLAFWILE 1YPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLA YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFO PAKHQLVKNIR  5521 546 911 KILNMQKSCENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQSFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	LDDVLK LYNRDL SKKTGL AFFSLS WPDWKS
RTKGGKDI KPLTAFROLLFTTLAFPVSTFVFLAFWILE IYPKVLDTVI PVWLNHAMHTFI FPITLAEVVLRPHSYF TLLAAASIAYI SRI LWLYFETGTWVY PVFAKLSLIGLA YVFIASIY LLGEKLNHWKWVSVQI LQRWRLESVGI CFQ PAKHQLVKNI R  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	LYNRDL SKKTGL AFFSLS WPDWKS
1YPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYF TLLAAASIAYISRILWLYFETGTWYPVFAKLSLLGLA YVFIASIYLLGEKINHWKWVSVQILQRWRLESVGICFQ PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	SKKTGL AFFSLS WPDWKS
TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLA YVFIASIYILGEKLNHWKWVSVQILQRWRLESVGICFQ PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	AFFSLS WPDWKS
YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQ PAKHQLVKNIR  5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP  5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	WPDWKS
5521 546 911 KINMOKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP 5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	POPSEE
5521 546 911 KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGN GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRG LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP 5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	PQPSEE VDELER
5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	POPSEE VDELER
5522 1224 637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	VDELER
637 GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	
WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	
WQGSTDHKGVPGKPGRVVTLVEDPAGCVWGVAYRLPVG	NYSRRF
AVI DEDEVOCATION OF THE PROPERTY OF THE PROPER	KEEEVK
AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCD	NPDYLG
PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPE	EADEHL
FALEKLVKERLEGKONLNCI  5523 3 1280 SKCKKPMGSSMSAATARRAUGANGANGANGANGANGANGANGANGANGANGANGANGANG	
SKOKKENGSSMSAATAKKPVFDDKEDVNFDHFQTLRAT	GKGSFG
KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELE	ILQEIE
HVFLVNLWYSFQDEEDMFNVVDLLLGGDLRYHLQQNVQ RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAH	FSEDTV
ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFE	TOFNI
GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVP	DWWSV
VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSE	TWSKEM
FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKS	CKVEPG
SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREP	CDNSRD
RDAAEPVEDEAERSALPMCGPTCPSAGGG	PEAPES
5524 85 2318 RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFS	22029
NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEPN'	WTDDG
CABTEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQS	T.VSOS
MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRF	IEGEGA I
TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLD	TVVUD
ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDT:	TPPPP
RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDP	AUTUR
. RLPVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPD	VIHPA
IYGAKAVILIYHHVHSRLNSQSSSEHQPSSCLPPDAPVSI	LEKAN
NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPOX	SAGLE
ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDF	STOVE
NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGOSKI	GSGRV
AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASI	PPPPA
FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHS	SLTNL
RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLE	VSCSE
NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSPPFHGS	RPAGL
PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWG	ĸ
834 SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLV	RESGS
LTYEEFLGRVAELNDVTAKVASGOEKHLLFEVOPGSDSS	APWKV
VVRVVCTKINKSSGIVEASRIMNLYOFIOLYKDITSOAA	GVLAO
SSTSEEPDENSSSVTSCQASLWMGRVKOLTDEEECCICM	DGRAD
LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWV	VSDAP
TEDDMANYILNMADEAGOPHRP	1
5526 3 853 RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIR	TRAVT
QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRK	PAOSR
LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKK	EMLKI
KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEK	
AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEY	HRKDK
YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAA	HRKDK FFPPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	
1	to first	1	L=Leucine, M=Methionine, N=Asparagine,
1	i .	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u> </u>	\=possible nucleotide insertion)
[	<b>}</b>		RRNPDSPAKAI PKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
	<b>{</b>	l	KFQTKGIKVVGKWKEVKIDPNMFADGCMDDLVCFEELTDYQLVS
(	ŗ	1	PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKKIKLKKS
}	ł	Į	KNVATEGTSTQKEFEVKDPELEAQGDDMVCDDPEAGEMTSENLV
1	1		QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
ŀ	Ī	ſ	AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
}	1		AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
1	Ì		AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
ļ		i	ŧ .
1			VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN
	ł		LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
			FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
	)	j	YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
1	1		ROTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
1	i	l ·	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
]	<b>!</b>		RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
1	İ		FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
ł	Į	}	RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
1	1	<u> </u>	YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
1		[	EDMYKCGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK
ļ	į	ł	YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP
1	İ	ì	QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
}	•		YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
1	Į		QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
ļ	<u> </u>	1	FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
ì	l		LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
Į		Į	AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL
1	ſ	ĺ	PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
		1	LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE
i		i	KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL
Į.	ł		IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
1	1		AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
3330	1511	2000	, ·-
1			FOPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
(			VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
1	}		DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
		Į .	SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
		1	QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
1			ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
1			PASLKPTASGRKCLFRVEEDEEEDEEDKKPMSLSTQVVLRRKPS
1	ĺ		VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
1		l	ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
			TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
1	1	[	GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
1			LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
1			GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC
L		L	EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF
1			ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV
1		,	TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
1			LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMI I EDETEFCGEELLHSVLOCKSVFDVLDGEEMR
1			RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
)			KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
1			GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN
1			FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
1			LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL
	<u> </u>	L	WELLINGTH A A CUGINA CATANA CATANA CALLA C

SEQ	Predicted	I brodies - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
· }	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVODTTI.
J		į	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIOGTEI
1		Į	DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSOI
	} .		YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAORKI
į	•		SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1	1		PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
Į	1.	}	VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
i	I .		IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
5533	94		MHRA
3333	34	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
	ł		TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
l	-	i	LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
ĺ	i		LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
{	1		HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
i	į	005	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
			AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
}	]		CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
ŀ			RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
j	1		NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
			SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM
1	}		KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
1.	1		ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
J			LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
1	1		DAVYTELQPTSPTPTWFADETPQPQTQTQQLEGTDGPLVTDPET
	1		HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
5537	3	2391	FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
	1 - 1	2331	RARVSSPOLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
	·		PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
	ŀ		YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH YNKDLLTEHCTBASFQKVISRRHGSCDLENLHLRKRWKREECEG
i	1		HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
	'		FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1	1 1		EXMYHCMMSEKTLMQSSSPKNHQEMYFLEKQYKCKEFZEVFLQS
1			MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
1			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP
ì	}		TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
	]		FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1	, [		EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
1	'		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTOHRKIHTGENLY
1	1		KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
[	. 1		RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
1	1		CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHOR
1	. [		SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
	1		FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
5538			EKL
3338	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
1 1	!		IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
l i	j	Į	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATOKIAFSATRTI
1 1		1	NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
] [	ļ		SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
5539	38		GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
	30	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
; ;			IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
l l	}		DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGOVCS
	<del></del>		SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

GEO	Drodiend	T 8 37 3 3	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
, NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			ELEKVHOLCONFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY
1	1		PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
j .	}	1	
	l	İ	SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
1		}	RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
į.	ţ	1	QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
	<u> </u>		LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
ļ	)	1	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
Į.		1	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRBKDEI
1	ì	t	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
<b>{</b>			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
}	1	<b>}</b>	KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
İ		1	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
j	}	}	
1			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
J	1	j	LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
F 5 4 3	ļ	[	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
Ì		l .	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
j	l .	}	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1	i	1	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
l .	Ì	j	FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1	i		KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDONNIWIRDHED
}	1	ì	SGSVHLGTPGPSSGGLASOSGDNSSDOGVGLDTSVASPSSGGED
1	1		EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEOKKO
i	]	1	LAQDTGLTILQVNNWFINARRIVQPMIDQSNRTGQGAAFSPEG
1	1	·	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWROHRG
3212	140	1440	
l	ļ	1	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
Ī	i		GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDBI
1	)	1	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1	}		FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
l	1	1	KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
1		}	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
J	}	1	EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
Į.	1		LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
1	}	1	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1	l	i	KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
İ	ŧ.	Į.	SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEO
1	1	1	RESKARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
1	i	]	DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
1	ì	l	
ł		Í	ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK
l	l	1	LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
1	]		SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
ł		ł	ESARDVEALMERMOQLQESLLRDEGTSQEEMESRFELEKSESLL
t			VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ
ŀ		)	DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
1	ļ		DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
l			ACYPEKTTRRMYNLFWRHFRHSEKVIIVNLLLLEARMOAALLYAL
			RAITRYMT
5544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
l			PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
ŀ			
1			QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEEEEEV
l		1	ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR
l	1		FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
			LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK
!			LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
			FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRD1YGGDYERFG
			LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR
			MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF
			SEHEGYFGAVGALLELLKIP
	· · · · · · · · · · · · · · · · · · ·	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence	<u> </u>	\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
j	}		KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
ì		[	GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
}	į.	1	SAFGEDGEGDDLDLWTVRCSGCHWEREAAVRFQHVGTSVFLSVT
			GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
1	1		DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
(	ł		RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
ł			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1	<b>[</b>		SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
ì			FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
1			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
[			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
ļ			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1	-		KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1 1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
j			FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
Į j	·		RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
)			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
5548			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
3346	1	2153	DQTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
1	-		DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLLVLLLAAYFFRF
1 1			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
; 1			PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
1 1	-		REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
1 1	Į	'	FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
1	ļ		WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
1 1	}		LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
i i			SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
1	1		TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
, 1	1		IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
ļ Í	{		RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI
}	į		KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
{	j		IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
, ,	1	,	SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
<u>[</u> ]			DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
ļ .			CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
] [	ĺ		KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAP
	į		RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
	<u> </u>		NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
,	1		SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
	,		TVAMKCQYVGADVLDIAFTMVASADGLVYEPTVFDISPQQKENQ
			RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
į į			ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
		ļ	FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
1	1	ľ	KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
ļ .	j	1	MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
		(	CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	MQRDHTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

CEO	Dradiated		
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	sequence	1 . · · · · · · · · · · · · · · · · · ·
<del>                                     </del>	sequence	<del> </del>	\=possible nucleotide insertion)
1			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK
i	i	ł	QRRAGINEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
Į			DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
I	}	1	LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
Ì		4	PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
}		1	FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
	l .		KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
l	ł	1	EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
		ļ	EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV
1	}		AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
L			FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
}		1	SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKSEKEKHL
1	}	]	DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
1	1		PVRACRTQPAENESTPIQQLLEHFLRQLQRKOPHGFFAFPVTDA
į			IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
1			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
1	1	1	EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAEEHVL
i			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP
1			DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
ì			ALSMONNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
ł	1		GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG
1			DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
1	1	1	HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL
	ļ		GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
			VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
1	ł		AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
1			EANLRAQELAKROGWENVPPFDHPLIWKGHASLVQELKAVLRTP
į	]		PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHCAHCFNA
<u>l</u>	ļ-		AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE
1			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL
5554	166		PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
3334	100	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
ł		ļ	GRSFFWVLPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
ł	ľ	i	WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ
1			VHTFEIFQKFLNESENSVFQAVYGLQRALQGDYKDVVNMKESSR ORLEALREAAIKEETEYMELLAABKHOVEALKNMOHONOSLSML
<b>!</b>		}	
1	,		DEILEDVRKAADRLEERIEEHAFDDNKSVKGVNFEAVLRVEEEE
1	1	1	ANSKONITKREVEDDLGLSMLIDSONNOYILTKPRDSTIPRADH
1	1		HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
1	1	{	SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
1			YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM
1			GSARGDXEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
1	ł	1	ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
İ		-	LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
}			VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
1			TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
1			SEPSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
FFEE	<del> </del>		TRCVPRPERRSSL
5555	212	1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR
1	1		GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK
j .		1	KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
1	1	<b>f</b>	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
1			GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE
}	}	}	MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
			GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV
}	1	<b>{</b>	TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
I			PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQG\$VQK
	j ·	1	VYNGLQGY
5556	5835	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

CDO	15		·
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
l.	sequence		\=possible nucleotide insertion)
			LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
1			YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
1	1		DALWII TEW NEIGEBURGA OF DE DEUT DE DESCREAVENRYE
ł	1	1	DALVLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
ı	l l	1	QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
[	i	l	GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYPIGDVFAAR
1	1	1	FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
	1	ł	SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
1	l	ì	KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
1	1	•	LRLVDKAQVLVCRALSNILLLPWPNLPENEOOWPVRSINHASLI
		Į.	SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
	1	Į	SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
	i	}	TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
1	[	į.	VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1	]	J	PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
l.			QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
i	1		TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
<b>,</b>			ARI DEEL TO CONCURATION CONTROL CONTRO
1	1		AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
5557	1712	491	RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
		491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
ĺ	[ :		KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD
1	}		RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV
			ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
	[		AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
1	1		DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
	1 1		WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDOLOOKLY
i	i i		LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
ļ	•		LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
	L		KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
}	}		TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
1	1 1		LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
l	! }		YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
1			LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
1	i	•	GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1	j j		SI ODCI SEDI WWW.DWG.FDG.DW.DDST.T.
	[ _		SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
1	1	•	CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
1	ļ ļ		NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
1 1	i		FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
5559			LNAMSVYTLSPEKYHALCSQTQVMBVGNEE
2007	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
1 1	1		ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
]	1		LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG
1 1	! <b>[</b>		KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
[ ]	·		VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
1 1			MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
! !			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
( /	ļ	i	PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
j l	Į.		ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
1	ĺ		KTITEI NI DENUTTE VOTE TENTE TO THE TENTE TO
, ,	Į.		KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
ļ I			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQ
j 1			RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPK
	1	•	PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
5560			GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
2200	9	921	SSVVEFSALSVSMACLSPSQLOKPOODGFLVLEGFLSAEECVAM
ŀ	1		QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
	!		IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
[	j		FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
! !	i		EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
l	!		SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
1	i	j	SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	sequence	
	sequence		\=possible nucleotide insertion)
			QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPPHLYPNTQAPS
ì	1	ł	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVT_KPPPPEVVSRGS
			S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
J	ļ.	1	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1			LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
ł	1	ł	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1	1	1	IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
	1	į	INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
1	ì	ł	DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
	1		GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1	1	1	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	1	1	LASFLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSFE
ļ	1	1	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
ł	1		INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
1	1		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
Í	1		GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
		İ	LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
ľ	1		VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT
	1		GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
		1	PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
}	}	ļ	GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
ļ			TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
5565	993	138	RWNSPNPARAGSISRPORAPGSVSAVAMTAAVFFGCAFIAFGPA
j	ļ		LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID
Į	į.	}	NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN
1	1	ì	PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
Į.	ļ	į	GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
1	į.	(	LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
j	j	·	LKLCLLCQDKNFLLYNQRSR
5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
ł		ł	KNVKEYVRWMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
1	1	į.	IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
ĺ	į.	İ	MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
ł	J	1	DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
l			EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK
1.		1	RPQVYP
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEACANINA
Į		1	CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
1			CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ
			AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD
I		(	GNEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE
			EVRAKLLELKHKHDALLRAGSRGRSLLRRRTSSAGSRGKVVRRV
i			SLTORTDLYRKOHAQEAIVWOOPPPTSPEPPEDNDDRQTGAELR
1		1	PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
1		1	STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
1	1	1	GLPGDTVTPOPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
	1		SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE
1			NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
1			SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
1	1		MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS
}			IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL
1			NPVPGSYPTQSCHPHLSPSHPVSOTOHASGOKLASWPSCTPGHM
ł			PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
			VNSPGTVYSGALGTPGAAGSKESSRVPMP
5569	2	835	OTPCPLAWERGSRSEDISVPGOKPPTCSSFSGMDVGPSSLPHLG
1		035	511CETHURYGOYGENTOALGAKKAICDOLDGIDAGLOOPRHING

SEO	Predicted	Prodicted and	· ·
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	J	\=possible nucleotide insertion)
			LKLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
	1	ľ	KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
i		ļ	PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVI.
	1		TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLL,YRSGVK
-	1.	1	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
	ļ		SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
- 1			MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
			PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCI.
		[	DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
	ì	į	RPEBYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
5571	<del> </del>		EAQDMEL
23/1	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1		l	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
ŀ			PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
1			DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1	<b>!</b>		RPEBYKOKIKEYIOKYATEEALKEQEEGTGDSSSESSMSDFSED
5572	2802	2085	EAQDMEL
	1	2005	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
ļ	1		DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
			RWGRRGLGAGAGGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
1	1		RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
1	<u> </u>		KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE EPSEYTDEEDTKDHNKQD
5573	2562	219	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF
	ļ		SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
	]		GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
1	j		MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
	1 1		VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
	)		NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
	!	-	QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
1			SOHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
	i i		IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
( )			GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
			LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
1 1	]		VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1 1	,		IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEOYFIOOGGG
1 1	}		PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA
	. [		RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
1 1	l		TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMOLLSEIFE
, ,	Ţ		HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
5574	123		APTVQELAALEKEAQTSFLHLGYLPNOLFRTF
1 22/3	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
] ]			LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1 1	f		TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
<b>}</b>	1		RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
1 1			FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
5575	456	265	RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
	.50	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
] [			LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
5576	249	2146	SPDIGRNSPHYLMFP
1 1	. ]	4440	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLLHRDVSSR
	1		EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
1.	1		QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
1	)		SKWTPLETQEKBEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
1 .	1	ſ	DQKFRCCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
1	i i	ì	EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL
1	<u> </u>		LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI
] [	į		VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR
·			KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=pcssible nucleotide deletion,
	sequence	Doduction	\=possible nucleotide insertion)
	sequence	<u> </u>	SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFDKGTSVIARNQVR
	1	1	LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC
	İ	1	HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLDVGENNRG
	į	ļ.	HNESWYLHNVYPEMEVPDLIPTETGATANDGINGCDDVGBNARG
		i .	GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
	1	ì	LGSCHFTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA
	1	1	MAPCNPSDPHQLWLFV
5577	3	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
55			YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
	1	[	SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLL
	1	Ì	QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV
	{	ĺ	GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
	· ·	}	SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS
	(		
	1	1	IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK
	1	1	
	Į.	1 .	EXPCHPERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV
			WPSLRSDRNNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
	•	· ·	WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
		l .	TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL
	i	1	EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
	Į.	l .	SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
	ŀ	}	LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR
5579	1 3	1540	CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL
	1	l l	REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
	1	1	RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK
	1	1	
	1	l .	ELLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
	<b>\</b>	l l	VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
	1	(	DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
			ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
			KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
	]	1	CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
			LHGEVILDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
	)	1	EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP
2200	1		WRLLOCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS
		1	GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG
		1	SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT
			ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
	[	i	DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLINGNGC
		į.	
			INILSYPELKPYQSINAHPSNCICIKFDPMGKYFATGSADALVS
	1	1	LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
	l	1	EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
	5	1	EAGTVKLFGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
	}		CSPDPOSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA
		[	YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG
			TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY
	i		SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
	1	1	TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
			TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	IITMNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI
		<b>!</b>	EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ
			ALVOYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
	i		EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC
}		1	SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
	}	1	1 STALPHDESVIOLGOELHOKUGERVKKAI KREQEDETI SDEDIO
			TARCVADOCTSNGLGSTDDIETDCYVDPRGSPALLPSTPTMPLF
			TAAGVADOGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
			TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
:			TAAGVADOGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLI

SEQ	Predicted	Predicted end	I Amino poid comment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<b>———</b>	- Sequence		\=possible nucleotide insertion)
1	l .		DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
ł	}	}	TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
1	1		RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
	1		KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT
1			IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
1	l		HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL
			REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
1			AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK
i			YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
- (	1		LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY
	1		DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
(	[		CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
1	}		LCDRLQKGKAC?DGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
	ļ <u> —</u>		KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1	i		IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
ł	1		QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
	i I		HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
l	ł :		CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
t			SGAKVIREKKI1EVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
í	1		IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1	}		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1	1 '		PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKEFCPNEQN
5504			WRQHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1	i	•	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
1	1		QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
1 1	1 1	_	HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
	i	·	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
	1 1		SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
j	] }		IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1 1	[		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1	] ]		PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
5585	253		WRQHREAYEEDEDGPQAGVQCQTA
2585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1 1		•	SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
1	1		ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
		•	VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
			GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
			YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
}	]		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
1	]		RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITX
	Ì		AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
1 1	1		ISANBKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
			NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
j · 1			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1 (	1		SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
1	ŀ		ENMVSF1KGG1KVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
] [	· I		VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
}	J		GHSFRSVLCVMLLLCYHTFLTPVLGTGNVNIEEAEKLLKPYLNR
] [	Í	· í	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
1. [	]		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
[ }			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
1			RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
1			AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
[ ]			ISANEKKIKYDHYLIPNALLELALLLMBQDRNEEAIKLLESAKQ
<u> </u>			NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

SEQ	Prodicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G≈Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
,	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	l .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	w=Tryptophan, i=Tyrosine, k=onkhown, -scos
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
į	1		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
ł	(	(	IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
•			DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
1		l .	KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
l		}	TLAOYLASEFORSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
	1	1	
1	1	ł	ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
1	1	1	NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
ŀ		Į.	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
l	1		SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
1	}		EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
i			GKCEAISIEIAS
	<del> </del>	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
5588	3	503	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
			TAPTEVI KROADDAMADECRI IDAUI WITTATAMADECAL AMBORTA
ì		j	VLAFFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
Į.		1	AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
)	}	1	RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
1		1	PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1		1	GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
	1	1	ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
1	1	1	RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
i	i	(	
1	į.	1	KEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
į	1	1	VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSG?
1	İ	1	TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV
1	ĺ	1	TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
1	ļ	1	SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
1	•	į	DNCA
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
3320			EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
1		(	LDDODDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
1			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
{	1	i	KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
}	l	1	
ı			QQKKFCFS1QQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
L		<u> </u>	PPPPPEPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
1	1	[	LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
1	[	1	DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
ł	i	1	PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1	)	1	CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
1	1	<b>\</b>	RQLEEEQAVRPKYLLGREVTGMMRAILIDWLVQVQMKFRLLQET
1	į	1	MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI
I	}		GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
ł	1		GREAT A I DATE I TRUMPER TO THE BALL OF TH
1	1	i	KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
1	į.	1	ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
i	Ī	}	TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
			VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1	1		TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
}	1	1	IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
	1		ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
1			
			MITKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
	•		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1			DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLEELQSLR
1			BLDLYDNOIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
i			KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1			SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1			ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
1			EPIPOUNCIEA TECHENIANTIAINTIANTIATATATATATATATATATATATATA
1	l .	1	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Pnenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Scrine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
į	sequence	1	\=possible nucleotide insertion)
	- <del></del>	<del> </del>	MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
Į			SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
1	į		ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
1	ł	ł	KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
J		j	SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
		1	ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1			EFWMNDNLLESNSDLDELKGARSLETVYLERNPLQKDPQYRRKV
			MLALPSVRQIDATFVRP
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1		[	PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
1	1	(	LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1	1	!	AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
İ		1	NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
ı	1		NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
1		ł	VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
j	,		DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
1	Į.	ł	LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
1	1		HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG GSWCDS
5595	698	219	
2020		219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
ì	i i	1	FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
ļ			KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
1			VFVIVGFVTL11FKRELHTISFLGGLALNEGVNWL1KNVIOEPR
1			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
l			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
	[		GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIPCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
	]	•	DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1	1		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1	}		GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1	}		NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
1			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1	[		TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1			YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
			HILGFGEDELGEVYILSSSKSMTOTHNGKLYKIVDPKRPLMPEE
l			CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
}			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1 .			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1			IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
į i	<b>!</b>	i	LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
] ]	]		SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1	{	ĺ	NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
į į	1		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
			TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
aı	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1	ļ	1	YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1	1	}	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
1	Ì		CRATVQPAQTLTSECSRLCRNGYCT?TGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
	1	1	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1		1	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1	l l	1	FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	ł	1	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
1	1	1	TFYHPTINVPPRHALKWIRPQTSE
	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
5601	1977	1244	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
· i	1	1	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
	ì		TFYHPTINVPPRHALKWIRPQTSB
L			YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
5602	246	766	NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
1	1	1	AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
1		İ	AAALKLINKIPLVVIGCQNEKFGGCGSVIXIABABBITTICKII VO
		<u> </u>	IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
5603	1	565	WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
1			
1	1		CFGFBDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
1		ļ	TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA
1	l		TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
1	ł	1	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
1		ł	GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
į.	1	Į.	RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
1	[	1	DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
1	1	ļ	VIDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
i	ì	ł	SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
Ì	1		NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
1	l l	İ	LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
		İ	ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
			ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
1			QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
1		1	MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
1			KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
1		1	GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
1			ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP
1	1		GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
1		1	GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
ŀ	1		GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
1			VWVAOETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
ì	1		KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG
	1		FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
	1		SGANTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
)	}	1	VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
1			ORNLGPALSRTLSQLYCSYGPLT
5606	3	1099	GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
3000	,	1	LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
i		ł	IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
1	1	l l	GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
1		1	VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
Į.		1	KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
1	1	1	SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
		•	1 STRUCK AND MANUAL VERT DEPART THE OF SY OR ADDITION AND A POSTOR
	1	1	TONUTERA TOGGET I COGRGENTAOVELAERCSCK PHWCCFVKC
			TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC RQCQRLVELHTCR

SEO	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	] -	\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMI.WLDLAMAGSSFLSPEHQRV
i	į		QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
			FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
	l		RIQTEPKYTGIWHCVRDTYHRERVWGFYRGLLLPVCTVSLVSSE
1			VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
1	1		SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP
1			KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFISYA
1			VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
ŀ	<b>[</b>		QADGQGQRRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAFPVN
			MVVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
ŀ	<b>[</b> :		KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
	į į		ALQLSVEEFVERYERPYKPVVLLNAQEGWSAOEKWTLERLKRKY
			RNOKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1	J		EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
Ì			GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
	i		NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
			WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
. I			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
5610	54	1196	R
	33	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG
1 1			CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS
	l		VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
	j		VIJFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
!	1		DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
	į		VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
1	1		TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
1 1	1		LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
			ELSNRFQGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPE
1 1			KLTAFKEKYMBFDLNNEGEIDLMSLKRUMEKLGVPKTHLEMKKM
1' 1	- 1		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
			KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS
	İ		SLLTLENLILNEFSYTATEARRLYLORKTVPSALLVOLIOERLA
}	· .		EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
i i			IERNLGKRIDPQTGEIYHTTFDWPPESEIONRLMVPEDISELET
1			AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVOS
5613	115	7.55	NHRTNAPFTPRVLLLGPVGS
1 2013	++2	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
			KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
1	1		AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
1 1	r		FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
1 (			GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
i I	į		AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
1 1	. 1	1	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
	j		TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
5614	3	1268	IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
	-	-400	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER
	<u> </u>	İ	APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
		l	EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
	İ	İ	LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
1	ł	İ	QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
1	1	ł	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
l i		,	SLASAGSAEGVGGAPTKGQAAPPAPPLPSSLDPPPPPAAVEVP QRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDELGLPPPPPGF
1			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

NO:	ID	1		Amino acid segment containing signal peptide
NO: nucleotide corresponding to first amino acid residue of first amino acid residue of amino acid residue of amino acid sequence		pedruurud		1 /A Alamina C-Cuchaina D-Aspartic Acid F-
Cocation   Cocresponding   Coffee   Corresponding   Coffee   Coffee   Communication   Coffee   Communication   Coffee	NO:	1		
to first amino acid residue of amino acid residue of amino acid sequence sequence  5615  9  1558				
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence  sequence  5615  9 1558  1558		1		
amino acid residue of amino acid sequence solution acid sequence solution acid sequence solution sequence sequence solution sequence sol			1	
residue of amino acid sequence (20dm., %-possible nucleotide deletion, %-possible nucleotide deletion, %-possible nucleotide deletion, %-possible nucleotide insertion)  5615  9 1558 ALGRERFGDPREMERAATPAAAGAARREELDMDVMRPLIN DGTSDERHEGELLPVQKHYQLDDGE15FVQTHHALKON. LLCLPLAIKANGIVLGPISLPVGHISLVGHILLVGCHELLGCHELLVGCHELLGCHELLVGCHELLGCHELLVGCHELLGCHE			l e	
amino acid sequence    Codon, /=possible nucleotide insertion,		L		S=Serine, T=Threonine, V=Valine,
Sequence   \_possible nucleotide insertion)				W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Scop
SDOWCEGUSSETGFPGGNYEPSC   ALGERRADTPARAGAMREELDMDVMRPLIN    ALGERRADTPARAGAMREELDMDVMRPLIN    LICLPLAIRNAGIVLEFISLVFICTISVHCHILLVRCSHF    FKSTTLGYSTDVSFMSUSPMSCLQKQAAWGRSVVDFILV    GFGSVYIVFLAENVKQVHEGFLESKVFISNSTNERSKFCER    LRIYMKCFLPFIILLVFIELRULFUSFLANVSMAVSLV    YVVRNNPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVULP    MKSKRFPQALNIGMGIVTILVYTLAIGMCHBEIKSS    LRIYMKCFLPFILLVFIELRULFUSFLANVSMAVSLV    YVVRNNPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVULP    MKSKRFPQALNIGMGIVTILVYTLAGMCHBEIKSS    LRIYMKCFLPFILLVFISTCAGALILFRIDVISFVCAVSS    LILPPLVEILTFSKEHYNIHMVLKHISIAFTGGVGFLDFIKSS    KWROICEFGIRSFLVSTSTCAGALILFRIDVISFVCAVSS    LILPPLVEILTFSKEHYNIHMVLKHISIAFTGGVGFLDFIKST    KWROICEFGIRSFLVSTSTCAGALILFRIDVISFVCAVSS    LILPPLVEILTFSKEHYNIHMVLKHISIAFTGGVGFLGFT    EEIIYPTPKVVAGTPQSPFLNINSTCLTSGLK    TOPPERGFGSAAMAGARARLEGVARAFTGGKLFTOWGFLLGFT    EEIIYPTPKVVAGTPQSPFLNINSTCLTSGLK    LKHLSSGDLLKRNMHLGTEIGVLAKAFTGGKLFDDWTT    LKHLSSGDLLKRNMHLGTEIGVLAKAFTGGKLFDDWTINLAW    IKORLTARNIHPASGGVYNIEPNPPKTVGIDDLTGSPLIQ    KPETVIKRLKAAPEDDTKPVLEYYGKGVLETFSGTETNNI    YAFLOTKVPQRSQKASVTP    DPRGGGSSPFRGAGAMAEGVNRSAGLAPDCEASATAETTV    TCEAAGKSPEPKOVDSCVECRIAGROPDCEASATAETTV    TCEAAGKSPEPKOVDSCVECRIAGROPOCHLHCENSTON    KORLTARNIHPASGGVYNIERNPTVKGVGVLHENWTVG    ERNNFTTEDAVKRIENCHTERKOVELVERWATVG    CERNSTTOFTNVKRIGHCHTERKOVELVERWATVG    CERNSTTOFTNVKRIGHCHTERKOVELVERWATVG    CERNSTTOFTNVKRIGHCHTERKOVELVERWATVG    CERNSTTOFTNVKRIGHCHTERKOVELHILGSSACPS    CHIQMIKGINSPULIGKSNDPSCULHILSSSITHLISSISILHSSISISHMKK    SGKVKWSOLIGBRIESSACVSKGNVYEGKRALIGISSACPS    CHIQMIKGINSPULIGKSNDPSCULVGCNIGLVVLK    SKYMMFTTEDAVKSSATNDPTGLIVIGSHDHMKA    SGKVKSOLIGBRIESSACVSKGNVYGGKRALIGUSVANDATV    KHSCGCVLPSSPQCCSQVICTGCUDGNLLCFPHFGEDWA    GPISSSCTISSEQKIFFGSHDCFIYCCNMKGHLQWKFT    VARKSCGSTPSSPQCCSQVICTGCUDGNLLCFPHFGEDWA    GRYSSSPVULESMLIIGCRNNYVCLDLLGGROR    SEPTEMPTORTISTAGASSTRPOPLTKUGGLIAVNDATV    CHARACTAGGGSGSPSPOCCLHPPAQHSQDLLPUNDVGNO    CESPPATP    DEPULTSGNVTISTAGSSTRPOPLTSVENIGLIAVNSTAGAR    ALGERSSPVULESMLIAGSSTRPOPLTSVENIGLAVNDATV    CHARACTAGGGSGSPSSPOCCLHPPAQHSQ		1	sequence	Codon, /=possible nucleotide deletion,
S615   9   1558   ALGRREPGDPREMEAATPAAGGAARREELDMUNRPLIN     DGTSDEEHEQELPVQKHYQLDDQGI 5 TYOTIMHLIKON.     LIGLPLATKINGGI VIJEGISLVPI GTISVHCMHLIKON.     LIGLPLATKINGGI VIJEGISLVPI GTISVHCMHLIKON.     GFGVYI VIPLAENWAGWESPLESKYTISSTRINSSPICER     LRIYMLCFLPFI ILLVFIRELKILEVLSFI JANNSMAVSLV.     YVVRNPOPHINLPI VAGWKKYPLFET SISTRINSSPICER     LRIYMLCFLPFI ILLVFIRELKILEVLSFI JANNSMAVSLV.     YVVRNPOPHINLPI VAGWKKYPLFT SISTRINSSPICER     LRIYMLCFLPFI ILLVFIRELKILEVLSFI JANNSMAVSLV.     YVVRNPOPHINLPI VAGWKKYPLFT SISTRINSSPICER     LRINSGI STEPT VAGWAGY SOLVEN JANNSMAVSLV.     KWGICEFGI RSFLVS ITCAGALLI PRIDI VIJSVGAVSS     LLIPELVEI LIFTSKEHTNIHMULKNI SI AFTGVVOFLLGER     EBILYPT KEVVAGT PGSPFILLINSTCLISGIK     DDFVRCGPGSAAMGASARLERAVI IMEAPGSKGTVSERT     LKHLSSGDLLRINNIHMCREIGGULARAFIDOGKLI PDDVWT     HELKINLTOYSWILDGFPRTLPGAEALDRAYQIDTU INLWY     LKRILTARWI HPASGROVYNIERPH PKY GIDDLITGSPLIQ     KPETVI KRILKA PEDOTKPVLETY QOKKUPLET SIGNEM     KRILTARWI HPASGROVYNIERPH PKY GIDDLITGSPLIQ     KPETVI KRILKA PEDOTKPVLETY QOKKUPLET SIGNEM     KRILTARWI HPASGROVYNIERPH PKY GIDDLITGSPLIQ     KPETVI KRILKA PEDOTKPVLETY GOKKUPE SIGNEM Y TA FOLVETY OF THE SIGNEM Y TO TECHNOLOGY ELHEN MYT GOKKUPE PKY GIDDLITGSPLIQ     KPETVI KRILKA PEDOTKPVL PKY GARATA PLOT TO TECHNOLOGY ELHEN MYT GOKKUPE PKY GIDDLITGSPLIQ     KPETVI KRILKA PEDOTKPVL PKY GARATA PLOT TO TECHNOLOGY ELHEN MYT GENNAT MYT GEN	_	sequence		
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LRIYMLCFILDFIILLVFIRELKNIFVLSFLANVSMAVSLUV YVVRNMPDPHNLPIVAGMKKY PETGAVPA PEGIGVULP MKESKRF POALNIGMGIVTTLYVTLATLGYMCFHDEIKGS LPODWNLYGSVKILYSFGIFVTYSIGFYVPAEIIIFGITS KWKGICEFGIRSFLVSITCAGALIJPRLDIVISFYCAVSS LIJPPLWEILTFSKEHYNIMMVLKNISIAFTGVVGFLGF EEIIYPPFKVVAGTPGSPFLNIKTCLTSGLK  5616  1 719 DDFVRCGFQSAMMGASARLLRAVIMGAPGSGKGTVSSRIT LKHLSSGDLLROMMLRGFEIGVLAKAFIDGSKLIPDDVMT HELKNLTOYSWLLDGF PRTLPGAEALDRAVQIDTVINLMV IKQRLTARWHPASGRVYNIEFNPPKTVGIDDLTGEFLIQ KPETVIKRLKAVSEQOTKPULEFYKKGVLETFSGTETNNI YAFLOTKVPORSGKASVTP PWRGGSRPBGAGAMAEEQVNRSAGLAPDCEASATAETTV CEAAGKSEPFKDYDSTCVFCRIAGRQDPGTELLHCENED KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENNAVTOG ERNNFTDFTNVRMGFHMPPFGILHHLULAVPOLGFL YRVMSVMFITADHLIBKLAT JINNINLSEBNKLGSKEDLWEKLGYLWKSTINLFEDLLKV LFLNSGGBIKSIRPLSGEIEKLUGTSVPGLLEIILSSRI HILQTVVPDEDVTFRKSCATKRKLSNINOEEASGTSLHQK FTCHNEINAFVVLSRGSQILLSHSTRFLTKLGHCSSACES QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTOR VRMRSDTGKCUDASPLVVITPTBKSSTTVYIGSHIRMKA SGKVKNSQILGDRIESSACVSKCGMFIVVGCYNGLVVLK EKYMMFTTEDAVKSAAMDPTGLYIUGSHDHAYALDIY VWKSKCGGTVFSSPCLNIPHHLYPATLGGLLLAVNPATC KHSCGKPLFSSPCLSSPCLICIGCURGNLLCFTHFEGDVM GPIFSSPCTSFSSRKIFGSHDCFIYCCNMKGHLQWKFET YATFFAFHNINGSNEMLLAASTDGKVMILESGSGOLGSV GEVPSSPVLESMLIIGCRBNYSCLLGLUGNSLLCFTHFEGDVM GPYSSPVLESMLIIGCRBNYLCDLLGSNORX CGEVPSSPVLESMLIIGCRBDRALLCFTHFEGDVM GPYSSPVLESMLIIGCRBNYVYCLDLLGSNORX CGEVPSSPVLESMLIIGCRBNALLAGSTDGKVMILESGSGOLGSV KRSCGGTFSSPCCSQFICHPAPARSDGLVPSLG LWGTKGRSGSSPSSPGCCCHPPAPARSDGLVPSLG LWGTKGRSGSSPSSPGCCCHPPAPARSDGLVPSLG LWGTKGRSGSSPSSPGCCCHPPAPARSDGLVPSLG LWGTKGRSGSSPSSPGCCCHPPAPARSDGLVPSLG LWGTKGRSGSSPSSPGCCCHPPAPARSDGLVPSLG ECSPPATP  5620 930 182 PIPPPFTLAMFITRSEVDRGVNTFSFEGRLFGVEYAIEAI ALGIOTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETONHMFTYNTETMTVESUTJOANSNL BEDADPGGMRSPFGVALLFGGVDEKGPQLFHMDPSGTFV ALGSASEGAGGSLQEVYHKRMTLKEAIKSSLIILKQVMEI TTIELATVOPGQURPHMFTKEELEEVIKNI		1		FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQI
YVURNMEDPHINLDIVAGWKKYPLFEGTAVFAFEGIGVULP    MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGS     Lippuwilygskilysrgirviysigfyvpariiipgits     KWKGICEFGIRSELVSITCAGALIIPGIVGYLOGAVSS     Lilphuwilitpskehnimmulkinisiaftgvogflight     EBIIYPPTKVAGTPQSPFLINIMSTCLISGIK     DDFVRCGPQSAMGASARLLRAVIMGAPGSGKGTVSSRIT     LKHLSSGDLLRDMMLRGTEIGVLAKAFIDQKLIPDDVMT     HELKNLTDYSWLLDGFPRTLPQAEALDARYQIDTVINLMV     KQRITARWIHPASGRVYNLEYYQKKGVLETFSGTETINKI     VAPLOTKVPQDSQASSVTP     T76		}	1	GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVI
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GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK  5619 2160 1477 DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRG AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSG RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGF LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQE TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFOVEYAIEAIF AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLA EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVG AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI		1	1	YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYEL
5619 2160 1477 DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRO AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSO RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGF LWGTKGRGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQE TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP 5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIF AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLF EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVG AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			i	
AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSC RSCPQPRPLEEILRAGSSTRPQPLTSSCCGMSCMYSFLGF LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQE TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIE AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIKARVETQHWFTYNETMTVESVTQAVSNLF EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVG AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI	5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPC
RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGF LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGMQE TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIR AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLF EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			1	AOSLHSHOLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLG
LWGTKGRGSGPSSPGCCLHPPAQHSQDLPLVHVDVGWQE TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIR AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLJ EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			1	
TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPS ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIR AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLI EEDADFGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVV AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI		1	1	
ECSPPATP  5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIR AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLA EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVALAGASSEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			1	
5620 930 182 PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFOVEYAIEAIH AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIG LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLJ EEDAGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFV AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			1	- 1 · · · · · · · · · · · · · · · · · ·
AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGO LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNL# EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI	EC30		102	
LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLJ EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI	2020	930	182	
EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQ AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI				WIGITIDEGACING SEVETIDENSINE STEVE ACTION OF THE SECOND SE
AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEI TNIELATVQPGQNFHMFTKEELEEVIKDI			ì	DIADANI DI DIAMA MENDECINI I ECCUDENCO OLI ERMODECA ELICADIA DI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADANI DIADAN
TNIELATVQPGQNFHMFTKEELEEVIKDI		1		
I FOR I THE PROPERTY OF A PROP				
	5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDG
				ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSL
		1		MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVE
		l		GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWI
QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQG				QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDIL
HTQTQDLQVFLKEBALHGFRVSDYFEYMEILEQNYRTVLI		Į.		HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDM
NIRLQST		ł		NIRLOST
5622 1122 456 AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNP	5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAM
PGTFYFOFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTC		1	1	PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFR
THE PROPERTY OF THE PROPERTY O		1	1	QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDC
I DADSELHCHWERCRESMECDDTDSENTRIANTISMSEC		Į.	1	

C PA	Dradiated	Transition 1	
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid E=
1.0.	location	t .	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
j	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	1 2242222	<del> </del>	\=possible nucleotide insertion)
- [			EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL O
5623	3	954	
		333	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
ı			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
<b>!</b>		i	TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
	ļ	ľ	ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
1	İ		SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
1	ł		SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
1			SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
1	1		SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1	}		IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
1		•	NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
1			EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK
1			LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
	!		AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
Į			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
i i			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
ı	l i		GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
I .			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
	}		ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
	[		RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1	. [		TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1 :			ITVQKKVSQWWBRLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
i i			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMONKAVVFFVFYLWSATE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIO
1	<del>]</del>		SIPIFNETGRESETLPYPVKIKVRESPELQIYLIMIFLGLYINE
5627	3100	<u> </u>	RHLYKQRRRRYGQKKKKIH
362/	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1 1	1		TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1	ļ <b>,</b>		ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
	· •		EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
1 1	į		LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1 1			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
1			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
1			SIPIFNETGRESFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
5628	75	1455	RHLYKQRRRRYGQKKKKIH
]		7433	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
1			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
1		!	GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR
i			IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
1 1	1	j	DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
1	1	•	LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
] [	•		DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
1	1		QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
<b>,</b>	i	}	SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC,
1	İ	1	EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
5629	2287	938	ARTNCSARPICVPCPGGRF
}	/	230	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
1 1		` [	PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
	l	į	NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
			QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
1 1	J	1	DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
<u> </u>			PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
l		l.	LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
l			DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
1			NOFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
	ł		EVTALKVPE
5630	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
3030	122.	2,0	TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
i	1		GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
1	1		KSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
1	l	1	
1	1		LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC
1	]		LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
		<u> </u>	LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARKAATMSVFGKLFGAGGGK
l		1	AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKHG
l		ļ	TKNKRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN
1		I	TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS
1		1	TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP
ļ	j	Į.	LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
i		ł.	SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
1	1	ı	FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
1	1		GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
1	I	1	NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
1	Į.	1	LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
ì	1	1	VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY
1	1	1	FLSLYTGV
5633	771	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
7633	//*	100	CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
į		1	LLLLSGHRPWGSSMV
E 53.4	1445	055	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
5634	1446	855	ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVD
1			
1	1		GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
1			SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
			ALAVGGLGSIIRVLTARKTV
5635	3	943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1			RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1			GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
1		•	EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
1			LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
1	1		KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
ı	1	l,	KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
1		ľ	HYRWW
5636	2253	1143	LEDTICOHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG
1	1	1	LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
1	1	1	ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
1	1	ł	YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
1	1		ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR
1	1	1	CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI
1	1		
l			QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
1	1	1	LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
ļ			HWDALFSYVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPPHLH
1		1	ниниронилирозаалинруоонтssаллалалалалалынро
		1	QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
ĺ	1	1	QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
1		1	VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEEIYVVTE
I	1		LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
İ	1	1	IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
1	1		PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
1		1	ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA
L			T. P. D. D. D. D. D. D. D. D. D. D. D. D. D.

SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ſ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
1			CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQP
5638			ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
3636	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
1			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
1	ł	1	TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
i		· ·	EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	1		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
	Ì		CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
1	i		MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125.	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
1		1200	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
1	1		TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
	1		EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
1	]		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
ı	]	•	CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
1			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS
1			IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAOI
Į.		,	NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP
1			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLEALYPK
1	1 1		LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
i l	ì		LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA
i		200	EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
			NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ
			IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
1 1			TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
i			KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
1 1			VHRPDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
l			LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIOYLFLTFPRIVFM
	i		LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL
5643	1	047	VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQB
	• [	847	PSGGVRDVETRGPGSRAARGPRVVMHRRGVGAGAIAKKKLAEAK
1 1			YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
1			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
1			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS
] [	Į		EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF
L I			TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
			KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
1 1	-		YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
( . I			IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
į l			GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDOLEALRD
j		l	ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
[			RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNI.
1		<u> </u>	VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSOVPTL
- E	3845		YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
1	j		AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
}	<b>[</b>		LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
5647	288	800	RAEGGAQ
/	200	000	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH
	<del>l</del> .		EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEQ	Predicted	Predicted end	T
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
140.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
i			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVD
			RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
			APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEK
j		1	SSTKETERKETKAEEELDAEVLEVFHPTHENQALQPGQAVPAGS
<b>1</b>	†		HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
	1		ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
			IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
1	ŀ		LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
ĺ	ì	İ	BGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
			LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT
		1	QEMSPEKLQQYRQVHLLPGLWEQGNCEITVHLLALPEHDAREKV
<b>!</b> .		1	LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE
	<u> </u>	1	DEGYFQELLGSVNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
]		1	KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
i	ļ	ļ	MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1	1		TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
	1		KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMOEPM
ļ	Ì	į	VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
1	1		LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
l	1		TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
i		ĺ	DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
ļ			HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG
		į	TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
Į	}	Į.	GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEBIETRVTSGSMEALNL
1	1		KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAODLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1		]	TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
1	1		KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
l	Į.		VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
	1		ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
1	Į.		LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
l	1	1	TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
l	1		DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
l	1	[	LEXRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
ŀ		l	HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG
1	1	1	TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
L		1	GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
l	i		AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
l		ł	WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
ł	1	}	ADP+LPGHSSQSPPRG+RWGRSRSAPAPAHPEHPAPAGSASASQ
Ī	I		QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPORGFPLGTLGS
	1	I	PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
ļ ·	1	1	PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
			GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA
	1	1	CMPSPPVEGSLGLSRKGHGDLPSOAR*GWHECRRARHLVPLPRL
	1		LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
		1	1
}	ł		CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW
5653	66	1401	HORKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
2023		1401	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
	i		CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
1	}	İ	GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
		,	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSOEI/SRDVIO
!		(	GWLLELQFRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ

SEO	Predicted	Dwodiate	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- [	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
- I	sequence	•	\=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
	1		PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
1	İ		LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
			ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
			THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
Į.		Ì	NWKPFVYGGLASITAECGTFPIDLTKTRFQIOGOTNDAKFKEII
1	1	Ì	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
5655	2		EKLFYYIQVQTDNNKKICLFKNI
""	"	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
1	1		PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC
1	1		ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
		-	EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
i			PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
ŀ			AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
1	,		LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
į			PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
1			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
			WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERATNAHVNLGV
4			TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
5657	10-		GVRESVNYL\VSQQNM
3637	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAABMNGEEEESEEER
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKOFSELKEXT.
1 1			FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
1 1			KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
			LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
			PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL ALVWTPPL
5658	2346	3541	TERRYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
1 1	1		NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
1 1	1		RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
l i			RTMLEDIWVTLSELDNVTFSFKOLDENYVANTNVFYHTFGSROA
į į	j		LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
	į		PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
1 1	l		TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIDIS
]			SELCYRLGACQMVMCGTGMORSTLSVSLEOAATLARSHGLT.PKC
l l	Ì		IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
5659	2	696	GDL NVPCCRUGDVGDVGDVGDVGD
	-	V 70	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
[			GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
	)		EREGEGORGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
			FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
1	1	•	CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
. 1	1		QRKAFPHHEFVALIGALLAICCNIFLGFADDVLNLRWRHKLLLP
	1	. [	TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
			PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
1	ļ	1	AGMAVTCDPKAFLSICFVTLVFLOLPLASICON*GTDSCASRGK
1	ļ	İ	ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCOP
5662			SLAVHMHERGMDMDGEQKWQYRGRT
3002	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
L	————— <u> </u>		PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLP

	7 - 37 - 5 - 3	1 500 28 200 200 200 200 200 200 200 200 20	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO:	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
	<u> </u>		LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
	1	· ·	QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
	1	1	NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE
	1	1	LFQLEPSGKLKVPEENFFNVPAFLTVSGQLHLEVMSGAFTQVFT
	1	1	FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
			ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
		1	AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
	į.		VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
ŀ	į	1	NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP
	İ		QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
			KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
	1	ŀ	GPPPGWDAAPPERGCE1FIGKLPRDLFEDELIPLCEKIGKIYEM
	1		RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
			CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
	1	1	ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLPEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
ŀ	1	<b>\</b>	GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
			FYYAKDEWPFGEYFCQILGA
5667	. 1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
1		į.	SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
i		1	ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
l			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
		İ	PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
3000	031	1 334	VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	<del>                                     </del>	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
3003	1	_	ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
Ī	<b>}</b>		ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
i	•		NSQ
5670	3	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
			ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
			STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
5671	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
			FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
			SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
ļ		·	FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP
i	1		WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
1			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
Į.		1	KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
1			DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE
1		1	AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
1	1		LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ
1			DLVFLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
i			MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN
]			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
1			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
1		.[	MFLKVAVTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
			KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKVT
	1	1	
	ł		LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
-	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
ļ			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
5676	2	930	HKCL
	1	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
1			RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
1	1		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
1			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
1			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	1		WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
5677	. 1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
			VTAETHPLPLLAPLAVCQSVKSPAACOVRPRPRAVALPAALGGP
1	]	•	GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
I	1		RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIONSKRKGPEP
İ	1		TREFESVLVDAFSHVAREADEGCKKPLERLLNIWOERSVYGGEF
			IQQLKLSMEDSKSFPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
1	l i		SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
5678	3	593	DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
1		333	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
}			GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIEE
1	ł I		SLAEFTEOFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEE PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
I	1		AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
]		•	DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
1			LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
			FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
5680	252		MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
3000	258	592	RRLTSTSEKLONRNSHTPLESLIHPOPSYKGFGIMFGKKKKKIE
			ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
5681	45	869	DPSCITPIQLAPMKTIVRGNKPC
		003	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
			RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
1	i		PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
	-[	•	LCLASFGMTLLGNFQLTNDBEIHNVGTSLTFGFGTLTCWIQAAL
1			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
]	İ		QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
			PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYO
.l	i		GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
5683	89	778	LRHRSFGDYQGRVHLRQD
	"	118	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
			HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
			ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
		İ	NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFECQAKKLAKHSEDD
		İ	SEDEEHDLC SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMXALDEPPYLTVGTDVSAKYRGAFCEAKIKT
	1		AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
j j	j		QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
			LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPATVTPO
ļ į		Ì	VKQEHPHTDSDLMHVKPQHEQRKEOEPKRPHIKKPLNAFMI,YMK
· .		ļ	EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
5686			RQLHMQLYPGWSARDNYVSPSSIPVALHS
2000	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
[		1	VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
	<u>-</u>		PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEO	Predicted	Predicted end	I bring sold comes
ID	beginning	ľ	Amino acid segment containing signal peptide
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	Walling, Tainteonine, Vavaline,
1	1	I .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u> </u>	\=possible nucleotide insertion)
			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
1		į	RMDFLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST
Ì			
1	1	į .	STLT1HVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
1	ł		NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
		<u>1</u>	YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
1			QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPELLPGP\SSS
1	Į.	1	LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
1			ENGONDOTO OF AN ANGERPOON SEPPOPPELI VP/ADA/PMPVI
1	į		SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPQTSEPAPSP
Į.	1		LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
1	ŀ		PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS
I	1	I	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
1	1		VLDI
5688	1	420	
1 3335	1 *	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
i	Į.	l .	*SHNIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV
i		1	LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
	•	1	DGYIPAVF
5689	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGEIPAL
ļ	1	1	
	l .	]	IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPFQPCEGPRSTSRG
i	1	1	GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH
į	Į.	ļ	GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
	Į.		PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
1	1	i	KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
1	<u> </u>		PQTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
	i	1	
	ł	l .	GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
		ł	EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
	1	1	GQELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
1	i		SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
i		i	GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
		1 30	CAMPROVICATION TO CAMPAPING TO CAMPARIAN CONTROL OF
		1	GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP
1	i	l .	*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
	1	į.	DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
1	i		GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
i			PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
l	1	}	
ł	1	Í	KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
1		1	SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP*
1	•	j .	GNFVR*LLLMP/GVA*RHGTSPFLGPSLGENGGQWDSGNLFGTP
1	1	1	KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE
l	l .	1	SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
1	1	ŀ	PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSGILSFIED
	I	1 230	
I	ł	f	VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
l	l	l	GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
	<u> </u>	ŀ	GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\QSVPCIOK
i	<b>{</b> ·	]	PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
	Į.		TERCURREDCAL PROCESS AND ASSESS A
l '	ĺ		TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ
l	l	1	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
i .	l	i	*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
1	] .	l	RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
]	l	1	
5001			PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
<u> </u>	l		QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
i i			
	i		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
[	İ		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
L			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	The sequent containing signal partial
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
J	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<del> </del>	\=possible nucleotide insertion)
1	1	ĺ	KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	1	1	VTGGRGGPRPVSSSIDPSLLSTKOGGLTPSRT.KEPTKUASCRTT
I		ſ	PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSDESTDYNODGU
)	1	1	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5695	<del> </del>		DITQCI
2695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
j			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVI.pTDSEKD
ł	1		SLAESGLSWFSESEEKAPK KLEYDSGSLKMEPGTSKWRRERPES
1	1		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1	]		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
	1	I	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1		1	KPVNGRKTSLDVSNSAEPG FLAPGARSNIQYRSLPRPAKSSSMS
1		1	VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1	1	1	PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	1	!	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
	<u>L</u> _	ĺ	DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1	1	ł	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAFSCI CHECKERA DATA THE TOTAL TOTA
	\$		SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
	1		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
ŀ	j i		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
}			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
i i			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1 .			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5697	1147	42	DITQCI
1		47	PSEALSPPACPSAPAPRRSI ISRLFGTSPATEAAPPPPEPVPAA
1 1			QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAROOGS
1 1			DSDGEALGGNPMVAGFQDDVDLEDOPRGSPPLPAGPVPSODITI
1 1	1		SSEEEAEVAAPTKGPAPAPOOCSEPETKWSSIPASKDRDGTADT
	1	•	RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEOASSSPEND
1 1			EGPIAAQMLSFVMDDPDFESEGSDTORRADDFPVRDDPSDVTDP
1	1		DEGPAEPPPPPKLPLPAFRL KNDSDLFGLGLKEAGPKESSPRCK
1 1			ECKTPSKENKKKKKKKKKEEE EKAAKKKSKHKKSKDKEEGKEERR
5698			RRQQRPPRSRERTAA
3096	2	666	GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
1	į		VEEWQQLDPEQKITYRDVMLENYSNLVSVGYHTIKDDVTCVIPO
1 1	j		GEEPWIVEGEFLLQSYPDEVWOTDDLIERTOFFENKESDOTTET
1		ļ	ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
	1		NASSBYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
<u></u>			FNQ
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
1	1		EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
1	[	1	RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
1 1	· i	· 1	DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1	j	}	TWI.VGGAPGPEGGCUPGGCUPGGCCAPTGCAPTG
[ [		ľ	TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
1 1		ŀ	WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
		j	VPILFQNPSGALRSRRTEPAGWVPPTRHE+DDG*TAAPASGGAP
į ,	İ		VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
1 1			GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
	1		GWOPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
i [	į		HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGI.
5700	923		FPPGRG
	323	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
ľ	į		KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLOCAYLD
5701			E*CSIASSLIKAILRVSVLSE
2,01	59	410	IFEKICSDTQEFISPEINPOICSWLIFDKGAK/NHATGYDSLEN
- 1		ľ	KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIBCETURI
			LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	- doquomo	\=possible nucleotide insertion)
5702	. 3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
1 -7	1	131,	ASESSASSDGPHPVITPSRASESSASSDGPHPVITPSRASESSA
1	İ		SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
	1		l '
	1		PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
1			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
1		•	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
	į		EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
j	1		PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
1			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
l	ì		PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ
1	l		KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
1	1		GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
	<del> </del>		LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
	l .		PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
1	1		RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
Į.	l		DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
i	1		ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
1	1		GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
1	1		RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
1	1		ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
			AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1	Į.		SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1	ł		QSSTAAAQSASATOTATPGAAGGATAAAASGATSAPEGDAARAA
	<b>{</b>		KSDNVAPRRP+LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1	ŀ		SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
1	<u> </u>		KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
L			SPQP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
1	]		DYVANTDNCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
ł	<b>j</b> :		WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
L			LFFIIFLF
5707	28	609	GSPAPTPGFRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
Ī			MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
ł	[		NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
Į			EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPBPACG
1	<b>i</b> .		TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGOPRPYLDLPA
1			QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPOAKPKP
			PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
1			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
			RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADLPCVGFVCSPP
1	(		LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
1			RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
į			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR*
1	1		LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
1			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTOPRAPSAH
1			GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
1	]		AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
	l i		1
1			QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
I			PPRPPRPPPPPARRP
5709	2	2031	1
1	<b>,</b>	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
J			LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS
L			LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE

C dec	I B 32 - 4 - 3	T.,	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
		j	ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM
	:	•	SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
		·	VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQOKIIPVVVK
1		İ	MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
			NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
1	1		RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
İ	1		LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS.
1			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
			VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1	}		TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1			DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
5710			GAKLPGATS*RYTAGQRV
1 3/10	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
		•	VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
1			\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
			QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
		1130	SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIF*LLM
			LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
1			OIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP
I			ETVIDI.I.NKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPPTKPA
1	'		SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
1			AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
i			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
1 :			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
1			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDROI
			EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
i i			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
1	<b> </b>		LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
5713	634	204	HKIFHLW\DTLLLGEFLFPILYWE
1 3,13	034	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
1			TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP
5714	212	613	*RAVLTSPCSHLGSADAASSHWLCGVSFH WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD
		013	KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
			HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA
i 1	Ī		MA
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
			QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
	ļ		GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
: I		İ	DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
1 1			PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
			QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
j j			TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGO*PPGL
			YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG
ļ			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
J			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
<u> </u>			VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE
i	•	i	EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT
			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP+E
	· 1	j	RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
5716	1713		TDLTEAQTSQH
3,10	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
		i	*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
5717	44	1489	RCPLVL*SGFFTIIVGGYSCCMPLKT
1		1405	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD EGPGALVLESDILLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE
		<u></u>	

SEQ	Predicted	Predicted end	Amino poid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
1			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
1			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
ŀ			SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
1			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
			RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
Í			Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
1			RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
5718	120		CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
3/18	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
5719	48	420	S**STADPLHL
1 -/	1	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
I			LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5720	1	1051	IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
1	1 -	1	RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
			GPCK/SLPN/SPSH/SAVSAASIPARAPINQGHE/SGGGSAFSD
i		į	Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
1	j	]	EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
1			KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
1			LHSERPLSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
1	}		CHPASG
5721	97	192	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
1		1	VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
<u></u>			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
1	İ		GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
	1		QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRPGAGVGAPRR
l			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
İ			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
1			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
5723	88	1043	KSSTREIPEMI
		1013	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
I			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
I			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
I			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
1	}		PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
j			KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAEEAADLDGEID
1			LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
1		•	MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP
1	İ		DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP
1			ADTH\DPWRPEAEHGELERERARREERRKRFGMLDATDGPGTE
j			DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK
			QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
			NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
1			DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
			RELEKSQRSQISSVNSDVEALRRQYLEBLQSVQRELEVLSEQYS
			QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
J			ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
E73E			TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSERTSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG
			SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
]			KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
L	1		PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

SEQ	Predicted	Predicted end	I project and a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown *-Ston
ı	amino acid sequence	sequence	Codon, /=possible nucleotide deletion
<del></del>	sequence		\=possible nucleotide insertion
			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
			NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
	ļ		SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR TSP
5726	2	486	
l	_	300	SRSLSMWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
		1	TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
}	}	}	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
L	L_		AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
1			NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
1			GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSO
1			GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPOGLWI.
- 1			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIOCKN/GAEDPPAED
			EPPQVPEAGEEDAVPAEEGPGGTPETOADOVRERPEAHLAEGGA
5729	1	1500	KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
1 3.23	-	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
	•		CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
			QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV
1			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
1 1			CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
1 1	į		PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
1 1			LHACTTGEEILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
5730			SCSPPGMVLDGSPKGAAVESVPVFG
3/30	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
1 1			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
1 . 1			KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AO
5731	122	443	GSSSREKGGQASWNPKLRVA
		443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
1 1	1		EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
5732	226	772	KPGRGRGKQRRQEWFFLRVY
1 1		112	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
	ļ		PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
1	ļ		QVSTNLLDFEVTALHTVYBETCREAQELSLPVVGSQLVGLVPLK
<u> </u>			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
			MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
1 1			AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS
<u> </u>			FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFTVFTVT
] [	. [		GSLFLMNLLTAIIYSQFRGYLMKSLOTSLFRRRLGTRAAFRVI.S
1 1	1	j	SMVGEGGAFPQAVGVKPQNLLQVLOKVOLDSSHKOAMMEKURSV
	1		GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYOSPFLOSAOFLFG
j l	ł		HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
	İ		VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVILFIC
	į	I	TL\VCTDCHTQAGGRRNW/RLLSLWDMTRMLNMLIVFRFLRIIP
5735	2		SMKPMAVVASTVLGL
	4	540	FFTPCVARAFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL
		j	ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNO
		}	YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
		<b>1</b> -	RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
5736	1	382	LKILT
			GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

WO 01/53312 PCT/US00/34263

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 -	\=possible nucleotide insertion)
			TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTEKLASDLRANKN
1			QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSORANLGPCRRKR
1		İ	LQTLMRLAAGFQYSSHKDPSLSAKEKETDYHNEARGPWPGWVG*
,			RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG
1		!	RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V
}			ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
		1	APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
5738	8	460	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1		}	VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT
i		ľ	ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI
	<u> </u>		FRILSEEAWALCAVETHR
5739	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
			FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
ı		1	SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
1	1	1	LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
1			VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
İ		[	HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
1			TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATS
1			PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
1			TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
1.		-31	YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
-			LQSELHKLYDEETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
1	1	4	
1	1	1	EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT
ļ			EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV
5742	2	362	TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG
5742	2	362	TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK
			TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5742	2	362 415	TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL
			TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE
			TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE
		415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLBETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLBETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLBETERE ISPQE
5743	2		TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLBETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTSPITTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA
5743	2	415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
5743	2	415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
5743	2	415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP
5743	2	415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
5743	2	415	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKKNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL
5743	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
5743	3	415 703	TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
5743	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK *CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEIKKNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQDGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVMLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
5743	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK *CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEIKKNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEEATGLLTEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVMLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
5743	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCGFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKHPBEGR EKSEEBRSKHKRKKSCEBIDLDKHKSIQRKKTEVBIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5743	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK *CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEIKKNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE  TRRTTTTSPITTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLIMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLKLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSDNSTSTHQASHKQIHOKRKHPBEEGR EKSEERSKHKRKKSCEEIDLDKKKSLQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLBEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEEATGLLTEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVMLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKHPBEGR EKSEEERSKHKRKKSCEBIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFNSILALHLRTHQPERPRSPAARLLLE
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE  TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL  GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVMSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGGERTEEEMLWDQSI LGF  SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLBTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPPTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVMSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFRQQE EKSEEBRSKHKRKKSCBEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGCRETEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGFAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPUDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCGFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKKRHPBEGR EKSEEBERSKHKRKKSCBEIDLDKHKSIQRKKTEVBIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGGERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILAHLBTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHIHILHRPNKCGLCSFGSSGEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSVPQPEPEPQPER
5743 5744 5745	3	415 703	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGREISPEENGPEE VKPUDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSDNSTSTHQASHKQIHOKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERFPCPVCGKFFFNSILALHLRTHQPERPSPAARLLLE LEERALLREARLGRASSGGMQATPATEGLARPQAPSSSAFCP YCKGKFFTSAERERHLHILHRPNKCGLCSFGSSQEEELHHISLT AHGAPERPLAATSAAPPPQPQPQPPPPQPEPRSVPQPEPPEPQPER EATPTPAPAAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA
5744 5744 5745	1400	41.5	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLDERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT YENRLPQWLPAHDSRLRLDSLSYCOFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHCKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHLHILHRPNKCGLCSFGSSGEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGMRKKKASFDUPS
5743 5744 5745	3	415 703 599	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMYRDILQCNPDTEICTKDG GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEB VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE TRRTTTTSPTTTRQMTITPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLITSKESKVWDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVMLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVMSRPTYRMFDQRLPSETIQTYPRSCNIPQT YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHOKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGGERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELHHSLT AHGAPERPLAATSAAPPPQPPQPPPPPEPRSPARRLLLE EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
5744 5744 5745	1400	41.5	TCPYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK  TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK TALYWAVEKGNATMVRDILQCNPDTEICTKDG  GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE ISPQE  TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA VFTTANTCLSLTPSTLDERATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT YENRLPQWLPAHDSRLRLDSLSYCOFTRDCFSEKPVPLNFNQQE YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHCKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHLHILHRPNKCGLCSFGSSGEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGMRKKKASFDUPS

	1		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
10.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	Беquence	• • •	\=possible nucleotide insertion)
			SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
ł			KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
1			AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
			KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
1			ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYORTLTPPLRRS
			ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSOSHDRRH
			ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
5748			RE
3/48	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
i			KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
ŀ	1		FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
5749	552	<del> </del> -	FFSYEFFCNVFHCMNRTASQR
1	""	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
	1		SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
1	1		LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
1	1		SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
			IILEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
			QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
			ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
1			VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
			TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIFEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLOGLEO
			DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
1 1			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
1			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA
5752	3	471	LMASGSGGHNTMPSGGNSVSSGSSVSSCI GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
1 1		-/-	VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE
			HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
L 1	,		AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
			TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
1	ļ		ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
5755			WPTPATPSPLTAPFSME
1 7/33	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
1 1	ĺ	•	WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
j i	Į		PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
1	]	•	RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
1 1	i		AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
] ]	ł	•	DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
	ļ	<b>-</b>	WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
1			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
1			HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
I		İ	AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
1 1			LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
1 1			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
H			ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
<u> </u>			WAEGQRLFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
<u> </u>	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	_	\=possible nucleotide insertion)
			SGSQLLVGCEDGSVKLFQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
1 3,33	-	1240	
i	1		MARSSPYPTDVARVVNAPIFHVNADDPEAVIYVCSVAAEWRNTF
Į.	1		NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA
1	1		DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILHIKHWL
ı	i		DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSV?LEDF
1	1		KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
l	1		NGQDVERGTFSHREHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
ì	1	į.	SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAOCIIDOF
1	į.	i	ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLOMSNDD
1	1		SDAYPAPTKDFEVSQL
576C	<del>                                     </del>	1201	<del>1</del>
3/66	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
l	1		GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
1			PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
1	1		LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
1			QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG
1			SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
ļ		]	VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
	1	•	TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
ì	i	1	VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR
•	I		RLGPVSAIGVT
5761	3	1275	- I
3,61	,	12/3	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
		ĺ	VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
	1		RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
			AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
1	1	l .	GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
1		ŀ	EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
	1	1	FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
	1		EHMESRMVTETEETOEKKAESKEPIEEEPTGAGLNKDKETEERT
ļ	1	ì	DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
1	1		AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGGGGGGRRTPRGMPKEKYEPPDPRRMYTI
	1	317	MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
	1		
E363	<del> </del>		SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	129	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEETTGRVRINV
ł	1		LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
I	1		ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
L	L	*	TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK
ì	1		LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
1	1		MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
l	1		TPEAORDKL
5765	3	825	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
105	1	025	
1			VQASAPQGNSHKETSKSKVKRSKTSKDANKSL3SAALYGIPEIS
į.			STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS
I			AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
1			GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
l .	1		GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF
L	<u>l_</u>		TVPAPPPHV
5766	1608	663	SGLFSVDPASSOAMELSDVTLIEGVGNEVMVVAGVVVLILALVL
!	1		AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
1	ĺ		PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
	1		1
1			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
I	1		TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL
1	1		RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
1	1		SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVPFSFLV
L	L		FGMYGR
5767	2	892	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
I	1		SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS
1	l .		LTEVKVEEEBRDPQSPEFEIEEEEEMLSSVIPDSRRENELPDFP
	<del></del>	L	T TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

SEQ	Predicted	1 5 - 32 - 5 - 3	
ID	beginning	Predicted end	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, R=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
· I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ľ	\=possible nucleotide insertion)
- 1			HIDEFFTLNSTPSRSAYDEPHLLVNIEKOKLELEKRRLDIFAER
1			LQVEKERLQIEKERLRHLDMEHERLOLEKERLOIEREKLRLOIV
			NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLOLEKORLO
	<u> </u>		FLKFESEKLQIEKERLQVEKDRLRIOKEGHLO
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
1			AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPI.
1			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
5769	38		WSRNAAPSSTKRRDSKLWSETFDVC
3763	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
1		Į	TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
1			DRCVEVIAKEGONLKELYLVSCKITDYALIAIGRYSMTIETVDV
1		[	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
5770	1	404	PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
1	1 -	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
I			FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
1			AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
5771	168	741	WEQAFLRWLPSLSPDCINVVVTGKDRLTA
	-00	147	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQPAMLLRE
1			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
<b>f</b>			LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ AFHRLLADITHDIE
5772	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
1 i			DESTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
1 1			LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
			RRLNISYTRNMTLKDGKNSK
5774	2	592	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1			VTEECVHILHGHRNLVTGIQLNPNNHLOLYSCSLDGTIKLWDYT
1			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFOLVSV
1 1			KLPKSSSQEVBAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
5775	3		YLSVYFFKKETTSRVTLSSS
1 3//3	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
1 1			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
1 1	.]		RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
1 1	. 1		EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP RP
5776	2	484	
1 1	=	-20-2	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
1	ł		IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
]			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GODPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
[			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
			GGGGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
1	]		YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
·			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
1 1		1	DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
; !			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
			NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
ļ f	j	1	GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1 1	ļ.	. 1	WAPLGAPERPEHLINRVLERLAGGATRDSAASDILLDDIVLTHS
	1	•	LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
	Į		TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
1	[		CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLOYSEEPAGREDS
<u> </u>			LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methioninc, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l		1	
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ł	\=possible nucleotide insertion)
			PLPEEIOVSPGDTEIHRVEPEDVANHLTAFHWELFRCVHELEFV
1	1	1	DYVFHGE
5779	138	1571	EAVOVLIKHSADVNARDKNWOTPLHVÄAANKAVKCAEVIIPLLS
5779	138	12/1	) === <b>-</b> · · · · · · · · · · · · · · · · · · ·
1	Į.	1	SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
!		1	ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
ł .	i		NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
•		İ	NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
I	1	1	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
1	Į.	1	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
	ł	İ	
	1	1	QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
ł		1	KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
l	<b>!</b>	1	ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
1		1	EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
1	1	}	RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	OFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
3/00	154	624	<b>1 -</b>
Į.	1		EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
ł	I	1	DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQQACLREK
ì	1	1	KKGLNVIGASDQSPLQSPSNLRDNP
5781	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
1	1	1	PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
ĺ	1		OAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
1	i	1	VOPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT
1	I .	i	
ì	ł.	Į	QHSIHTVTCKSPRQKEDRSPKPPQAPKHPEEHGRQS\QAPPPLP
1	1	1	VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
j	1	1	CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
l .	1	· ·	NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
!	1	1	PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
1		İ	SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP
1	1	1	PEPESSITLTPVESAVVABEHEVVPBRPVTCMVSETPAMSAEPT
1	1	1	
		1	VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
l	i	1	ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
	i i		EPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVLEPAVSVIQ
İ	i .	1	PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM
	i	1	ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE
i	į.	i	EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
Į	ł	1	IGEEKILPTSETKORTVLDTYPGVSEADAGETLSSTGPFALEPD
i		1	ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
1	1	l .	
1	ı	1	SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ
i		1	TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD
i	ì		LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV
	1	1	\ssmp\erasgs\ssgekgg\yeifvkvkDThekskknknRDkg
Į.			EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS
1	1	1	HRS\QTRSRSRS/RDRRRRSSRSRSKSRGRRSVSKEKRKRSPKH
ì			RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR
1		1	1
	ı	<b>J</b>	
1		İ	SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRS
•			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEEEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFPNLNIAAAK PTTPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKRGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDVIVNKPHVSDEEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
5783	1693	698	RTPSRRSTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
5783	1693	698	RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGGWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRRNGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
5783	1693	698	RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGSMGAVLMRKNGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ
5783	1693	698	RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGGWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRRNGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM

SEQ	Predicted	Deodi et ed eed	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ī	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
}	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1 .	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	sequence	boguence	Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
į	1		LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYI
Í	1	İ	GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS
	1	l	NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE
5784	2669	1388	LFSVCTNEDPKDRPSAAHIVEALETDV
	1	1300	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
	1	}	GILSNTHROAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
ı	ì	٠	RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
ı			QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
l l	ı		GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
<u> </u>	ļ		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
}	ļ		VDSGCFEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
ł	1		E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
	1		HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
5785	2669	1388	WPAMKFRRGSGHPAYAEVEPVGEXEGFIVSEQC
	2005	1300	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
	1	•	GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
	1		QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
	1		GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
	i i		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
	i		VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
1	1		E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1			FAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
5786	2532	1674	WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
i		2074	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPOM*SGTP
j	f		APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M
			S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
	l		SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
			GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
			TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
	ļ <u>i</u>		T/RYCEIP/GPD/LEESP/TCP/LCKEPFRP/GSFRPNWQLANV
	1		VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR
1	ŀ	•	EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS
f 1	l i		RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES
	[		QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARELLTD
	ľ		IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF
,	· }		LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS
1 !		•	PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
}			EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
1 1			RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG
			RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG
		į	SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR
1 1	ļ		AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV
1 1	1		SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
ĺ	į.		ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP
1 1			HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI
]	1		KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL
] [	i		FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
] [	[		SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
j	į	ļ	FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
] [	j.	1	SSPAPVAASSQATTQSKSSTKKSKKEEKEKEKDGETSGSQBDQ
. 1		ļ	LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
1		l	IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
] [		İ	TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF
j }	j	[	DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI
]			GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
ŀ		j	RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS
		1	TETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF
			XOT WOOD VERWEGACON CORNOR NO NO CHACKS IN A DEKDPP

Deginning nucleotide location corresponding to first amino acid residue of summarian and residue of amino acid residue of amino acid residue of amino acid sequence s		B - 32 - 4 - 3	Predicted end	Amino acid segment containing signal peptide
Notestich   location   corresponding	- ,			Amino acid segment containing signal peptide
corresponding to first amino acid residue of amino acid of amino acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequence of acid sequenc				Clutamic Acid E-Phenylalanine G-Glycine
to first amino acid residue of amino acid residue of amino acid sequence    P-Proline, Q-Goltumine, R-Arghaine,   S-Serine, T-Threonine, V-Vuline,   S-Serine, T-Threonine, V-Vuline,   S-Serine, T-Threonine, V-Vuline,   S-Serine, T-Threonine, V-Vuline,   W-Trytpophan, Y-Tytooine, V-Vuline,   W-Trytooine, V-Vuline,   W	NO:		T .	
to first amino acid residue of amino acid residue of amino acid sequence    Seserine, T-Miremaine, V-Waline,   Sequence				Hamistidine, laisofeddine, kabysine,
amino acid residue of amino acid sequence  Sequence  Sequence  Locacoffcxfargpfmlyfakpccavbfieledburkson, *mstop Codon, /mpossible mucleotide deletion, /mstop Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Locacoffcxfargpfmlyfakpccavbfieledburksonsingt Strangpfmlyfakpccavbfieledburksonsingt Strangpfmlyfakpcdfieledburksonsingteringthieledburksonsingthieledbur			1	b=Leucine, M=Methionine, N=Asparagine,
mein acid sequence    Sequence				
Sequence   Sequence   Codon, /-possible nucleotide deletion.		amino acid		S=Serine, T=Threonine, V=Valine,
Sequence   Sequence		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
LCNACGFCKYARFDFMLYARFCCAVDP I DNEEDRKAAVSUNTL LDKADRVYHOLIADGYCGDCKNSFDELSKIIQKVPASRELL STSASVNRYIIQLAQGYCGDCKNSFDELSKIIQKVPASRELL TOLQQREAATKSSRTSVOPTFTXSYPASIAVLAGGTSSTKCYG CASAVTEHCITLIRALATNPALRHILMYGGLIRELPDYNLRRGA AAMEESVRQIAUCHITDHPEATOCONNOLIIGKSKIIGKVBASRELL TOLQQREAATKSSRTSVOPTFTXSYPASIAVLAGGHASPITYKRYCM CASAVTEHCITLIRALATNPALRHILMYGGLIRELPDYNLRRGA AAMEESVRQIAUCHITORISKEDSCNELRILCALSIFJAMVNIKAGHANP UVVENTITMICLERILORIK PEPPATSKRINDVDVPALTYTVKYYCN EHAQAQUALITORISKEDSCNELRILCALSIFJAMVNIKAGHANP VVVENTITMICLERILORIK PEPPATSKRINDVDVPALTYTVKYYCN EHAQAQUALITORISKEDSCNELRILCALSIFJAMVNIKAGHANP VVVENTITMICLERILORIK PEPPATSKRINDVDVPALTYTVKYYCN EHAQAQUALITORISKEDSCNELRILCALSIFJAMVNIKAGHANPA VALVOKITSKALDELSKYEVESIKKHKSRINDVIKAYCY LCLRKLVVQRTKLIDETODMILLAMEDMITGTESETKAFMAVCI ETAKRYNLODYRTPVS I FERLCSI I YPEBREVTEFFVTILRODY LCLRKLVVQRTKLIDETODMILLAMEDMITGTESETKAFMAVCI ETAKRYNLODYRTPVS I FERLCSI I YPEBREVTEFFVTILRODY LCLRKLVVQRTKLIDETODMILLAMEDMITGTESETKAFMAVCI ETAKRYNLODYRTPVS I FERLCSI I YPEBREVTEFFVTILRODY LCLRALVVQRTKLIDETODMILLAMEDONITORISCHEMIN RICHARD SERVICHIMINI VIMICAL SILVENTONICOLORISCHEMIN RICHARD SERVICHIMINI VIMICAL SILVENTONICOLORISCHEMINI VIMICAL SILVENTONIC		amino acid	sequence	Codon, /=possible nucleotide deletion,
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IDAGPENYLOBELKI RESISTYHORITHUCLUFISPTCHSIKTI, DILITMKNIDSKYII PVIAKADTYSKELGKFIKIKISELUSKO VOIYOFPTDDDTIAKVINAMMGQLPFAVUSMEWKONKWYKA ROYPMGVUVQNEMERAILICTMMEDLREGOTHTRHYBI. VERCKLEEMGFTUVGPENKPUSVQETTEAKRIBEPIGGERGKEEB MKQMPVQVVENKEKAILIKEARERLOKTMENLAGERKEEB MKQMPVQVVENKEKAILIKEARERLOKTMENLAGERKEEB KKRIBEBIIAFSKKKATSSIPHSQSPLATGSMIRKUKDKINNSGF PVKQKVQPEHRRSSOANFIKKKLEVCTDFAVICTITSIFGEOPO LLITMEKYPOVGOVISGSE ARARPSKAWGGFVVYVVHTCWWMGIVYTPCSGDASCIOPY LARRPKLQLCHSTTTTSHIGABINIDLVINVEDFDVESKFER TVNNSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT WYMVKVDERINLITGSDTOQLEFAKUFSALDEPVSHIPPRLAL NVNADMEVPDGSSLPADHRYMKNIQLGKTVHYLPILIFIDOLSN RYKDLAWVINRSTTELPLTVSYBVKYTSALDEPVSHIPPRLAL NVNADMEVPDGSSLPADHRYMKNIQLGKTVHYLPILIFIDOLSN RYKDLAWVINRSTTELPLTVSYBVKYTSALDEPVSHIPPRLAL NVANADMEVPDGSSLPADHRYMKNIQLGKTVHYLPILIFIDOLSN GFGFSEKDADEVKGIFVDTNILYFLALTFFVAAFHLLFPILAFKND ISFWKKKSMIGMSTKAVLUKGESRLFWHIMOLAVYSLOO FGFSEKDADEVKGIFVDTNILYFLALTFFVAAFHLLFPILAFKND ISFWKKKSMIGMSTKAVLUKGEVATISHLINKFVKESGDASCIOPY VARGFIFMLPOLFVNYKLGSVARIJHKKAFTVKAFNTFIDDVEFA IITMPTSHRLACFRDDVFLVYLYVGRWLFVDKRRVNEGGSSYE EKATRAPHTD  5793 2263 653 ARARPSPAWMCGVFVVVVVHTCNVMYGIVTTPCSGDASCIOPY LARRPKLOL\ARSFTTTRSHLGBENIDLVLNVEDFDVESKFER TVWSVFPKKTRNNGTLYAYIFLHHAGVLPMHDGKQVHLVSPLTT YMPKYBEEINLITGSSTOTQIGBAKGHRYHHMODAVYSLOQ FGFSEKDADEVKGIFVDTNILYFLALTFFVAAFHLLFDFLAFKND ISFWKKKSMIOMSTKAVLUKGFSTVVHFLLDEGTSILVIVP AGGAALELWVVKALKMITIFRGLMPFFFOGTYSESEKKTEEY DTQAMKTLSFYLLYFLCVGGAVYSLLNIKYKSWMINSFYNGV YARGELFBLOQLFVNKLKSVAHLBVKFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVPLVVLYQRMLYPVDKRRVNEFGESYE EKATRAPHTD  5794 1 5016 MGPRISVWLLLLLPAALLLHEENSRAAKGGGCAGGGCKDCHGV KQKGERGLPGLGGVGFPGPGDFGPGPGPCDCKGTGFBCHDG KQCGPGFGTLGFGLGGFGRGFGFGFGFGFGFG GGLGFPGLGFGRGFGFGRGFGRGFGFGFGFGFGFGFGFG GGLGFPGLGFGRGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGF				NVKLKAQTYELOESNVOLKLTIVNTVGEGDOINKERSVORTUDV
DILTMINLDSKYTI I PVI KADTYSKTELOKFKIKLMSELUSNO VOI VOFTDDDTIAKUNAMMICOJENUSMODEVKONKOVKA ROYPHGUVQUVENENHCDFUKLREMLICTMINEDLREOTHTRHIYEL VRRCKLERMOFTDUVGPENKPUSVETAKRIEPIGEROKKEEE MKOMFVQRVKEKEAILKEAREELOAKFEHLKELHQERMIKLEK RELLEEELIAFSKKATSEIFHSQSFLATISHIKOKDRINISGF FVKOKVPEHRRSSSQANFIKKKLEVCTPEAVICHTISTIGEOPO LLIPMIKTYPOVGOVISOSE  AAAAPSFAWCGUVVVVVHTCWWWYGIVYTEPCSGDASCIQPY LARRPKLQL_KHISFTTTRSHIGAENNIDLIVINVEDFDUFSKFER TVNNSVVPKTRINIGTLYAYITLHHAGULEWHIGKOVVHLSPLITT YMVPKPEEINLLIGESDTOQIEADKKPTSALDEPVSHKPRELAL NINADNEVPOGSSLEADHVRYKKHOLGKTVHYLPILFIDQLSN RVKDLWINRSTTELPLTVSYDKVSLGRLRFWIHHQDAVYSLQO GFSEKDADEVKGIFVDTNIYFIALITFFVAAFHLLFPIAFKND LSFWKKKKSMIGMSTKAVLWRCFSTVVIFLFILDEGSLUVLVP AGVGAAIELMKVKKALKWITIFWRGLMPEFOGFTSLSERKTEEY JTOAMKYLSYLLYPLCVGGAVYSLLNIKVKSMYSWLINSFVMGV YARGFIFMLPOLFVNYKLKSVAHLPHKAFTYKAFNTFIDDVPAF LITMPTSHLACFRDDVVFLVYLYQRWLYFPUKRKRVNERGESYE EKATRAPHTD  5793  2263  653  AAAAPSPAWCGVFVVVVVVHTCGWAWYGLVYTPPCSGDASCIQDY LARRPKLOL_RRSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNSVVPKKTRNIGTLYAYIFJHHAGVLPWHDGKQVHLVSPLITT YMVPKPEINLITGESDTOQIEADKERVHMYDLUKVPDFRVERESSE EKATRAPHTD  AAAAPSPAWCGVFVVVVVHTCGWAWYSLUFFLHEDFOLGSVE EKATRAPHTD  SRYKLKKKSMIGMSTKAVLWRCFSTVFJALDEPVSHMPRIAL NVMANNFVPCSSLPADVHRIVMMIQLOKKTVHYLPLLFIDDCISN RVDLMVINRSTTELPLTVSYNKSTALDEPVSHMPRIAL NVMANNFVPCSSLPADVHRIVMMIQLOKKTVHYLPLLFIDDCISN RVDLMVINRSTTELPLTVSYNKSTALDEPVSHMPRIAL NVMANNFVPCSSLPADVHRIVMMIQLOKKTVHYLPLLFIDDCISN TYMSTYNKSTLIFLUCGGAVYSLINKYKSMIVSHLINSFVNGV YAAGGAAIELMKVKKALMMITFRGLMPFDFGTYSESERKTEEY DTOAMKYLSYLLIPLGUGGAVYSLINKYKSMIVSHLINSFVNGV YAAGGHALLUPAALLUPADRACHTYLFLULDFOLDLIVLVP AGVGAAIELMKVKKALMMITFRGLMPFPDFGTYSESERKTEEY DTOAMKYLSYLLIPLGUGGAVYSLINKYKSMIVSHLINSFVNGV YAAGGLFFRIDDFOLFGYNGCGEGEGGGGCGCCCCHGV KOGKGERGLLDFAALLUPARALLUPERGRAGGGGGCKCCCHGGF KOGKGERGLLDFAALLUPARALLUPARALLYPONGRRVNERGESYE EKATRAPHTD  5794  1 5016  MGPRISWULLIPRAALLUPARALLUPARALUPARAFTYRAFNTFIDDVFAF ITMTTSTRRLACFRDDVVSLVYLVYGREGEFGFGPFDFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGF	1	1		IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLVFTSDTCHSLVTI
VOITOFPTUDITAKVINAMICOPKIRENLICTIMEDLERGYTHENISL.  ROYPMGVUQVENINGOPKIRENLICTIMEDLERGYTHENISL.  YERCKLEEMGYTUVGENKUVGEVALITAKENEELIGENGERGRKEEE MKOMPVQVENEKEALIKENEELIGASPELIKELHQEERMIKLEEK RELLEEELIAPSKKKATSEIFHSQSFLATGSNIERKOKDRINGSF FVKQKVPBHRRSSGANFIKKKLEVCFDEAVICFITSIFGEOPO LLIPMERYPOVGGOVISGSE  AAAAPSPAMWCGVFVVYVIITCWWYGIVYTPCGGDASCIOPY LARPKLOLINETTTISHIGASHNIDLVIAVEDFOVESKFER TVNNSVPKKTRINGTLYAYIFLHHAGULPHHOGKQVALLVSPLIT YMVKPEEINLLIGESDTQQIEAMSVTSALDEPVSHWRPRLAL NVNADMEVPDGSSLDADVHRYMKMIQLGKTVITLPILIFIDQLSN RYKOLMWINRSTTELPLIVSYDKVSLGRIRFWHMQDAYYSLOQ FGFSEKDADEVKGIFVOTINLYFLALFVAAFHLLEPHJAFKND ISFWKKKKSMIGMSTKAVLURCFSTVVIFLFLLDEQTSLLVLVP AGVGAALELMKVKKALKWITFWGENEPOGTYTSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSWLINSFVNGV YARGFLFMLPQLFWYKKLKSVALIPBEPOGTYTSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSWLINSFVNGV YARGFLFMLPQLFWYKKLKSVALIPBEPOGTYTSESERKTEEY DTYANSVPKKTRINGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEAMKPTSAAPTHDDVEAY ITIMPTSHRLAGFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAPSPAWGGVFVVVVVHTGWVMYGIVTTRCCSGDASCIQPY LARREKLOLINSTTTRSHLGAENNIDLUKTHVLPLIFLIDDVEAY ITIMPTSHRLAGFRDDVFLVYLYQRWLYPUDKRRVNEFGESYE WAYNANDFVPCGSSLPADVHRYMKINGKUKTHVLPLIFLIPQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYLLATIFVAAFHLEPTLAFKND ISFWKKKKSMIGMSTRAVURRCFSTVVIFFLILDECTSLLVLVP AGVGAALELMKVKALKMTIFPRGLMPEFOFGTYSESERKTEEY DTQAMKYLSYLLYLECGGAVYSLLNIKYKSWYSMLINSFVNGV YARGFLFHNLPQLFVNYKLKSVAHLDWKTYNEFTSLLVLVP AGVGAALELMKVKALKMTIFPRGLMPEFOFGTYSESERKTEEY DTQAMKYLSYLLYLECGGAVYSLLNIKYKSWYSMLINSFVNGV YARGFLFHNLPQLFVNYKLKSVAHLDWKRYNEFTSLLVLVP AGVGAALELMEVKKALKMTIFPRGLMPEFOFGTYSESERKTEEY DTQAMKYLSYLLYLECGGAVYSLLNIKYKSWYSMLINSFVNGV YARGFLFHNLPQLFVNYKLKSVAHLDWKRYNEFTSLLVLVP AGVGGAPLEFORGFOFGFGFGFGFGFGFGEFGGM GLSFGGFRGKDGGOGVGSPGPGPGGRGCGCGCGCCCHGV KOCKGERGLEGLGGVGGFGFGFGFGFGFGFGFGEFG GGLGFFGGFGFGFGGFGFG	1	1	1	DLLTMKNLDSKVYIIPVIAKADTVSKTELOKFKIKIMSELVSNO
RQYPMGYVQENEMEDFUKLERGITHRHIYEL YRRCKLERMGTUDG PENKPUS VGETYEAKRHEPIGERQRKEEE MKQMFUQRVEKERAILKEAERELQAKFEHIGERQRKEEE MKQMFUQRVEKEKATSEIFHSQSFLATGSHLERDKDKNKNSOF FVKQKVPEHRSSSQANFIKKKLEVCFDFAVICFITSIFGEOFO LLIFMEKYPOVGOYISOSE  5792  2263  653  AAAAPSPAWWCGVFVVVVYTTWWYGIVYTRPCSGDASCIOPY LARRPKLQLKHSFTTTRSHLGAENIOLLMVEDFOVESKFER TVNVSVEKKTRNSGTLYAVITHHAGVLPHENGKQVHLVSPLTT YMVDKPEEINLLTGESDTQQIEADKKPTSALDEFVSHWRPKLAL NVNADNEVPKGSELPADVHRYMKQLGKTVHTYLFLIFTDOLSN RVKDLMVINRSTTELPLIVSYDKVSLGRLRFWIHMODAVYSLOO GFGFSEKDADEVKSIFVDTNLYFLATFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEGTSLLVLVP AGVCAATELMKVKKALKMIIFWRGLMSPFGGTYSESRKTEEY DTQAMKYLSYLLVPLVCVGGAVYSLLNIKKYKSWSMLINSFVMGV YARGFLFMLPQLFVMYKLKSVAHLPWARFTYKAFNTFIDDVRAF IITMPTSHHLACFRDDVVFLVYQRAVLPVDKRVNDEGSYE EKATRAPHTD  5793  2263  653  AAAASSPAWWCGVFVVVVVHTCWVMYGIVYTRPCSGDASCIOPY LARRPKLOLVRISTTTRSHLGAENNIDLLNVCDPDDVESKFER TVNVSVPKKTRNNGTLAYAIIFHAGVLPWHDGKQVHLVSDLTT YWDYKDEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPKLAL NVMADNVFDGSSLPADVHRYMKNIQLGKVTWLPILTEDQLSN RVKDLMVINRSTTEIPLTVSYDKVSLGRLRFWHMODAVYSLQ FGFSEKDADEVKGIFVDTNLYFLALTTFVAAFHLLFDELAFKND ISFWKKKKSMIGMSTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGMSTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGMSTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVVIFIFLINDGTSLLVLVP AGVGAAIELMKVKKKSMIGHTKAVLWRGFTVXIFITKDGTSLLVLVP TRATGPPGASCYPGNPGLVGFCOGPGPGOPGORGDTGERSLEP FGIGTFGPGLGFGFGFGPGFGFGFGFGFGFGFGFGFGFGFGFGFG	1	i		VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA
TRRCKLEEMGTTOVG DERNOVS OF STYPASKHEPHIGERORKEER  MKQMPUQRVEKER AILKEAERILQAKFEHLKRLÜGERMILEEK  RRLLEEEI JAFSKKKATSEI FHISGSFLATGSMLEROKDRKNSOF  PVKQKVPEHRRSSQANFI KKKLEVCFDFAVICFITS I FGEOPO  LLI IMEKYPOVGGOYI SOSE  AAAAPSPAWWGGVPUVYVVHTCWVMYGI VYTRPCSGDASCIOPY  LARRPKLQL KHSFTTTRSHLGAENN I DLVLINVEDFDVESKFER  TVANSUPKKTRNNGTL YAVI FLHHAGVLPWHDGKQVHLVSPLTT  YMUPKPEEI NILI TGESDTQQI EAKKPISALDE VSHWRPILAL  NVAADNEV FGSSLPADVHTWKMT QLGKTHYL PLILI FIQLSN  RVKDLMVINNSTTELPLITTSVALGKRIPA I HUHDDAVYSLOQ  FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLEDFLAFKND  LSFWKKKKSMIGMSTKARULWRCFSTVVI I FPLLDEGTSLLVLVP  AGVGAAI ELWKVKKALKWI TEWRGLMPEFOFGTYSESERKTEEY  DTQAMKYLSYLLYPLCVGGAVYSLLNIKKYKSWSWLINSFVNGV  VARGFLFMLPQLFVAYKLKSVAHPWKAFTYKAFMYFIDDVPAP  LITMPTSHRLACFRODVVFLVYLVQRWLYPVDKRRVNEFGESYE  EKATRAPHTD  AAAAPS FAWNGGVFVVVVVHTCWWYGI VYTRPCSGDASCI QPY  LARRPKLQL KRISFTTTRSHLGAENNI DLVLNVEDFDVESKFER  TVAVSVPKKTRNNGTL YAYI FLHAGVLPWHDGKQVHLVSPLITT  YMVPKPEEINLLTGESDTQQI EAAKKPTSALDEPVSHWRPILAL  NAMADDAFVPDGSSLPADVHRYMUN IGKVVHLYPLIFIDDLSN  RVKDLMVINRSTTELPLITYS DKVSLGRLFFWIHMODLAVYSLQQ  FGFSEKDADEVKGI FVDTNLYFLALTFVAAFHLLFDFLAFKND  LSFWKKKSMIGMSTKAVLWRCFSTVVI FIFLIDEGTSLLVLVP  AGVGAAI ELWKVKKALKMTI FWRGLMPEFOFGTYSESERKTEEY  DTQAMKYLSYLLI YELCVGGAVYSLLNIKKYSWSWLINSFVNGV  YARGFLFMLPQLFVNYKL KSVAHLPWKAFTYKAFHTFI DDVFAF  LITMPTSHRLACFRODVVFLVYLVQRWLYPVDKRRVNEFGESYE  EKATRAPHTD  SO16  MGPRISVWLLILFAALLLHEEHSRAAAKGGCASGCGKCDCHGV  KGQKGBRGLPGLIGGVIGFPGMGPPEGFOFPGORGDTGEPGLPG  GELGPFGLIFFGRANGPGPFGLFGKGPDGPFGRGRGRG  GLEFGCGPFGLFGFGARGPGPFGFGFGFGRGRGRG  GLEFGCGPFGLFGFGARGPGPFGFGRGRGRGRGRG  GLEFGCGPFGCWGGVGSPGPGVGAVQDEKGDPATKGEKGQNG  GEGFGCMPGVCEKGEPGKPGPRGKPGKDDKKERGSPFFGEPG  GPGLGFFGKDKGDGVGSFGPGPGPGAVQVGEKGDPATKGEKGQNG  GEGFGCMPGVCEKGEPGKPGPRGKPGKDDKGEKGSPGFPGEPG  GEGFGCMPGVCEKGEPGRAGPGPFGIVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGRAGPGPFGTVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGRAGPGPFGTVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGRAGPGPFGTVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGRAGPGPFGTVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGRAGPGPFGTVIGTGFLÆKKERGD  GEGFGCMPGVCEKGEPGBFGGFGCLLI			ł	RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREOTHTRHVEL
S792 2263 653 AAAAPSPAWCGUPVYVVYTCWVMYGIVTRCSGDASCIOPY LARRPKLQL\RHSFTTTRSHLCAERNIQUETSHERGES TVNVSVPKKTRNSGTLAYSHLAGUNERNSGF FYKQKVPEHRSSSQANFIKKKLEVCFDFAVICFITSIFGEGPQ LLIFMEKYPOVGGYISGS  AAAAPSPAWWCGUPVVVVYTCWVMYGIVTRPCSGDASCIOPY LARRPKLQL\RHSFTTTRSHLCAERNIOLULNVEDFDVESKFER TVNVSVPKKTRNSGTLAYAIFLAGUPNIOLULNVEDFDVESKFER TVNVSVPKKTRNSGTLAYAIFLAGUPNIOLULNVEDFDVESKFER FYKDLMVINRSTTELPLTVSYDKVSLGRLERFHIMQDAYYSLQ FGFSEKDADEVKGIFVDTNLYYLALIFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAULWRCTVVIFFLELDEGTSLLVLVP AGVCAAIELWKVKKALKWTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVSTULTKYKSWYSWLINSFYNGV YARGFLFMLPOLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVPAF ITIMPTSHLACFRDDVVPLVYLVQRALYPVEKRWNEFGSSYE EKATRAPHTD AAAAPSPAWWCGVFVVVVVVTTCWWMYGIVTTRPCSGDASCIOPY LARRPKLQL\RHSFTTTRSHLGAERNIDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHHAGVLPHDCKQVHLVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHHAGVLPHDCKQVHLVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHHAGVLPHDCKQVHLVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHHAGVLPHDCKQVHLVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHHAGVLPHDCKQVHLVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHGSDTQOIEAGRNTDLUNVSPLTT YMPKPEEINLITGESDTQOIEAGRNTDLULNVEDFDVESKFER TVNVSVPKKTRNNGILXAYIFLHDLAFFVHDCKTHLIFDELAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVUIFFLIDDCTSLIVLVP AGVGAAIELWKVKKALKNTIFRGALMFVIAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQKKLYPVKKRVEPGESYE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPRKAFTYGAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQKKLYPVKKRVEPGESYE EKATRAPHTD  MGPRISVWLLLLIAPALLILABALLILHEHSRAAARGGCAGGCGKCDCHGV KGQKGBGLIGLQGVGPGPGPGPGPGPGPGPGPGPGPGPGPGPGFGFGERGENG GLSFGGFKOMGOGVGSGPGPGPGPGPGPGPGPGPGPGPGPGPGPGFGGERGKG GLSFGGFKOMGOGVGSGPGPGPGPGPGPGPGPGPGPGPGPGFGGERGKG GLSFGGFKOMGOGVGSGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGP	1	<b>[</b>		YRRCKLEEMGFTDVGPENKPVSVOETYEAKRHEFHGRRORKEER
S792 2263 653 AAAPSPADULTENSESTATISHINGERSORSE TURKESSOAMS IKKLESUCTOFATICFITS IFGEORO LLITMEKYFOVOGOYISGSE  AAAAPSPAWGGVEVUTTOWWYGIVYTRUGGASCIQPY LARREKLOL\RHSFTTTRSHLGAENNIDLVLNVEDFOVESKEER TVNVSVPKKTRINGTLYAYIFLHHAGAENNIDLVLNVEDFOVESKEER TVNVSVPKKTRINGTLYAYIFLHHAGAENNIDLVLNVEDFOVESKEER TVNVSVPKKTRINGTLYAYIFLHHAGAENNIDLVLNVEDFOVESKEER TVNVSVPKKTRINGTLYAYIFLHHAGAENPHOLKOVHLVSPLITT YMVPKPEEINLLTGESTDQIGADKKPTSALDEPVSHKRPRILAL NVNADNEVFDGSSLPADVHRYMKMIQLGKTVHYLPILIFIDOLSN RVKDLMVINRSTTELPLITVSKVSLGRLEFHHMODAVYSLOQ FGFSEKDADEVKGIFVDTNLYFLALTFFVARFHLLDEVISLKVLVV AGVGAAIELMKVKKALKMTIFWRGLMPEROFGTYSESERKTEEY DTQAMKYLSYLLVPLCVGGAVYSLLINIKYKSWYSMLINSFVNGV YARGFLEFMLPQLFVNYKLKSVAHLPHKAFITYAFHTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLVQRWLYVPVDKRRVNEFGESYE EKATRAPHTD LARRPKLQLLARSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLAYIFLHHAGVLPWHGKGVHLVSPLIT YMVPKPEEINLLTGESDTQOIBADKKPTSALDEPVSHKRPRIAL NVMADMFVPDGSSLPADVHRYMKMIQLGKTVHYLPILFIDLSIN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIIMODAVSLQQ FGFSEKDADEVKGIFVDTNLYLATFFVARFHLLPDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFFLDEGTSLLVLVP AGGGAAIELMKVKKALKMTIFWRGLMPFFQGTSTSEERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSMLINSFVNGV YARGELFMLPQCLFVAYKLKSVAHLLFWKAFTYKAPNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLVQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MPRILSVMLLLEAFRDDVVFLVYLVQRWLYPVDKRRVNEFGESYE EKATRAPHTD  GGLGFPGLGFRAGNGGPGGPGGPGGPGGPGGPGGREGLEG TKGTKGPPGASGSYEORDCLPGIPGGPGGPGGPGGREGLEG GGLGFPGLGFRAGNGGPGGLGGMAGDGELIGHTVGGREG FFGIGTTSPPCLUGGLGSPUOPPGFTGPPGPGGREGLEG GGLGFPGLGFRAGNGGPGGLGGMAGDGELIGHTVGGREG FFGIGTTSPPCLUGLGSPUOPPGFTGPPGPFGFFGFG GGLGFPGLGFRAGNGGPGGVGRAGGREGKGG GGLGFPGLGFGRAGPGPGGFGFGFFGFGFG GGLGFPGLGFGRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ł		MKQMFVQRVKEKEAILKEAERELOAKFEHLKRLHOERRMKLEEK
5792  2263  653  AAAAPS PAWGGVEVITOVITCWWYGIVTREPCSGDASCIQPY LARPRKOLO   RAFPETTT RSHLGAENI DLVLAWEDFOVES KFER TVANVS VPKYTRINGT LYAY I FLEHAGYLPHIDGKOYHLVSPITT YMV PKPEE INLITGESDTQQIEAD KKYTSALDEFVSHMEPRIAL NVANADNEV PROSS SLPADVHRYMKHI QLGKY VHYLPILFI DQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRIRFHI HMODAVYSLQQ FGFSEKDADEV KGI FVDTNLYFLALTFFVAAFHLLFUFLAFKND LSFWKKKKSMIGMSTKAVLWRCFSTVVI PLFILDEGTSLLVLVP AGVGAAI ELWKVKALKMTI FWEGLMPERQFCTYSESSERKTEEY DTQAMKYLSVLLYPLCVGGAVYSLLMI KVKSYSLINSFYNGV YARGFLFMLPQLEVNYKLKSVAHLPHKAFTYKAFMTFDDVFAF LITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPS PAWGGVFVVVYVVTTCWVMYGI VYTRPCSGDASCIQPY LARRPKLQL RHSFTTTRSHLGAENI DLVLWEDFDVESKFER TVWSVPKKTRNINGTLYAYI FLHHAGVLPWHIDGKOVHLVSPLTT YMVPKPEE INLITGESDTQGI LARKKPTSALDEPVSHRRPPLIAL NVAADMFVFGSSLPADVHRYMKMI QLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRIRFWHIMQDAVYSLQQ FGFSEKDADEVKGIFVDTNILYLALTFFVAAFHLLFPDLAFKND LSFWKKKKSMIGMSTKAVLWRCFSTVVI FLFILDEGTSLLVLVP AGVGAAI ELWKVKALKMTI FREIGMPEPGFGTYS SEERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSML INSFVNGV YARGLFMPDQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF LITMPTSHRLAGFRDDVVFLVYLVQRMLYPKRAFTYKAFNTFIDDVFAF LITMPTSHRLAGFRDDVVFLVYLVQRMLYPKRRVPREGSYE EKATRAPHTD  5794  1 5016  MGPRLSVMLLLIPAALLLHEERSRAAKGGCAGSGCKCDCHGV KGQKGERGLPGLQGYIGF PGMQGPEGPGPGPGPGPGFGENGM GGLGFPGLDGGFAGNGPGFGFGERGENGD GGLGPPGLPGGFAGNGPGFGFGERGROPFGFGERGOR GGLGPPGDFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGF	1		ľ	RELEGEITAFSKKKATSEIFHSOSFLATGSNLRKDKDRKNSOF
5792  2263  653  AAAAPSPAMIGUVVYVUNTGWMYGIVYTRPCSGDASCIQPY LARRPKLOL\RHSTTTRSHLGAENNIDLVLNVEDFUVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQLGAKKFTSALDEPVSHHRPRLAL NVMADNFVPDGSLPADVHRYMKMIQLGKTVHYLPLIFIDQLSN RVKDLMVINRSTTELPLTVSVVSLGRLRFWIHMODAYSLOQ FGFSEKDADEVKGIFUDTNLYFLALTFFVAAFHLLFUPLAFKND LSFWKKKKSMIGMSTKAVLWRCFSTVVIPLFLLDEGTSLLVLVP AGVGAAIELMKVKKALKMITFRWGLMPEPGFGTYSESERKTEEY DTQAMKYLSYLLYPLCUGGAVYSLLNIKKKSWISMLINSFVNGV YARGFLFMLPOLVPNVKLKSVLHPPKAFTYXAFNTFIDDVFAF LITMPTSHRLACFRODVVPLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAPSPAWGGVFVVYVVHTCWWYGIVYTRPCSGDASCIQPY LARRPKLOL\RHSTTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEVSHWRPRLAL NVMADNFVDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMODAVYSLQQ FGFSEKDADEVKGIFVTDTNLYSLALTFFVAAFHLLFDFLAFKND LISFWKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEGTSLLVLVP AGVGAAIELWKVKRALKMTIFWRGLMPEFGGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSMLINSFVNGV YAFGFLFHUPQLFVNYKLKSVANLLBYKAFNTFIDDVFAF LITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEPGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KGQKGERGLPGLQGYIGFPGMGGPEGFOGPPGCBGPGE GPLGFPGIJEGFFGROPGPGPGPFGFCRCGM GFLGFPGIDGFGFGROPGPFGLPGFGFGFGFGFGFG FFGTTSLPGPFGCRCGAGOPGPFGLPGFGFGFGFGFG FFGTTSLPGFGRGREGFGD GRGFPGTSLGCGFGFGFGFGFGFGFGFGFGFGFGFG FFGTTSLPGFGRGREGFGD RGFFGTSLGGFGFGFGFGFGFGFGFGFGFGFGFGFG FFGTGTSLGGFGFGGFGGFGGFGGFGGFGGFGGFGGFGGFGG GLSFPGFGCGGFGGFGGFGGFGGFGGFGGFGGFGGFGGFGGFGGF		1		FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEOPO
ARAPAS PAWWGSVVYVYHTCWWYGI VYTRPGSGDASCTQPY LARRPKTGI, PRISTITTSHLGAENNIOLUNIVEDEPUSKERER TVNVSVPKKTRNNGTLYAYI FLHHAGVLPWHDGKQVHLVSPLTT YMVVPKERINLITGESPYOLEADKKPTSALDEPVSHWRPRLAL NVMADNPVPDGSSLPADVHRYMKMI QLGKTVHYLPILEI IDQLSN RVKDLMVINRSTTELPLTVSVDKVYSLGRLRFWIHMQDAVYSLQO FGFSEKDADEVKGIFVDTNLVFLALIFEVAPHLLIDEDTSLLVLVP AGVGAAI ELMKVKKALKNI FWRGLMPEFQFGTYSESERKTEEY DTQAMKXLSVLLYPLCVGGAVYSLLNI KYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITNPTSHRLACFFDDVVFLVYLVQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSSPWGGVVVVVVHTCWWNYGI VYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIOLUNIVEDFDVESKFER TVNVSVPKKTRNNGTILYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEE INLITGESDTQQI EADKKPTSALDEPVSHWRPRLAL NVMADMFVFDGSSLPADVHRYMKNIQLGKTVHYLPILFIDQLSN RVKDLMVINISTTELPLTVSVDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIONSTKAVLWRCFSTVVI FLFLLDEOTSLLVLVP AGVGAAIELMKVKKALKNISTTELPLTVRGUMPEFGGTYSSESERKTEEY DTQAMKYLSYLLYPLCGGAVYSLLNIKYKSWYSMLINSFVNGV YAFGLFHMLPQLFVNYKLSVANLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLTPVKKRRVEGGSTE EXATRAPHTD  5794  1 5016 MPRIJSVMLLLIPBALLLHEEHSRAAAKGGCAGSGGKCDCHGV KGQKGBRGLPGLQGJVGFPFFGPPGPPGPPGPPGPPGEFGCM GPLGPPGIPGFRGNCPPGLPGJPGPPGPPGPPGPPGPCBCQM GLSFQFRGNEOEPGLQGSVGPFGPFPGPPGPPGPPGEKCQM GLSFQFRGNEOEPGLQGSVGPFPGFPGPPGPPGPPGERCQM GLSFQFRGNEOEPGLPGFPGPFGPFGPFGPFGPFGPFGPFGPFGPFGPPGPPGPP	5792	2263		LLIFMEKYFQVQGQYISQSE
TUNNSVPKKTRNINGTLYALPHHAGULPHHOGKONHUNSPLIT YMVSKPESINLITGESDYQQIEADKKPTSALDEPVSHWRPRLAL NVWADNFVPGGSLPADVHRYWKMR QLGKTVHYLPILT IYMVSKPESINLITGESDYQQIEADKKPTSALDEPVSHWRPRLAL NVWADNFVPGGSLPADVHRYWKMR QLGKTVHYLPILFIDQLSN RVKDLMYINRSTTELPITVSYDKVSLGGRIREWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALITFVAAFHLLFDPLAFKND ISFWKKKKSMKGMSTKAVMCFSTVVITPLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YARGFLFMLPQLFVNYNLKSVAHLPWKAFTYKAFNTFIDDVPAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAFSPAWWCGVFVVVVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTILYAYIFLHHAGULPWHDGKOVHLVSPLTT YMVPKPEINLLTGESDTQQIEADKKPTSALDEPVSHWRPLAL NVMADMFVFDGSSLPADVHRYMKMIQLGKTVHVLPLFIDQLSN RVKDLMVINRSTTELPLITVSYDKVSLGRLFFWHMODAVVSLQQ FGFSEKDADEVKGIFVDTNLYFLALITFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLRCFSTVVI FLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLHKKYKSWYSMLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCKCDCHGV KQQKGERGLPGLQGYIGFFGMGPPBGPGPPGPPGPPGPCBCGQM GPLGPPGLFGGPGFGFGFGPFGPPGPPGPPCPPCBKCQM GUSSPGJRGDKGDQGVSGFGFFGPFGPPGPPGPPGPCBKCQM GUSSPGJRGDKGDQGVSGFGFGFGPFGPPGPPGPPGPCBKCQM GLSFQFKGNBCDQCVSGFPGFFGPFGPPGPPGPPGPCBKCQM GUSSPGJRGDKGDQCVSGFPGRFGRFGKGOKG EPGCPGPBCVGEKGFPGRFGPFGPPGPPGPCBKGCMM GUSSPGJRGDKGDQCVSGFPGFGFGFGFGFGFGFGFGPGPPG PGPRGPPGPPGVFGFFGPGPFGPFGPFGFFGFGFFGFFGFFGPGPPGPG GPGGPPGFFGFGFGFG	3,32	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
TVNNSVPRKTRNNGTLYAYIFLHHAGVLPHHDGKQVHLVSPLAT YMVPKPESINLITGESDTQQIEADKKFTSALDEPVSHWRPRLAL NVNADNFVPDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTYSYDKVSLGRLFFHHMGDAVYSLQQ FGFSEKDADEVKGIFUPTVASFHLLFPVASFHLLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVIPLFLLDEQTSLLVLVP AGVGAJELBLWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLVCGGAVYSLLNIKYKSWYSWLINSFVNGV YARGFLFMLPQLFVNYKLKSVAHLPHKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLVQRWLYPVDKRRVNEFGESYE EKATRAPHTD AAAAPSPAWMCGVFVVYVVHTCWUMYGIVYTRFCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIPLHHAGVLPWHDGKQVHLVSPLTT YMWPKPEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFGSSLPADVHRYMKMTQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSVDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFTNLYFLALFFVAAFHLLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEGTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCAGAVYSLLNIKYKSWYSMLINSFVNGV YAAFGLLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLEPALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGRRGLPGLQGYIGFPGMGPGFGPGPFGPGFGRGKDTKGER GPLGFPGLBFGAGNFGFPGLDCJDGPWGPFGPFGPFGPFGPGFG GPLGFPGLBFGAGNFGFPGLDCJDGPWGPFGPFGPFGPFGPGFG GPLGFPGLBFGAGNFGFPGLDCGNGTKGER FFGISCTPGPFGLPGLDCGPWGPFGPFGPFGPFGPGFG GPLGFPGLBFGAGNFGFFGFRGKNGDKGEKSSPGFPGBPG GPLGFPGLBFGAGNFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFG	1			LARRPKEQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKEED
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TONUSUPKKTRNACTLYAYIFLHHAGULPHHDGKQVHLUSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLAGFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQFPGPPGPGKGCMGTGEFGLPG KGQKGERGLPGLQGVIGFPGMQFPGPPGPPGPGFGLPG KGQKGERGLPGLQGVIGFPGMAGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQSPVGPPGFTGPPGPPPGPPGFKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGRPGPGRFGKPGKDGDKGEKGSPGFFGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPPGFFGFPGLPGQPGPPGLPVPGQAGAPGFPGERGKGD RGFPGTSLPGPSGFGLPGQPGPPGLPVPGQAGAPGFPGERGKGD RGFPGTSLPGPSGFGLPGGPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	1			LARRENTOL DESERVED OF THE TOTAL
YMVPKPEEINLTGESDTQOIEADKRPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLFFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGLPGLYGG GPLGPPGLPGFAGNPGPPGLPGIPGQDGPPGPPSIPGCNGTKGER GPLGPPGLPFFAGNPGPPGLPGIPGDPGPPGPPGPPGPEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGERGQKG EPGFQCMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGPKGERGEAGPPGPPGIVIGTGPLGEKGERGYBGT PGPPGTSLPGPSGPPGQPGPPGLPVPGQAAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG	l i			TVNVSVPKKTPNNGTLVAVIELUNGVEDENVEDEDVESKFER
RVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGNSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPQBPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGIFGDMCGDPGELLGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGVGPPGPFGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPPRGEPGPKGPFGPGPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP	1			YMVPKPEEINLITGESDTOOLEADKKDECAL DEDIGGEDDAY
RVNDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQDFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGDGPGPPGPPGPPGPRGKGR GPLGPPGLPGFAGNPGPPGLPGIPGDGPGPPGPPGPPGPPGPFGRPGF FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPPGPPGPKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFFGLPGQPGPPGLPVPGQACAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	1			NVMADNEVEDGSSI.PADVURVMVMIOLCVTURVU DIV ETDOLGV
FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHILFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSILVLVVP AGVGAAIELWKVKKALKMTIFWRGIMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWILNSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPCMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPCMQGPEGPQPPGLPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGLQGPUGPPGPPGPPGPRGEKGQM GLSFQGPFGDKGDQGVSGPPGPPGPPGPPGPPGPRGKPGKGQKG EPGFQGMPGVGEKGEPGKPGPGAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGRKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPPGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGGPGPGPGVTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	İ .			RVKDLMVINRSTTELPI.TVSVDKVSI.GPI.DEWIUMODALIVSI.GO
ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGIMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER GPPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFPGPPGPPGPPGPEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFCMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QBEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGP\QBEKGEAGPPGPPGLPVPGQAAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGOG	1 1			FGFSEKDADEVKGI FVDTNI.VFI.AI.TFFVAAFULLEDELAEVAD
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWIINSFVNGV YAFGPLFMLPQLPVNYKLKSVAHLPWKAFTYKAFNTFIDDVPAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQPFGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFPGPPGPPGPPGPEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQCMPGVGEKGEPGKPGPRGKPGKGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPPGLPPGQAAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGPTNGIVECQPGPP GDQGPPGIPGQPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	!	ļ.		ISFWKKKKSMIGMSTKAVIWRCESTVVIELELLDEOTSLLVIVD
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGJPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPG1PGQDGPPGPPB1PGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGLQGPWGPPGPPB1PGCNGTKGER FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGEKGSPGFPGP YPGLIGRQGP\QGEKGEAGFPGPPGIVIGTGPLGEKGERGYPGT PGPPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPFIGEIGEKGQKGESCLICDIDGYRGPPGPG		1		AGVGAAIELWKVKKALKMTIFWRGIMPEFOFGTVSFSFDVTFFV
YAFGLEMLPOLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPG1PGQDGPPGPPGPPGPGCAGTKGER GPLGPPGLPGFAGNPGPPGLPGLWGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	1	ľ	1	DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLTNSFUNGY
11TMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGPKGDTKGER TKGTRGPPGASGYPGNPGLPGIPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQCMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFCTTSLPGPSGRDGLPGPPGSPGPQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG		l.		YAPGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
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MGPRLSVMLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV  KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGCKGDTGEPGLPG  KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGCKGDTGEPGLPG  TKGTRGPPGASGYPGNPGLPGLPGDGPPGPPGPPGPCGKGTKGER  GPLGPPGLPGFAGNPGPPGLPGMKGDPGEPLGHVPGMLLKGERG  FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM  GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG  EPGFQCMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG  YPGLLGRQGPYQEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT  PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAAPGFPGERGEKGD  RGFFGTSLPGPSGRDGLPGPPGSPGPQAPGYTNGIVECQPGPP  GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	F = 700			EKATRAPHTD
KGQKGERGIPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCMGTKGER GPLGPPGLPGFAGNPGPPGLPGIPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQCMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPPGLPVPGQAGAPGFPGEKGEKGD RGFFGTSLPGPSGRDGLPGPPPGSPGPPQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGPPSPGPQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	3/94	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCTCHGV
TKGTRGPPGASGYPGNPGLPG1PGQDGPPGPPG1PGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGE1LGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKKQQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG	1	ł	ł	KGQKGERGLPGLQGVIGFPGMOGPEGPOGPPGOKGDTGEPGT.PG
GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPKGKDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPGPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPOG	1		ĺ	TKGTRGPPGASGYPGNPGLPG1PGODGPPGPPGIPGCNGTKGER
FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPFGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKFGRKGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPOG		[	I	GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG
GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGRFPGKFGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG		1	1	FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGOM
EPGFQCMPGVGEKGEPGKPGPRGKPGKGEKGSPGFPGEPG YPGLIGRQGF\QGEKGEAGPPGPPGIVIGTGFLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG		1		GLSFQGPKGDKGDQGVSGPPGVPGOAOVOEKGDFATKGEKGOKG
YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFFGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPG				EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPOG	i i	Į.		YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPOG			i	PGPRGEPGPKGFPGLPGQPGPPGLPVPGOAGAPGFPGERGEKGD
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Deginning		Predicted	Predicted end	laming agid commont containing gignal montide
No:   nucleotide	SEQ	)		Amino acid segment containing signal peptide
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amino acid residue of amino acid sequence  ##TTP/ptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possible nucleotide deletion /=possibl				· · · · · · · · · · · · · · · · · · ·
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STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE   PLAKIILESNOPROFFFKYVELISTDIASDAFATFKOLLTRHKVL   VADFILEQMYDTIFEDYEKLLQSENYUTKROSLKLLGELILDRIN   FAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFKVFVASPH   KTQPIVEILLIKNOPKLIEFISSFQKERTDDEQFADEKNYLIKQI   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RTQPIVEILLIKNOPKLIEFISSFQKERTDDEQFADEKNYLIKQI   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RTGPIVEILLIKNOPKLIEFISSFQKERTDDEQFADEKNYLIKQI   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKTAP-RALRDSKY   RDLKKKEPTORE   RTKKKPYNSNIGFYTKRNALRVAEVMODDYSKYNYTANNEP   RTKKKPYNSNIGFYTKRNALRVAEVMODDYSKYNYTANNEP   RTKKKPYNSNIGFYTKRNALRVAEVMODDYSKYNYTANNEP   RTKKKPYNSNIGTYTKRNALRVAEVMODDYSKYNYTANNEN   RTKKKPYNSKY   RDLKKKKPYNSKY   RTKKKPYNS	<b>!</b>	<u> </u>	l	
PLAKI ILESNOPRDFFKYVELSTFDIASDAPATFKOLLTRHKVI, VADFILONYDTITFEDYEKLLOSSNYVTKRQSLKLIGELILDRHN FAIMTKYI SKPENLKLMMILLRDKSPNIQFEAPHVFKVFVASPH KTQPIVEI ILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR  5796 2 1078 GRVGWELWGMY159PKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVMDDYKSHVYIAWNLPLENF GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTITLPDTRCLVDNNSKSRLPQLLDCDKVXSSIYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLIRSCTTGGWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQILKMKVESSQEANABVWREMYKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAITEBANKKMQAARISLEEKDQRIGEL DRLIERMEKERHQLQLQLEHETEBANKKMQAARISLEEKDQRIGEL DRLIERMEKERHQLQLQLEHETEMSGELTDSDKERYQQLEEAS ASLBERIRHLNDMVHCQQKKVKQWVEELESLKKKLQQKQLLILQ LLEKISFLEGENNELOSRLDYLITETOAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSTWKSINSNOEKOPYYEEQARLSKHHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTEDSCSTSASPEPSLPVIQSTYGMKT DGGSLAGRENINGEDEMEMVDDYEDDPKSDYSSENERPPRAVSAN 5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPPFPERESSILAKKRKGGPGAGSAL DDGRRDPSSNDINGGMBPTPSTVSTPSPSDADLLGIRAAPPPAAP PASAGAGRILLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLINKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVFRRYGGAPQALTLKLPVTINKFFQPTEM	5795	1192	61	
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GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKARDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMMKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGTARGRQVLDGPPRASPG QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETISPLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMYHCQQKKVKQMVEBIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLITETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPESLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN 5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	. 2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFTQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVNREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGGL DRLIERMEKERHQLQLQLLEHETENSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKVVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETTEIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  5798 644 115 KILGSRWKSNSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLDVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDVEDDPKSDYSSENEAPEAVSAN 5799 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILLVDVFDGPAAQPSLGFTPEEAFLSFGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	. 2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASHDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETEIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASHDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETEIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKN9IK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLILKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSPLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  S798 644 115 KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  S799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNPSPTVVHPGDLQTQLAVQTKRVAAQQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*KALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG  PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASIDKKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  S798 644 115 KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKKKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL
QHRDPG  5797 2 891 PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSPLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  5798 644 115 KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMSKFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTTSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASIDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETINSFLKAIEEANIKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVESIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  5798 644 115 KIIGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQDQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTTSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPCDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R
VAQVENQLIKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNTTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNPSPTVVHPCDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5796	2	1078	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPFKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTI KNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
KHSAEKEALLEETNS FLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETENSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  5798 644 115 KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQENRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN 5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFIHL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG
DRLIERMEKERHOLQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPFFPERSSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILIVDVFDGPAAQPSLGFTPEEAFLSFGPEDIGPFIP EADBLLNKKVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGFPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQGTYEASMDKLREKQRQLE
ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT  5798 644 115 KILGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN 5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLIGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEI LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQGTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR
LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTTSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL
SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT  5798 644 115 KIIGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTTSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPFKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQSPLENHTAILYPCHGWGPQLARYTKEGFHLL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS
5798  644  115  KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799  2679  1435  LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFONPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP*RALRDSKR GRVGWELWCMY I SPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEI GLLDPGMDVYGGENI ELGI KVWLCGGSMEVLPCSRVAHI E RKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYI AWNLPLENP GID I GDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAI LYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLI LRSCTGQRWTI KNSI K*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNI KDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABEWREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAE I SLEEKDQRIGEL DRLI ERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ
TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	-			FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP+RALRDSKR GRVGWELWCMY I SPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEI GLLDPGMDVYGGENI ELGI KVWLCGGSMEVLPCSRVAHI E RKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYI AWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTA I LYPCHGWGPQLARYTKEGFI HL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKV KSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLI LRSCTGQRWTI KNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNI KDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANAB WREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKNQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797	2	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP*RALRDSKR GRVGWELWCMY I SPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVY I AWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFIHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797	2	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVE I LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLI KQI RDLKKTAP*RALRDSKR GRVGWELWCMY I SPPKDWDDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGI KVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVY I AWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFIHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN  5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797	2	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQKKVKQMVEBELSLKKKQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIWMPSRNYTPYTRVLELTMKKTLT
5799 2679 1435 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTTSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797	2	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFHLL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLACIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR
TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNILIVDVFDGPAAQPSLGPTPEEAPLSFGPEDIGPPIP EADBLINKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVOFQNPSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797	2	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIBLGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLETNSFLKATEBANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLITETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASHDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKLLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIGSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMY I SPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQGTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLLEHETEMSGELTDSDKERRYQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTBVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KIIGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFTVGQQPQIPITTGTG VYYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
EADBILINKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASHDKLREKQRQLE VAQVENQLLKNKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEBLESLKKKLQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIFITTGTG VYYPGAITMATTTPSPQMTSDCSSTASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
KTSVOFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFHLL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLACIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEBIESLKKKLQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKKKKGFGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
NIECLROFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPFKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIBLGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKATEBANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLITETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP
	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIBLGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEWMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTBVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVILELTMKTLTT KIIGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQITPITGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEMPPFPERESSILAKLKKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGRILLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
A A A B B B A B A B A B A B A B A B A B	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMY I SPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERRYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLKIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAQPSLGPTPEEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL
AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA	5797 5798	644	891	FAIMTKY I SKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI RDLKKTAP+RALRDSKR GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPPTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK+R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASNDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEBLESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIFITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLFPETKATIGGVLRAGSGLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQVL NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM

	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal pertide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucinc, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
1	i		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
	Į.		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	1		PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
1	}		EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
1	{		KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVOQVL
į.	1		NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
	1		AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
l.	}		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
l .	ì		· ·
5801	3	1413	RTSKEPVSRHLCELLAQQF
3301	1 3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
1	1		QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
}	1		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1	l		QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
1	1		DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
]			NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
	1		GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
}	1		BVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
		,	NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
1	]		GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
L			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMOLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
j .	j		GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLIYISIMYREV
L	į.		ITQRLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIBIVKVKAIGRQRFKVLELRTQSD
1	į		GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
	1		SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
	}		WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
1			LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
			SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
ļ.	i		rcr .
5804	2.	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE
l			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
l			REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
			ESLSPGKLKLTFEELERQRQENRKKQAEEBARKRLEEEKRAPEE
1			ARROMVNEDEENODTAKIFKGYRPGKLKLSFEEMERORREDEKR
l			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
1			GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
<b>]</b>			GEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS
ł			
i I		•	EKEIQKKIEEERARRAIDLEIKEREAENFHEEDDVDVRPARKS
<b>j</b> i	•		EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQPEQREI
	•		DAALQKKREEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
			SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
			AFKESQQQSBDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
			YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA
			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
			RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
			ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
	<b> </b>		RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIOPACLGLYCGKTLLFKNGSTEIYGECGVC
	2201	1302	
ļ <b>l</b>			PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
			LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

WO 01/53312 PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		<del></del>	LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLOAVGG
i			GLLYYAFPYIILVLSLVTLAVYMSASEIENCYDLLVRKKRLIVL
ł	í		FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
1	ł		EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS
1			EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
ŀ			LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
		1	LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
			RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
1	ĺ		EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
1	1		
l .	1		ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
	1	1	INSRRINPKISYVISIKGORLDPMESVREETVNLTTDSRTPEVC
		1	LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
1	<b>1</b>		SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
		i	FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
}	}	j	VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYOKEF
ł	1		AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
1	1	i	TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
	i		LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
	Į.		EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
1	l	1	WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
	1	1044	BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAOSFEE
1	ł.		VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
	İ	l	SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDOMLK
1	}	ļ	QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
			EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
1	į.		TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
1	1		TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
1	ł	1	RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
(			SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
i	l	İ	SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
1	İ		VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
j	Ì	Į.	KCTLHLGIBPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRPLKSSLGYEITFSLLNPDPKSHDVY
1	1		WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
1	1	1	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
1	1	j	HSPLYIODKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
1	1	1	RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
1	i	İ	WELDRLLWARSVENLATATTTLTSLAOLLGKISNIVIKDDVASE
1	1		VYKAVAAVOKSAEELASGHLASAFVASOEAVTSSELAFFDPSLL
1		1	HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
1	1	[	KTD
5812	5204	2744	GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
I	1		LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGO
1	1	]	DMVSILQLVQNLMHGDEDEEPQSPRIQNIGECGHMALLGHSLGA
1	[	<b>[</b>	YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEERE
1	1		GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGO
1	1	]	YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
1	1		RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
1	1		LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
1	Ī		LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACOLS
1		l	QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
1		l	PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
1	1	l	EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
ì			EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ
1	]		GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
1		1	AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS
1			EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES
L	L	L	PPUTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

SEO	Predicted	Predicted end	1 América de la Companya de la Compa
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	T	<del></del>	TEPIYYYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
	1	1	LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
1	1	1	TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
	1	·	LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
1	[		GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
ļ			RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
1	Į.		SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
		ļ	KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
			SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
1	[	1	ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
1	İ		PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
1		İ	GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
1		İ	AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
1	1		QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
ı	1		LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
			ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
ł			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
1	<b>\$</b>		RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
1			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
L			VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
ì			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
			AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
]			GQFHGHFSQKI+EVFLDREFLLRVSYMEIYNBTITDLLCGTQKM
i			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
	l i		TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA
<b>i</b>			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1 .			NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALOFAST
			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKOLEEVSLETRAO
			AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLOOFI.
			KAKRKRRVTWCLGKINKMKNSNYADOFNIPTNITTKTHKISTNI.
	ļ.		LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNOENIESELN
			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
ŀ	i		KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
]	i i		QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
} }	,		ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYQSQLE
			AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK
1	İ		ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD
i i			KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
	I		SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE
!	·		AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE
i	ľ		NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
	1		QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHQETINTIKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
	}		TADVKDNEI IEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
	i		KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
i	i		TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE
	1		NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
j		}	KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
ſ	[	'	TIDELRRSVSEKTAQI INTQDLEKSHTKLQEEIPVLHEEQELLP
!			NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
	1		QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
ı	1		SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
1	1	}	LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
j		1	AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ
Ī			LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEFR
ŀ			KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA
-		1	LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE
1			IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
			DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH
			THE TAXABLE TA

000	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	1	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of		
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
1	1	i .	IAHMHLKEQQETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
1	i	i	IOELKANEHOLITLKKOVNETOKKVSEMEOLKKOIKDOSLTLSK
i	1	1	
	l .	}	LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLK
1	i		ESLQETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
1	Ī	1	ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
1	1	1	EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
1	1		LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
ł		1	
1	ļ		HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
I	ľ	1	RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVEKQKELLIK
1	1	į.	IQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKDFSESEFPSIK
1	1	1	TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
1	1	i	NNFFNNRITAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
1	{	1	
1	1		KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE
1			NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC
	1	1	LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
1	t		KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
1	1	}	DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
1	1	1	EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
ł	•		
l l		1	SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS
	1	1	LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
1	ł	1	DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
	ì	1	TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
i	i	I	SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
1	i	ì	
į.	1	1	CNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELFQFSIVDY
1		Į.	KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
1	1	1	SWYSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
i		1	AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
1	1	1	NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
i	i	l .	TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
1	i		OLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
		<u> </u>	
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
1			TVYHERQRLELCAVHALNNVLQQQLFSQEAADBICKRLAPDSRL
i		1	NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
1 .			VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
1		1	K\LRAPEGPGGLRTE\*GPFLAAALAQGLCEVLLVVTKEVEEKG
-	1	1	
<u> </u>			SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
ı			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
1	1	1	KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
l	1		RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
1			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
1	1	İ	
<u> </u>		J	HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
1	i .	ı	DRRIGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
1	1		NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
	I	1	TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
1	i	I	
	1	1	TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
1		i	PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
1	i .	1	TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
Į.	1	1	NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
1	1	1	NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
1		1	AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
1	i	i	HATDUMITTERMARKANINA OF HISTORY AND AND AND AND AND AND AND AND AND AND
1	1	1	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
1	1	1	DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
1	•	j	PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
i	l .	1	HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
1	1	1	NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
1	l	1	MOME ACTIONS TOWNSTAND TONGON WELL COME SANDANG
Į.	1	1	LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Amino acid sogment
ID	beginning	nucleotide	Amino acid segment containing signal peptid (A=Alenine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
*	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleotice deletion
	sequence		\=possible nucleotide insertion)
	· .		ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPEVG
			WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSODD
			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNIRTEV
	l		MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIP
	ł		GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPOOF
			GIINLAFEDATENECREFSANKKFKRSVLLSVDECRELGSDEG
			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNIL
İ	ĺ		CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDV
			SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCH
			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTE
			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFE
			KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNS
			PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLI
5819	1	5557	SSASITMASFSSEDCSPQGEWTILELETQH
	_	3331	AAAGLIGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGI
			LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMI
			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
1			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
- 1	j		RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHI ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIF
l			TNASDSTEFILEPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPK
ĺ			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
į			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
ŀ			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
- 1	j		NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
1			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
J	j		IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1	j		DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKT
1	i		VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEDG
			KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVOPGVAMOEDM
- 1			WDADWD_HQSLFKGWTGIKENSGHRLSAIFEVNTDLOKNIISKI
- 1	]		TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SODVPV
1			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
1			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
ŀ	1	i	ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
- 1			ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
ľ	ł	1	ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRLS\FEASNPPFD VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
l		1	GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
			SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
	1		PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
j	]	. ]	SSEDSDITSLIBAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
		j	KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
	ľ	.	TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI
i			KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
			SRNAQKTKGTSKLVDNRPPALAKFLPNSOELGNTSSSEGEKDSP
- 1		ł	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKOROTSPTPAS
İ	}	ſ	PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKOPNGSKHKLTKAA
	1	1	SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
		,	HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
			VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS
1	1	}	SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
	ĺ	- 1	TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
820			RSSDPWSNSHFPHEN
020	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
1	ļ	i	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
		í	ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
- 1	i	1	
		I	SSSSDSSSSSSDSEDEDKKQGKRRKKKKNRSHKSSESSMSETES

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			H=Histidine, I=Isoleucine, K=Lysine,
i	location	corresponding	,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
<del></del>			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
1	1	1	ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKKKAA
l	1	ł	SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
1	1	1	GIIPGLFSSHSDATV
5821	179	915	KWRNOSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPOT
2027	1 1/3	) 313	**************************************
İ	1	}	PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
1		†	TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1		1	SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
1	1	ļ.	SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
ł	}	ļ	RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
1	1	1	PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
1			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
1	1	1	LTRKDRLYKNIIRMOHTHGFKAFHILPQTFLLPAEYAEFCNSYS
1			KDRGPWIVKPVASSRGRG\VYLINNPNOISLEENILVSRYINNP
}	1	1	LLIDDFXPDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
i		1	NIRNOFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
	1		1 "
1	1	Į	LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
	1	t	FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
	1	1	MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
1	l .	i	SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
1	l .		RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
1	1	İ	APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP
l .			KYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF
1	1	1	LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
1	1	1	LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
ì	1	Į.	QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
	1	1	LERTRILAHOLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
i		ì	ENFORFIRQASEAELEEVLTFYTOKNKSASVFLGTHSKISKNNN
	1	1	
1		1	NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA
	1	1	EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
1		1	LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
	Į.	1	RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
i	ļ	1	GIAKTQKEGEDASLYSKRYNQSMVTAELQRLAEKQAARQYSPSS
		1	HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
1	1		SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
1	Ī	1	KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
I	,	1	LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
1			VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
ł			ITSSTDPAHTKIMNHKHTEKOPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
3023	1 1	1	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
1			
1	1		EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1	]		RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
i	l		EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
1	1		RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
1	1		CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
	I		L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1		i	GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
ı	1		OFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
i		1	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1		1	PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
j	1		
l	}	1	GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1	1	1	BALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
1	1		SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
L		L	ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDBPSACRAGDVNMDDPKKEDILLLADEKFDF
ı			DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1		I	TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
1			

SEQ	Predicted	I B 43 1	
ID	beginning	Predicted end nucleotide	The segment containing signal pentide
NO:	nucleotide	location	[A=Alanine, C=Cysteine, D=Aspartic Acid r_
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
-	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1		1	DSPIJGPPUGEDRI I ASCRAL DOGGA OAR I TOAT TOAT TO THE T
- 1	1	1	DSPLLGPPVGEPRLLASSPALPSSGAQARUTRAPGPPHSAHALP RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1	į.		EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
[	İ		RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
İ			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
ı	1	İ	L\PAGFVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1	1		GGG\QWLNSSCAWSESSQLNKTRSIRRDSCLNSKTKVMPTPTN
1	ł		QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1	j		RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
ł	ŀ		PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1		İ	GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1			EALLVDIKLEPLAVTPDAASOPLIDLPI.TDFCDTPEAHVAVGSF
1		!	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
5005			ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
1	1	Í	SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSEVEL
1	1		SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYVVFSG
1	1		KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONGS
ł			VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD
ļ	•		SQMQSIFTDIGXVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
1	1		GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
	ŀ		GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
1			YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
ì	1. 1		GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
1	i i		ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
	1		DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF
ı	} i		YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
1.	i !		HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
1	ļ í		DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ
í	1		[ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAOPLNIRMNLTOLV
	i j		GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
	f i		TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
J	1		LQHLSVLELTDSGALMANRFVSSPOTIVELFFOEVARKHIISHI
1	1	•	FSQPKAPLSQTGLNWPEMITAITSYLLOLLWPSNPGCLFLECLM
'		•	GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGOKAI.
1	! !		ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLOYYDKVLPLLD
1	1		VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
1			\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
1 1	ľ		YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
1			TVMFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
] ]			VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
			CSLARIRLTLAQHD?SAVAVAGSSSAEEMVTLLVQAGLFDTAIS
			LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQAEAWAWIAANQLS SVITTKESSATDEAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
l			VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
, I			AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
j !		·[	WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
} [			CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
]	1	İ	AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
l i	-	· 1	PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
ا ہے۔		_	WQGLVVDPSPHPLLAFPLLSSAOVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
	ļ	1	RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
	[	l	RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
1		. [	SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
ļ J		Į	EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEOVSADVI.S
İ		ļ	SPQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFT.KSI.
			TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP
			23111111

•			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	504	\=possible nucleotide insertion)
	sequence		VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
	1	į	EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR
	1	1	D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
	1	Į.	TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
	1	<u> </u>	SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
	l	i	
	l	l .	EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
	1		EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
		ì	GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
	į	1	EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
	İ	1	W
5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
		1	MAVGGGSRMTDLTSSIPKPLLPVGNKFLIWY?LNLLERVGFEEV
		į	IVVTTRDVQKALCAEFKMKMKPDIVCIPDDADMGTADSLRYIYP
	İ		KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI
			EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
	1	1	GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
			EL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
	1		SFY*KEANYTGTGAPY\D\ACWI
	<del> </del>	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
5829	260	1259	
	1	1	GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
ļ	1	1	YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
Į.		İ	ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
1	<b>!</b>	1	PRTPHPHEBKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
ĺ		1	LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
1		1	QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
	1	<b>!</b>	LTLTEDKLKDCLENQQKLFSAVQQKS
5830	4496	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW
ţ	1	1	NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
		1	PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV
1	į.		TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL
			LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE
1	1	1	GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
1	i		INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR
ł	ì		ADQEKERKKREERERKRRKKEEVQQQKLAEERRRQNLQEEKERK
		1	LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIHDF
,		· ·	LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
1	l		GLSHTEVLFVQDLTDE
		<u> </u>	
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
	1		TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
1	i		FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
		1	ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREEYR
		1	KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEE
	1		EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
1			QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE
1		j	RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
	1	I	RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
			VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
ł	1	1	VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
		1	GSPLELKODNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
1			GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
		1	VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
1		1	ADDENDAVAEMENDAVAEMANDAVA A VLIMADAVAMINITERINO
		1	KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
		Į.	QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEERRY
1		1	YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
		1	GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL
		1	AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
1	1	1	PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
			PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
1			NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
1 -002	1 3333		SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF
1			

SEQ	Predicted	Dradiated and	
ID	beginning	Predicted end	The signal pentile containing signal pentile
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- i	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine.
ĺ		residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	<u> </u>	\=possible nucleotide insertion)
			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
	i		RVHFHLPYRWQF'LDRGKWEDLDNMELIEEAYCNPKIERILCSES
	1 .		ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
İ	}	1	YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
}	· <b>!</b>	1	PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
	1	ſ	QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
- 1	1		YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
ļ	Ţ	1	GKAVDEBOLEUCTCA LEIDA LOCCHEDURIO IQWQKGQMQKQNG
i			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
- [	į.		ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
1			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
5833	170	3289	TPSILLALGSLFSSRQ
	1	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
		ľ	RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
Í	1	i	GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
	1	1	GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
	1	<b>}</b>	RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
1	i		EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
J	ĵ		DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
1		ſ	GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
ı	1	i	YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLORRYGR
1			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNONESVSEIG
ł			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
1			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYOGIDN
1			YPLDWELSYAYYSNIATKTPLEOHTLOGEOAYVETIRIKEDETI.
ł	1		KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
1	1		EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
	1		KKAASKGLEQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
1	1		PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
1	i I		WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
j	i i	•	AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
1	1 1		GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLE:S
J	] . [		VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
1			SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
1	i i		SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
	i		STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
1	ļ		SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
1			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
1 .	j		NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI
}			PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC
			GEVERI CUAERRY DEVICES VI THE CHERRY REPRESENTATION OF THE CHERRY REPRESEN
]	I		GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
	1		KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
1		i	QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
1 1	ſ		GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
, I	}		ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
<u> </u>	1		RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
]		ļ	SOWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
j	. 1		EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
1			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
] {	1	}	RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
1 1	]	1	KTLRSSLEGPTILDIEKPHRESFFYTHLINFSETLQQCCDLSQL
1	!		WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL
[ . <b>.</b> [	į	l	YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDOFVYKLADO
1	į.	İ	IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKOR
1 1	1	i	HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
[ ]	į	j	LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL .
	1	i	HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSOEFORDKOPNAOP
] [		1	QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYOGIAVV
, ,	ĺ	İ	MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
	f	1	EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
			EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP
			THE PARTY OF THE P

SEQ	Predicted	Predicted end	Desire said coment contribution desired
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	
<b> </b>	bequence	<u> </u>	\=possible nucleotide insertion)
	1		LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1	1		DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
]	<u> </u>	İ	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
ĺ			EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
5035	4000		HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
Ì			DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ
ļ	1		SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ
			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
	1	}	PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
1		İ	RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
}	ł		PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
1			SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR
1	1	1	TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA
1	i		NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
ſ		ļ	HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
ł			GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
(	{		LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
	ŀ		QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
i	ļ		KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
l .	1		QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
İ			HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
			CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
]	J		SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
İ			VZAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
	ľ		HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
i			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
i			VXFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
1	1		FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
1	1.		DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
1	<b>(</b>		PIDLLNVAFIAEEKTMPTTFNREGNKOKNKCEIPSEEFSKDVAA
1	-		AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
1	i		ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
1	1		VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
ł	i		MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
1			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
			KMEKINEKASDKCGRLQIMSLENLSIBKETKL
5837	4792	903	NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
1			KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
1		,	QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
i	]	·	RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
I	]		MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
ł	]		DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
1			GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
1			KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
[	1		HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
1			P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
I			VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
1			DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ
1	:		PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ
l			EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
			ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
1			VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
[			HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
			GYHVWLWAVEAFAKOLCFODQYVKAASHLLSIHKVYEAVELLKS
1			NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
}			CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
1			LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
1			EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
}			QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW
		<del></del>	1

SEQ	Predicted	Predicted end	I amino acid coment cost-initiation
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	0-1	\=possible nucleotide insertion)
	<del> </del>		DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
1	1		HQSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
	1		TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
i	1	Į.	LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS
i	ļ		TANGPDKNBPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
1	1	Ì	ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMOQ
ı			QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
		1	ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
Į.		}	LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH
1		1	RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
· §			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
•			IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
			FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
		İ	EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
		1	SQLNEHQRIHTGEKPYECKECGKTFRGSQLTYHLRVHSGERPY
1		· ·	KCKECGKAPISNSNLIQHQRIHTGEKPYKCKECGKAFICGKOLS
1		,	EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC
}		•	GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHO
1			RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
	1		GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
Į.			HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLPLRGRRQCGRWTVDFEECLKD\SPRFRAAL
ŀ	1		EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
ł		•	RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
1			EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
	İ		PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA
			AKEKREMECKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
			RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
	<u>[</u>		HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
	<b>!</b>		AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
			CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
1	. 1		VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPOPG
1	ŀ		QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
1			EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
			TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
1			AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
j			LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
			RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRAFMSALSKTQTQSAPALQ
			GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS
1			AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP
			SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ
]		·	RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
1			SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
j l			SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
1 1			PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
1			KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
1 1	ļ		SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
1	. 1		LFSPQNTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
			RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY
	ļ		RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT
	į		VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
1 1	l		SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
	į		LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
[	į	i	VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS
1	Į	İ	SGGSGVPFSTPPPPPPPVDHSGVVPPPAPPLAEHGVAGAVAVFP
Ll			KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEO	Predicted	Predicted end	Dring agid coment containing claral services
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			TLPSHSLEHLGPPHGGGGGGSNSSSGPPLGPSHRDTISRSGII
			LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
1	1	Ì	PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
1	ļ		TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
	i		RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
i	ļ		GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK
			SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
1	Ì	l	QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
1	ŧ		\VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHI
1			FP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
			LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
j			WSSRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
1	ļ		HRSRDTAEPSFPEIPLDGTLAPPESOGNGSTLOPNVVYITLRSK
1			RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQEA\EG
	[		KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGFDFLQPSS
1			RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
}		:	RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
1			GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
1			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
1	į		DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
į.	ţ		LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
			AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
Į.			DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA
1			EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
			LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCBLVVT
i			LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
1			LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG
5844	202	0.450	VQARAPGLGRA
3044	202	2471	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
Į.			KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
			QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
1	ì		PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
İ			PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGPHGLPGIGK
į.	[		PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
]			GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
1			PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
	]		PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
l	]		PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGOKGVP
1			GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
1			PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPOGOPGL
Į			PGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG
1	· [		AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY
I			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
1			EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
<u> </u>			SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
			GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
			KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
			PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT
1		ı	RQAARHNAAMKALQALQNEPIPERSPONGESGKDMDDDKDANKS
į			EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
]	i		IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
<u> </u>			EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ
L			DQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

SEQ	Predicted		
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
""	location		Glucamic Acid, F=Phenylalanine G=Glucine
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
	1		RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
1	]		NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
	1	1	DROSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
1		i	YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
5846	1126	456	
		=36	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
	1		KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
ŀ	Í		TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
- }	!		RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
- 1		1	KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
5847	2769	505	LQGVI
1	105	]	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1		ŀ	WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
1		İ	PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
1			HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS
1			WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
1	· I	'	KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF
	1		SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE
i	1		KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK
	1		CNECGKAFNGPSTFIRHMIHTGEKPYECNECGKAFSQHSNLTQ
1	1		HOKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
-	j .		GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
F			HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
1	[		SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA
			KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS
	1		HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK
1			CNECGK/TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
	1		KHORLHPGI
5848	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
1			GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
1 .	1 1		DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
ļ	i l		YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
l		,	GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
	1		VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAOKNPEEFKTSV
1	1 1		SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLOCY
1			PPPDPAVRGRLTECLETILNKAQEPPKSKKVOHSNAKNAVI.FEA
1	]		ISLIIHHDSEPNLLVRACNQLGQFLOHRETNLRYLALESMCTI.A
1	] [		SSEFSHEAVKTHIETVINALKTERDVSVRORAVDLLYAMCDRSN
1	]	1	APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\vvn
1	.		TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALO
1			APACHENLVKVGGYILGEFGNLIAGDPRSSPLIOFHLLHSKFHI.
1			CSVPTRALLLSTYIKFVNLFPEVKPTTODVLRSDSOLRNADVEL
			QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
.			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLC
]			LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
; !		ļ	RFVCKNNGVLFENQLLQIGLKSEFRONLGRMFIFYGNKTSTOFI.
] ]		ł	NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAOVOOVVNIECVSD
, 1			FTEAPVLNIQFRYGGTFQNVSVOLPITLNKFFQPTEMASODERO
1 1			RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLF-VDP
			NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
5849	3505	·	SQRLCELLSAQF
3049	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
1		ľ	P*DPCMSLSPPCFTEEDRFSLEALOTIHKOMDDDKDGGIEVERS
[ [	1	ł	DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
	ļ	i	TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMT
1 1		j	SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVST
j ·		1	VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEOSLMDLOER
}		. 1	LBKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE
[	1	!	CELSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLO
L			LTHEVEVQYYNIKRQNAEMQLAIAKDEAEKIKKKRSTVFGTLHV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding		1
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
İ		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
į	sequence	1	\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
1		[	IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
	İ		PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPOPORAOLA
1	İ		PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNBEE
ļ	<u> </u>		
1	<b>!</b>		EEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
5050			IIS/DERYQEMRCP+RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
1	i		LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
j	]	!	SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
1	<b>,</b>	Į.	EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
			QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
	1		QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
1	1	[	DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
i	1	I	RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
1	1	l	NSINWGRLLPOVVYHASAYLDLVSOGFISFGSPVDVCIPTGNFG
1		I	NILAAVYAKMMGIPIRKFICASNONHVWTDFIKTG\HYDLRGKE
1		1	
1	İ	l	N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
1		İ	QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
1	i	1	PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
)	1	1	NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
L			VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAIAAAEEPAGSPSVMTRAGDHNRQ
i	1	Į.	RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
	İ	1	GNSLLLTAVYGLVVAGSVLVLGAI IGDWVDKNARLKVAQTSLVV
1		1	QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
1	ł		ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
t	Į.		LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
1	1	ļ.	PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
ì	l	i	ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
1	Į.	l	LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
1	•	1	LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	
3032	1 -	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
ł	ł.	i	SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
	İ	į.	SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFFITSGPG/WFRQ
1	1	1	YYFFISGRH+VLFTESDFYYVAMDFGGHGL9SHYSPGVPYYLQT
ŀ	1	I	FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
L		<u></u>	ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
1			PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FP1FRP
	1	l	LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
1	1	1	GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
1			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
	1		SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIOEEGPDT
1		1	GWEREKRNPAEMGNPORWASPIHTPPLGPEILRAMPEALRAMPE
	1	l	
1	ł	ł	ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
ESEA		<u> </u>	LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
			LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
1	1	i	RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
	1	[	GAETIKDLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH
i	[	]	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
		į.	RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
1		1	LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
			FISLTHHVLSOSOSPLSSNCWICLSTHTO*FTALPADLLTWTOS
	i	1	
I		{	NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
1	ł	f	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
1			LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
ı	[		KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
Γ.	L	<u>t</u>	NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

SEC	Predicted	Predicted end	
ID	beginning	nucleotide	The state of the s
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
,	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Watrontonhan Variance
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
ı			PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
- !	1		ILPPNQTILISVEASISSSPIRNKWALHLITLTGLGITAALGT
	}		GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
	i	1	LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
ſ	1		RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
1			CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
		1	SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
1	Ĭ		FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
			IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
1			VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
1			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
j	1		LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
	<u> </u>		SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
1	1 1		VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
	1		PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
1			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
ı			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
1	1		NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
1			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTOPGSTPPISTMDD
5858	<del> </del>		LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
3030	355	1419	PPHQPAAASTSXHQQQQPPPPPPODSSKPVVAQGPGPAPGVGSAD
1			PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1	1		PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKGGPGGPKGGKMP
1	j		GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGROHHPPYHOOUUO
	i l		GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTOPCPEC
1	! :		LLGIYLLISRRMNSRRLFAKIWENOEKFLSTKAKDSEFIKI.EGD
ł	] }		ALA*NCPKFELG*YTP*GGROLPSSLFPTHACLPLSCSVIFGDP
	ļ į		MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
5859	307	1503	FAS
1		1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
1			NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
1	J		RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREYGSSQSFVT
İ	]		EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
	i		HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
4 1	1	1	VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
	!	i	YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ
	i	İ	SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT YOGMLKILFMWELFOLVWWYPAYHOAN AND THE TOTAL TOT
<u> </u>		}	YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ HGKNF
5860	2956	1270	
j l	1		TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
!!	. ]		SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI
1 1	Į.		TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
	1		PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
			NETATIISQYKLPPTRFARGRRITCVVKHPALEKDIRYSFILDI
			QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
	}	J	QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
ì	·	1	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
ŀ	1	1	PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIP
. 1		ļ	CYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV
1	Į.	i	KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
		1:	KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
1	j	1	SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC
- 1			TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
		<b>!</b> 1	LE+RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
	<del></del>	<del></del>	TODOURT OT STANKE ALLYGCH

SEQ	Producted	Decad about and	T 3
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	i '	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
l	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
l		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5862	1055		A
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
İ			PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
1			DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
			RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
1	<u> </u>		GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHĶI
	1		RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
1	}		LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
			ALASARRSSSVSLAVNDELTRCVLV+SVASAPVSRPFPSGSSGS
L			PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN
1			VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
	ĺ		TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
1			ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
ł	]		GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
ł			PICROPYSYDFPEDVAPALGTSFSHMLGATNPTOKTKESLGRKI
i			QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFEI
1			NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN
Ī			GTGTNTYAALNSVYLMMNNQMRLLGMETMAW\QEIRHAIILL\T
1			DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
l			DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI
1	i .		CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
į.			AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
			KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM
1			\EANLGFLRETFKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N
1			GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT
ŀ			D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
l			SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
ł	ļ		Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
L			EWATLRTL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
ļ			KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
ļ	j j		KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
			HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
			MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
ŀ			SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL
			GSFSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
J	]		LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
1			ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
l			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
	[		/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
Ì			VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP
1			CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
i			GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
			GGRGWVCAPPLNGPQCCCFS1KPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
1			KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
1			LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED
i .		•	DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPO
Į i			QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
[			KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
[			RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV
	•		AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
			CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTONRM
			TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
İ			NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
			RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD
			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
			PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
			KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	I=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	N=Truntophan V=Truncing,
j	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
Ŀ	sequence		\=possible nucleotide insertion)
		<del> </del>	NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR
- 1			TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
į.		ſ	AGSDVSKQAADMILLDDNFASIVTGVEEGRLIFDNLKKSIAYTL
1			TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
ſ			EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
	ł	1	YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
	1	Ţ	VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
į	ł	į.	GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
L	1		YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
1		1	GPVKTLTRKKNKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
			DPSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
	i		ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
1	1	1	WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
1	į	j	GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
ł	Ì	1	TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
1		1	ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
1			ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
Ĭ	i		PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
		<u>L</u> .	ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
	İ	ĺ	AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
i	ŀ		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSTILAN
	ļ		LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFC
1 .			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAOLOMLESNED
F-60-60			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAONL/CVTNAMREDLADIWYID
1			AVTVYDKPASFFKETPLDLOHRLFMKLGSMHSPFRARSEDEDDV
i			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV*T\MTLDGHNLPSLVCVITGKGPLRKYYSRI.THOKHFOH
1 1			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1 1			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAOLOMLESNED
5870	2122		DPAGKLNQFRKNLRESQQLRWDESWVOTVLPLVMDT
30,0	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
1 1	i		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEDEDDV
1 1	1		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
	ì		LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLTHOKHFOH
	. 1		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPWKVVDMFC
l l	ŀ		CCLPVCAVNFKCLHELVKHEENGLVFBDSEELAAQLQMLFSNFP
5871	3		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
	,	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
ł i	1	1	VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
j ,	1	i	LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
1	3		
	I		CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
1			KCMRGILYCYMRQADKVQQFKODPRPTTCLHSVFNVHTGDELLS
		·	KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLOIIYNTDEVSFIONLUF
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKPO
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNOTLCSLLDPRSP
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*\SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSOTLDKVVRKLKGKYGFKP
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSYGLGKRQ L*KOFNGFNLFGNGGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMYDDG
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVRYYYVDADFURYF
		1	KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGOALYIIAKLLADELISPKDI
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLUF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNROTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESORLOV
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPOOELVKAYLOLGIMEKIGLSGR
			KCMRGILYCYMRQADKUQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*\SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALLAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSODVFLLID
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*\SGSTELHSSYGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGFLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKNHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEOLDFLRISDTEELPEFKS
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*\SGSTELHSSYGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGFLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peotide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	•	S=Serine, T=Threonine, V=Valine,
1	5	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b>!</b>	sequence		\=possible nucleotide insertion)
l			AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
	1	i .	HEEEVISNPLSPRVIQNIIYYKCNTHCEREAVIQQELVIHIGWI
			ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
	1		SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
1	t		LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
i	1	ĺ	PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
]	1	}	KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
į.	i	i	EVKPNNDDPCLIS
5872	68		
3672	60	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
1		İ	NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGEKVLGDK
I	1		GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
1	1	1	TAPGVLSTANAGPTINGSQFFICTAKTEDG*QHVVFGKVKDGMS
L		L	IVEALERSGSRNGKTSKKITAANCGQL
5873	2240	506	RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR
1			HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
I	1	1	GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS
1	1		YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPOCLCP
I			SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH
1	ł	ĺ	IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC
i .	ì	i	KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
1		•	KKAKIKNVTPEPTRTPTPKVNLOPFNYEEIVSRGGNSHGG\KKG
1	1	1	
l l	ļ		NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
	1	ļ	FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
		}	EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
ļ	j		PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
J	1		DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
	<u></u>		GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
i		į	AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD
	1		VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
	į.		SYFRKECGROLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW
1	1	1	EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\
1		Į.	SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
	İ		. KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
1	1	j	QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS
İ	İ		FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET
İ	1		ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
1 .	1	1	NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC
1	1		NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGOTFSLAS
1			
I		l	SFROEKIL*AVGLODIAPSPAAFPNFEDSTLFGREYIDHLKAWL
1	1	I	VSSGCPLQVKKAEPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP
j	I .	[	QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMORMSENLRGADOKPTSADCAVRAMLYSRAV
i	1		
1			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIIMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNI\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIIMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNI\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HBQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGBA\AEGDL\ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGDDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKSVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESFEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDDDDGGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDLSEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPPG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTINELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGGLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS
5875	296	1848	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of	Predicted end nucleotide location corresponding to first	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Isoleucine
NO:	nucleotide location corresponding to first amino acid	location corresponding to first	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Isoleucine
	location corresponding to first amino acid	corresponding to first	H=Histidine, I=Isoleucine, K-Lucine,
	corresponding to first amino acid	to first	n=nistidine, I=Isoleucine K-lagino
	to first		
	amino acid	lamino anid	D=DeuCine, M=Methionine N-Asparagine
		amino acid residue of	P=Proline, Q=Glutamine R=Argining
		amino acid	S=Serine, T=Threonine, V-Valine
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	seduciice	Couon, /=possible nucleofide deletion
		<del> </del>	\=possible nucleotide insertion)
1 1		]	GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
3 1		1	I NGHEEV VACANDGOTYIIDHNRTVVRFOVDENTDARGAGI VA GE
1 1			EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETXP\ST
1		1	TACCESWAWILTTSL*LVPCFTKRSTIOTSHHEUT DOACRIDDO
5876	1122	224	WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ
1	· <del>-</del>	***	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPIPQYEV
1 1		İ	NEXT EILHHLSERNRVRDRDVYLVIEDLKOKASEVESER EVILO
1 1			DELMESVNFSPANLSSTGSRYLNALVDSAVALETKOTCLACETO
1 1			AVADLISDLERTKSKSEEIKIELEKLEKNI.TATIJA EVOLODOV
1 1		•	KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
]			SARGO LOARS VPIOSLVALIRENWPRIKOOTIDIK V KVI POVI D
5877	2030	1907	LMP\NPSHCSK*RIEEAK\RELA\SIEAELTRRVS\MMEL
1		2307	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
			LSRELIEMLAISRNOKLLQAGEENQVLELLIHRDGEFQELMKLA
1			LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
1			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
			PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
5878	950	2113	CPCSTVS/NGSQMTCR*INIILILQKSVCEL
1			GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
!	Ī		RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP
j			ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS
• 1			FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
1			LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
	1		PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
1			KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
			GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
5879	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
}			GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
- 1	1		AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTPALLEIVHCLIGIV
	1		PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
	1		EITRYSPYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
· ·			AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
1			YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
5880			NNKNKOTCEISMIAMETKI
3080	1138	1324	SLWCLVAGGLGLGPSSONPLQRAGILARPREARGTFSALTACSA
1		j	SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
- 1			*ARRIGRESS/WLSQPOHEREKEVVLLRRSMAFGFDADAACDUT
1		ł	CRSLANETHQLRRTLTATAHMCOHLAKCI.DEPOUAOPARICEPOP
1	j	ļ	DOSERT DGHTS VQSVIEKLOEENRIJKOKUTHUEDI MAVKODUNI
j			ASKLETVKGLHAQLRGLOIPHEPELMRKETSPINDOLEPVINDO
ŀ	1		ASVAQELAASKTARDAALERVOMLEOOTI.AVVDDPMGEDADDED 1
i	į		AUSKIQELEEKVASLLHOVSWRODSREPDAGPTHAGGETTAVVIA
1	1		ADMIEDRY PEGNEPGTGSOOPEPPAEGGHPGAAOPGOGDI OCDII
5881			CEQCESDEQGEELLRHVAECCO
2001	26	441	GGIHPSPTEAPRAOHLTMDCTW2TLFLVAAATCTHAOVOLLOGO
ļ		1	SEVKKPGASVMVSCYVSGYTLTKLSMHWVROAPGYGLD+MCDED
i		1	LQUVETI YPQKFQGRVSMTEETSTETTO/AYLELSSI RSEDTAV
5882	2407		HHCATOTV
3002	2407	2216	SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE
j j	1	1 3	KIRRD*QLPEAGGPGLOEPLOLGELDI7SDEFTI.DEVDG\vmrp
l		1 1	HISKQVELELQQIEOKSIRDYIOESENTASI, UNIQUEA CONTRED
1	ļ	1 1	MEQMLGAFQSDLSSISSEIRTLOFOSCAMNIDI DNDONUOCULO
I	1	ş 1	LVDGLVVPSALVTAILEAPVTEPRFI.EOLOFI.Dakaaaupeoe
- 1	j	1 2	ARGIAACADVRGVLDRLRVKAVTKIRFFILOKTVCFPVDMMNTVA
ı			PQTALLKYRFFYQFLLGNERATAKFTRDFYVFTT CV IVI CVVD
1		1.5	ILGKLMKVQYEEVAEKDDLMGVEDTAKKGFFGKDGI DCDNDIR
		1 -	LUGIRGSVISPTELEAPILVPHTAORGEORVDFFAI FROOUVAL
i	[	] 1	DNSCREYLFICEFFVVSGPAAHDLFHAVMCDTI CMTI VIII DOV
	l_	I	ADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<b></b>	1 1 1		\=possible nucleotide insertion)
	i		PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
i			SINQTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLI
Į	-		NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
j		ĺ	PPFGGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSWK
1		ì	SSVESLSQDVMRSFTNFRNGTSI1QGALTQL1Q\LYHRFHRV\L
5883	2		SQPQLRALPARAELINIHHLMVELKKHKPNF
2003	1 2	1374	EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG
			CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEE
ı			EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
1	Į.		EETRELAGOHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
1			ELRSLREEISLLEHEKESBLKEIEQELHLAQAEIQSLRQAAEDS
1			ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
1			MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALOESNS
	ľ		SLTGQLADLESERTQRATERWLQSQTLSMTSAESOTSEMDFLED
1	1		DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEELOHHROVSEE
1	1		EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL+A
F00.4			LVVISALLNCWNAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
1	1	•	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVPVV
1	ł i		FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLOF
1	į	•	SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVROM
			HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
			IPSTSDTKSDTATGGESAGHATSSQEPSGCSDORPAEDLNTRVE
-	<u> </u>		RLTKKLEERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKOER
1 .	l l		ELTKRMLEERNREKAEDRAARERIKOOIALDRAERAARFAKTKR
l	1		EVEAAKAAALLAKQAEMEVKRESYARERSTVARIOFRLPDGSSF
1	<u>[</u>		TNQFPSDAPLEEARQFAAQTVGNTYGNFS LATMFPRREFTKEDY
			KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASTVHSSSGDTW
	l		TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
l i			IYWFRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
	Í		YLQIDEEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
			VYSSQVLPIQSKGPS
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
j i			GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
1 1			EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQOVAKVVESKNVAL
			PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
( 1			MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
1			KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY
1			DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
1 !	<b>]</b>		PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
1 1	•		D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
<u> </u>			NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
j	İ	ł	RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP
į l	į		PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
	[	1	ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
; I	į	İ	FCIHITN\*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY
1 1	i		VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
	ĺ		AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
	1	I	KUDITUOG TUTOGI NUTI UDDDDDDDUU ODD TOTO
		1	KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
			LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
			ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI
		1	LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
		-	KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
[		j	DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
	I	•	SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFFPF
		i	V

C S	EQ	Predicted		
	מס	beginning	Predicted end	Amino acid segment containing signal peptide
	0:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid R-
1		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- (		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
ļ		residue of	amino acid	Water on han Value
- 1		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
. L		sequence		\=possible nucleotide insertion)
58	88	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
. [				LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
				CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
1		•		GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
				SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1	ļ			PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
1				QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLVF
1	- 1	•	į.	IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
- 1	i			DNELRICARDKEVGNLYDMFHTRNSLHRRAYOHKVGNT IDTMIT
	- 1		1	DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
	- 1		ľ	YSTDPKLKDAREILKQIEYRNLFKYVGETOPTGOIKTKREDYES
	1			LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
	- 1			FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
	ı		}	LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
588	89	1831	731	NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
	- 1		/31	LPAACGRPVTARPRQAPEGRSGRPRDL)PYPPQVFPPRPDRVAI VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
	- 1			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
				FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
	- 1			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
ļ	- 1			SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
1				AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
1	ľ			DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
589	<del>  </del>	1322		LWSKSCEMTGVLDVTL
1 303	" I	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
!				GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
				LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
[	- 1			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1	1			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1	- 1			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
	- 1			AYPHEVVRTRLREEGTKYRSFFOTLSLLVOEEGYGSLYRGLTTH
589	<del>,  </del>	1322		LVRQIP\NTAIMMATYELVVYLLNG
	_	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
	j			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
	1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1	- 1	j		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1				RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
	- 1			KQKLLBYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
				AYPHEVVRTRLREEGTKYRSFFOTLSLLVOEEGYGSLYRGLTTH
589	<u> </u>			LVRQIP\NTAIMMATYELVVYLLNG
303	<b>~</b>	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
1	- 1	1		DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
]	- 1	J	i	TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
			[	AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
ł	- 1	İ	į	CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
ł		ŀ		FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
l	ľ	1		TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
(	- 1	1		DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
ļ				AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG *TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
				PCAIGSWNGSPLPVFEYPWGT
5893	3	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
l .	-	j	. 1	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
İ			i	MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIOFOTTVLSVRKCP
ĺ			ł	DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
		}	Į.	GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
	- 1	1	ľ	
		}		NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
				NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

SEQ Predicted beginning nucleotide nucleotide nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence SEQUENCE PRODUCTION (A=Alanine, C=Cysteine, D=Aspartic A Glutamic Acid, F=Phenylalanine, G=Glutamic Acid, F=Phenylalanine, G=Glutamic, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagin P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletio \possible nucleotide insertion)	cid, E=
NO: nucleotide location corresponding to first amino acid residue of amino acid amino acid sequence coresponded sequence sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid sequence location corresponding to first amino acid sequence location corresponding to first amino acid sequence location deletion sequence location corresponding to first amino acid sequence location per location in sequence location in sequenc	ycine,
location corresponding to first amino acid residue of amino acid amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence (L=Leucine, M=Methionine, N=Asparagin P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletio \possible nucleotide insertion)  LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQ	ycine,
corresponding to first amino acid residue of amino acid sequence to first amino acid sequence to first Lebencine, M=Methionine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, N=Methionine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, N=Methionine, N=Asparagin P=Proline, N=Methionine, N=Asparagin P=Proline, N=Methionine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, Q=Glutamine, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin P=Proline, N=Asparagin N=Asparagin P=Proline, N=Asparagin N=Asparag	
to first amino acid residue of amino acid residue of amino acid sequence sequence to first amino acid sequence to first amino acid sequence sequence to first amino acid sequence to first amino acid sequence to the first amino acid	_
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid sequence Sequenc	e,
residue of amino acid w=Tryptophan, Y=Tyrosine, X=Uhknown, amino acid sequence Codon, /=possible nucleotide deletio (=possible nucleotide insertion)  LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQ	
amino acid sequence Codon, /=possible nucleotide deletio sequence \ -possible nucleotide insertion)  LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQ	
sequence \=\possible nucleotide insertion\} LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQ	*=Stop
LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQ	n,
AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRI	
QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAV	RLYFGPCN
SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALK	DSSNFSVS
FLLKILGLLAVVVAFF\CQLQWS	
5894 174 1673 RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKK	EGLRVVRE
DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEET	
RLRELCQOWLQPETHTKEHILELLVLEQFLIILPKE	
HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKI	
KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVT	
SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSERE	
LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERK	
LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQN	
IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPC	
FSQALLLTHHQRIHSKSHQCNECGKAFSLTSDLI	
EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSE SGLFOHORYHHKDKLA	CGEAFROR
	VAN-25
IN SUBSHIEL TEFFSSEWEFELI LEWINSTRASKIEL	
MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPE	
RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDD	
EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTL	
RO\NCPFLAGETESLADIVLWGALYPLLQDPAYLPE	
FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQ	KQPQPSPA
EGKGLSPIEPEEELATLSEEEIAMAVTAWEKGLES	
NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLS.	
RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEIC	
DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLL	
. TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQ	
NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRL	EEWLGRTL
PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\W	
GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KN	PEQVDLYQ
FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIAT	EYLNYEDG
K\fsksrgvgvfrdm\ahdtgippdisrfyl\lyir	
FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFG	3/YVPEMV
LTPDDQRLLA\HVTLELQIIYIQ\LLEKVRIRDALRS	ILTIS\RH
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNI	AALLSVML
QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAG	QIGTVSP
LFQKLENDQIESLRQRFGGGQAKTSPKPAVVBTVTT	AKPQQIQA
LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLK	KQLAVAEG
KPPEAPKGKKKK	
5896 2967 86 HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFII	QRGIHGE
MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPE	
RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDD:	TNOWLEW
EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTL:	THIDHSLS
RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPE	
FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQI	
EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESI	
NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLS	
RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICI	
DIY\RWFNISFDIFGRTTTPQQ\TKIT\ODIFQQLLI	
TVEQLRCEHCARF\LADRFYEGYCPFCGYEEARGDQ	
NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLI	
PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WG	
GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNI	
FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATI	
K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRI	
FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFG(	
LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSI	
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIX	
OPYMPTVSATIOAQLQLPPPACSILLTNFLCTLPAGE	
LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTT	KPQQIQA

SEQ	Predicted	Predicted end	Amino onid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ſ	to first	amino acid	N=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequeince	Codon, /=possible nucleotide deletion,
<b>—</b>		<del> </del>	\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5897	2967	86	
	1 2557	1	HPSLLCAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
į.	1	ł	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
h	ļ	ļ	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
1	ì		EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
1	Į.	]	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
i	1		FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
İ	1		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEXGLESLPPLRPQQ
1	Í	(	NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
	ł		RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
i			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
	!	[	TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1		ľ	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
j			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVPRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
1			LTPDDODLAN HIMLET OURSION LINGUISTED LINGUIS
1			LTPDDQRLLA\HVTLEIQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1			QPYMPTVSATIQAQLQLPPPACSILLINFLCTLPAGHQIGTVSP
			PEOKLEMBOLESI BORESCOON MECHANINE MENTANDO TON
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKILDLKKQLAVAEG
İ			KPPEAPKGKKKK
5898	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
1			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
i i	·		RQ\NCPFLAGETESLADIVLWGALYPLIQDPAYLPEELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1 1	l		EGKGLSPIEPEEEBLATLSEEBIAMAVTAWEKGLESLPPLRPQQ
1 1	-		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
[ [			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
l i		•	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1 1			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL
1 !	j.		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
j }	•		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEOVDLYO
1 1			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	- 1		K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
	-		FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
ļ i	1		LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
} !	İ	ł	GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
ļ [	<u>.</u>	İ	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
1 1	·		LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1 1	1		LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
F 5000			KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ
· · · · · · · · · · · · · · · · · · ·		1	EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKOIB
j i			QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
	ļ		EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVOKAI
		ļ	PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
F000			TLESRLDLSAKQKMPEIRMALFGANTNRKFFI
5900	64	1409	KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK
[		I	GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
		į	KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
		ł	KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI
l l		İ	LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
	Į.	1	VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA
			LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL

SEO	I B 32 - L . 3	1	
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
1	, ,		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	<del> </del>	<del> </del>	QKAPEEFELLSKSAI\KHEYIEDVGECHOPHDWDWAQS*ISTHG
1	ŀ	l	/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
1	1		
1		ļ	NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
	<u> </u>		NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
Į.	l .	į	KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
1	i	[	SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
1			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
	1		CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
1	l .		REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
į.	1		,
			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
1		1	AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKFYM
	1	1	CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
1			EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
1	1	1	GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
		1	CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
1		1	KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
	l .		QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
j	j	1	
1			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
1	li de la companya de la companya de la companya de la companya de la companya de la companya de la companya de	1	FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
	<u> </u>		HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
1	l	1	IPLXPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
1	l		VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
	1	ł	EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPOPLOGRGLPTT
1			PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
	1	1	GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
	Į.	İ	
1.	i		LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET
1	1		HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
· ·	ŀ	ŀ	KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
1	1	1	RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
ŀ		ĺ	ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
1	ł	Į	HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1	!	1	GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
1	ł	1	LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
1	_		ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
1		I	RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
1			
1	1	I	HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
	1	l	VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL
i	1	1	KEEEEKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKEI
I	i	l	REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ
1			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
<u>L</u>	j		ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP
1	1	1	DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
1	Ī	İ	ONSDGGOKNKPREHIIDCGDIVWSLAFGSSVPEKOSRCVNIEWH
i		1	
l		1	RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
1			TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
I	]	ļ	SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
1	1	l .	WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
1			SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
1			WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
1	l .	l	KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
1			LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
1	l		
I	1		*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
1	1		QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
l	1	)	REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI
			FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*
<u> </u>	<u> </u>		YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

SEO	Predicted	1 War of and 5	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
} 100:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence	ł	\=possible nucleotide insertion)
			IRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
}	1		EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR
į.	i		FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
			PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
1		2000	DCFUCTDANDENDO LOTANDANO COMO DE TOTANDO COMO DE COMO
1	4		PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1	İ		DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
1			A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
İ			HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
			DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
j			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
1			KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
1	1	٠	QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
ı	]		TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
1	1		SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
1 .	<u> </u>		ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
	1 1		DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
	i i		VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
L			SGIGSMQNEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
f	1		KATSKVPSAPHFVHPNDHANREAELKKKWVBEMREKQQAAREQE
1	i I		RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK
ļ	i l		AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
1			KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
1	l j		MPCCVDVDOACECLL VCVA CECAENT MADE CONCERNOS
1	l 1		NRCSVPVDQASESLLKSKACFGAENLMRVLGNYCRLGEVRTHIR
İ			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
1			IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
Į	l l		NLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK
į.	l i		AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
	ŀ		EÇANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
1	1		ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
	1		SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
5908	247		SDSMMSALDLSGNADDGVGD
3500	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
	1		HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
1	l l		GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
1			VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
<b></b>			VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
	i. I		SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
	[		CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
]			STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
1 1			ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
[ ]			SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
	1		DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
			IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
			GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
1			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
i 1	i i		SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM
ļ 1	1	· .	VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE
<b>j</b>			DCEADACTVEEDI BERATTOONA ONDOO
[ 1	1	ł	DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG
[	1	l	EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
	1		IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
[ ]	}		HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
j i	•		SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
			EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
		•	SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT
l l	į		IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWORPTAAATPDGMR
			RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

Degiming   No: uncleoted   location   corresponding   control   control   control   corresponding   control   cont	SEQ	Predicted	Predicted end	I Design
Cocation   Corresponding		1		Amino acid segment containing signal peptide .
Corresponding   Coffree   Contract   Contr	NO:	nucleotide		Glutamic Acid. F=Phenylalanine G-Glycine
L-Leucine, M-Methionine, N-Apparagine, to first amino acid residue of amino acid senion acid senion acid senion acid senion acid senion acid senion acid senion acid senion acid sequence   S-Serine, T-Threonine, V-Waline, M-TypCoplan, X-Unknown, *-Stop Codon, /-possible mucleotide deletion,	ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Sequence   P-Prolime, Q-Glutamine, R-Arginine,   serion acid   residue of   serion, T-Firenoine, V-Valine,   sequence   Sequence	1		to first	L-Leucine, M-Methionine, N-Asparagine,
Serime, 7=Threonine, V=Valime,   Seridue of amino acid sequence   Serime, 7=Threonine, V=Valime,   Sequence	1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
### ### ### ### ### ### ### ### ### ##				S=Serine, T=Threonine, V=Valine,
sequence    Sequence			1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
GGGGGGEARESGGETDJREGGIAFPORGTITLLIQS PAVERI TREPETYLAMSADRIVETS STOLEMBILDVRENDARIPETS THE PETPITLAMSADRIVETS CLIEMBILDVRENDARIPETS THE PETPIT IN PERPETYLAMSADRIVETS CLIEMBILDVRENDARIPETS THE PETPIT IN PERPETYLAMS CONTINUES AND THE PETPIT IN PERPETABLE PROMESTIC CONTINUES AND THE PETPIT IN PERPETABLE PROMESTIC CONTINUES AND THE PETPIT IN PETPIT		}	sequence	Codon, /=possible nucleotide deletion,
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IDPRIPLOMORIPHILITHONILORISYSAGRASEVSINIKGASL LARPGHSLUAM RISOHHURSH FLANDRUNT FOR IT FEMLLOR ROPSIARNHTHERIHITETSONIGLEKSCDADUVILLISIFEE EIMSVUPLOARHROYS FENCSCSSEPONSPOLGRASHARPEY YRRDFEAKLRIFYEKLEAKGPCGGFOKTKLITERDHILGETPRO UWAYSRRELGYRREYYKLEAKGPCGGFOKTKLITERDHILGETPRO UWAYSRRELGYREYRKLEAKGPCGGFOKTKLITERDHILGETPRO UWAYSRRELGYREYREVGOVTERELKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVCCOTERLIKSGCANTGOTEKNEK EYTERWVENVERGEVVERGEVGTSUPTERGEGGANTGOTEKNEK EYTERMVENVERGEVCOTERLIKSGCANTGOTEKNEK EYTERMVENVERGEVGCOTERLIKSGCANTGOTEKNEK EYTERMVENVERGEVGCOTERLIKSGCANTGOTEKNEK EYTERMVENVERGEVGEVGTOTEKNEK EYTERMVENVERGEVGEVGTOTEKNEK EYTERMVENVERGEVGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK EYTERMVENVERGEVGTOTEKNEK ETTERMVENVERGEVGTOTEKNEK ENGLELLINGVILLIKAPOLIKOTETTSTYPT  109 591 109 595 591 109 595 591 109 595 591 109 595 591 109 591 109 595 591 591 109 595 591 591 591 591 591 591 591 591 59	1	1	}	TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYQH
LARPOHSLVAATRSOHCHESUPLAYMOKIVAFLROPNITEMILOGE ROPSIARNITHERIHNYITERSINGLEKISCHULVILLISLEE EIMSYVPIQAARHOGYSFSPRGSPGSSPONSPGIGRASARAPSP YRRDFAKLRINFYRKLEARGFGGOPGKIKITEBULLROFTPRO VANYSRELQRRKLYVTFYGEGGIDYSGPSEFFFPLGSGLFAP YYGLFEYSANDTYTVQISTAGFVENHEWSGRIGHADLAND HOYLIDAFTTIAPFYKALLARGFVENHEWSGRIGHADLAND HOYLIDAFTTIAPFYKALLARGFVENHEWSGRIGHADLAND HOYLIDAFTTIAPFYKALLARGFVENHEWSGRIGHADLAND HOYLIDAFTTIAPFYKALLARGFVENHEWSGRIGHADLAND HOYLIDAFTTIAPFYKALLARGFVENHEWSGLFANDTOTTERIK EYIRRWINGRVENGUVGOTEALUNGDYFEVUSRIJSVEDARRELE LUAGTAELUNDARNINTTYKGCYHDGHLYDAVERTONTER GREALLOFVTGTSSVEYBEGFAAPPREPMIKEKLYAVERTSTPOTTE LEPRGAITCLOPDUDLPTYSTGCYHDGHLYAVERTSTPOTTE LEPRGAITCLOPDUDLPTYSTGCYHDGHLYAVERTSTPOTTE LEPRGAITCLOPDUDLPTYSTGCYHDGHLYAVERTSTPOTTE LEPRGAITCLOPDUDLPTYSTGCYHDGHLYAVERTSTPOTTE LEPRGAITCLUARGFSGKARALYTHIRDTDRAWHGAVERTSTPOTTEL REGALLYGSTISSAJCSTLLAHAGGSLAVERTYSTAVC FULLMUWWEGFGGKARALYTHIRDTDRAWHGAVITYKWYTLEG LITRKKLQAR*GWARTHANTGGITSGROCCCCPCCPEPH LITRKKLQAR*GWARTHANTGGITSGROCCCCPCCPEH LILTEFLHYTVITHYYTHRYDAVERTSTSPDLDLALKALRIM ATHMGCCTH LILTEFLHYTVITHYYTHRYDAVERTSSPDDLDLALKALRIM ATHMGCCTH CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS CCHRRGGAAFKYRFTPUVOPBORPTCOKHMRGGVSLLSPELGCS SOOYAHPACALARACHATATYTCHAND	1	į.		
ROPSIARNHTIREKIHYIRTEGONIGLEKISCOADUVILLISLEE ELMSYVELQAARHGYSER PEGSCSSENONSEGLORASARAPE ELMSYVELQAARHGYSER PEGSCSSENONSEGLORASARAPE YRRDFEAKLRNFYRKLEAKGFGOGPOKIKLI IRRDHLIKGFFRO WAYSIRELORIKLLYTFYEGEGLOTYGGFEVFLAGGLIPP YGLE FYSANDTYTVOLISMSAFVENHLEWERFEGGILJALI HQYLDAPFTI, PEYKALL, KIPC, DI, LSQUEBEHOSLOW MKDNNITDILDLTFTVMEEVFGCVTEREKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTEALWEGFYEVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTEALWEGFYEVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTEALWEGFYEVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTEALWEGFYEVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTEALWEGFYEVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTESSEPVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTESSEPVEKSGGANTGVTERNKK EYIRMYKWEVEGWUCGTESSEPVEKSGGANTGVTERNKK EYIRMYKWEVEGSVEYEGGSPAPWEWRALDERITTSYANC GRALLOPTGINGTSVEYEGFAPWEWRALDERITTSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC FILLMINGSAPTVVSULCCFGIMIPRSLULVENTITSYANC CHIRRGGAAFTYKETTVVGPEOGRETURGCTSSPLICSTNOTHT AMPUNICATION AM	1	į.	i ·	
EMSYVPLQARPHGYSTSPRCSPCSSPQNSPGLQRASARAPSP YRRDFAKLINFYNKLEASFGQGGCMCKILTBULLEGTPRO VMAYSRELQRNKLYVTFYGESGLDYSGPSREFFFLLSGLAYDA VMAYSRELQRNKLYVTFYGESGLDYSGPSREFFFLLSGLAYDA YGGLFVSANDTYTVQISTRASFVENHLEWFRSGKILG\LALI\ HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDWERFSGKILG\LALI\ HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDWERFSGKILG\LALI\ HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDWERFSGKILG\LALI\ HQYLLDAFFT\RPFYKALL\RLPC\GYTGFELKSGANTOVTEKNKK EYIRMWKWRGGVVGQTEALVRGYFWVDSRLVSVPDARELG LVIAGTAEZIDLDWGRNTTSKGYHGGHLVAVEVFBAVERFINDE REVIAGTAEZIDLDWGRNTTSKGYHGGHLVAVEVFBAVERFINDE REVIAGTAEZIDLDWGRTTGTSKUPYEGFAAPPWERPMAVERFINDE REVIAGTAEZIDLAFFTYDALLAGSILLFYNWADVERFINDE REVIAGTAEZIDLAGGTAFAYANGTHAMAY THE TOP THE THE THE THE THE THE THE THE THE THE	1		[	
YRRDFEAKLENNFYRLEAKOFGOGERIKHLITRIDHLLEGTING WANSTRELGRIKLLVTPVGEBGLIDYSGERFFFILLSGLIND WANSTRELGRIKLLVTPVGEBGLIDYSGERFFFILLSGLIND HQYLLDAFF\RPPYKALLKILE\CD\LYBESGLINDELGERIG\LALI HQYLLDAFF\RPPYKALLKILE\CD\LYBESGLINDELGERIG\LALI HQYLLDAFF\RPPYKALLKILE\CD\LYBESGLINDELGERIG\LALI BORLILG\tag{Price} ALICIPATION CONTROL PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PLUS PROPERTY CONTROL PROPERTY C	1			ROPSLAKNHTLREKTHYTRTEGNHGLEKLSCDADLVILLSLFEE
WAYSREELORBKLYVTFVGEEGLDYSGPSREFFELLSGGLIND   YUGLEYSBADTYTVOLSPMSAFURMERPSGRILG LALI    HOYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLUSEH\GSCGATQUTEKNEK   MXDNNITOLLDLTFYVEEVFGQVTEGLEKSGGATQUTEKNEK   EYIERMVKWRVERGVCQTEALURGPYEVUDGELUSVPDARELG   LUJAGTAELOLDAWBANTEVERGSYDDGINFPHANEKEVERNE   GREALOFVTGTSSVPYEGFAAPPEPMGLRERIP*KKMCKITS   ORLELOFVTGTSSVPYEGFAAPPEPMGLRERIP*KKMCKITS   ORLELOFVTGTSSVPYEGFAAPPEPMGLRERIP*KKMCKITS   ORLELAGFYTGLALTSILTILALGSIAIFLERAYLYKMTGTFSOFFT   AAQLIRALGFYTGLALTSILTILALGSIAIFLERAYLYKMTGTFSOFFT   AAQLIRALGFYTGLALTSILTILALGSIAIFLERAYLYKMTGTFSOFFT   AAQLIRALGFYTGLALTSILTILALGSIAIFLERAYLYKMTGTFSOFFT   AAQLIRALGFYTGLATTSILTILALGSIAIFLERAYLYKMTGTFSOFFT   AAQLIRALGFYTGLALTSILTILALGSIAIFLERAYLYKMTGTFTTSTAVC   FILLMLWWEGFGGKEAVLRTLRDTPMWATTGCCCCPCCCPRL   LLITKKLUGH, CWALSANTSILTILALGSIAIFLERAYLYKMTGTOFTT   REACLYGSTLSSA/CSTLLALMTIGIISRGARHLHGONGAKF   ALFOYLLILTALOPSISTS**LANGGIACSPYSSSTRSQWMNCH   LLILETFLHTVLTRMYYRRKDIKVGYETFSSPDLDLKRALRRM   AAFWOLGCH    KAFGCH    SP11	ł	1		VPDDEEAVI DNEVDVI EAVGEGOGDGVIVI I I DDDW I DOWN
HQYLLDAPT\RPFYRALL\RLPC\D\L\S\SLEYLDEEH\B\SL\G\ HQYLLDAPT\RPFYRA\L\R\C\S\C\S\C\S\C\S\C\S\C\S\C\S\C\S\C\S\C	Ī			VMAVSBKELOBNKI.VVTEVGEEGI.DVGGBGBBBBBI I COEL DVD
HOYLLDAFFT\RFT\RFT\RFT\RFT\RFT\RFT\RFT\RFT\RFT\			1	YYGLFEYSANDTYTYOT SPMSAFVENHI, EWEDESCRIT CALALI
MKDNNITDILDITTYNBEUTGGUTEREIKSGGANTGYTTEKNIKK ETIERMYKRVERGEVOGTEALVAGTYEVUGETUSPODARELE LUIAGTAEIDINDKRNTEYRGGTHOGHLVIRWFRAAVERFINE GRERILDFVTGTSSLYPEGFAAPMERILFEP,FYEKWGKITS GRERILDFVTGTASLYPEGFAAPMERILFEP,FYEKWGKITS LEPPRG\HTCLOPHOLDFYTS PRITMILYEK\LITA\VEETSTFGT   LEPPRG\HTCLOPHOLDFYTS PRITMILYEK\LITA\VEETSTFGT   AQLIRALGFVEHALTSILTILLAGSIAIFEDAYVIX/RTICP   IKRRILLMKSSAPTVVSVLCCFGIMIPRSLVLVEMTITESTYAVC   FILMINWSEGGGEAVAURTLERITEMWHTGPCCCCCPCCRL   LLITKKLQ\R*CKALSNTPS\**I**PWWATGPSSTTASMTQOTFL   LLILTFIHTVITRWYKRKDIKVGVESTSSSPIDJENLKKRGNIKAKRM   AATHMGCCTH	Ì		ļ	HOYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDKEEHOGLOW
BEYLEMWKMRVERGVVQOTEALVRGPYVEVDARELUS   LVIAGTAEIDLINDWRANTEYRGGYHDUNGRYKAVERFINE   GRERLLGFUTGTTSVPYEGFAAPBWEPMGLRFFLP*KKWGKTTS   LPPRG*  HTCLQDPWDLPTVSRTTMLYKLLITA\VEPTSTPGT   LPPRG*  HTCLQDPWDLPTVSRTTMLYKLLITA\VEPTSTPGT   AAQLLRALGFVELALTSTLITLLGISIALTFEDAVYLYKNTLCG-   IRRRTLLMKSSAPTVVSVLCCFGHIR JSLVLVEMTITSTYAVC   FILLMLWWESFGGKEAVLRTLRDTPMWHTDSPCCCCPCCPCL   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTPS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGGTLSPPYSKTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGTLSPPSSTSTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGTLSPPSSTSTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGTLSPPSSTSTTSGYMCH-   LLTRKKLQ\R*CWALSHTSS\R*TPSVLANGGTLSVLANGGTLSPPLOC-   RAGHVQAGCLEL/RVVIHDEPPKVLGLQA-   AMTMRGCTH-   GEHLVQAGCLEL/RVVIHDEPPKVLGLQA-   SGYSHBFDGDBEFYVDLERKETWQLFPLFRFRFFPDFALTN-   LAVLKHHAIN\XIKRSSTATNEVPSVTYGSSPVLAQSYGN-   SGQVSHBFDGDBEFYVDLERKETWQLFPLFRFRFFPDFALTN-   CLVDNIFPPVVNITNLSXGHSVTGQUSETRPSSFKSDHFILQDQ-   SGSQSHBFDGDBEFYVDLERKETWQLFPLFRFRFFPDFALT-   CLVDNIFPPVVNITNLSXGHSVTGQUSETRPSSFKSDHFILQDG-   SGSCXSHBFDGTVFGTSSTADTSVSTADTPSSFBJGHTLGATVAGGTL-   CLVDNIFPPVVNITNLSXGHSVTGQUSETRSSFKSDHFILQDG-   SGSCXSHBFDGTVFGTSSTADTSVSTADTPSSFBJGHTLGATVAGGTL-   CLVDNIFPPVVNITNLSXGHSVTGQUSETRSSFKSDHFILQDG-   DSEKCSYSQSSVKRQALVXSTTSTTGSLANGKSKGTNSTST-   A6				MKDNNITDILDLTFTVNEEVFGOVTERELKSGGANTOVTEKNKK
SPI1   SPI2	l			EYIERMVKWRVERGVVCOTEALVRGFYEVVDSRLVSVFDARELE
ORLRILOFVIGTSSVPYRGFAAPPWEPMGLREFP+KKMGKITS   EPPRG\  HTCLQDPWIGPTVSPRTTMYKLLITA\VESTTFOT   AVACHARMEPGETQIKLDPRYTADILEVILTTNYGTFSKCFSGPPT    AAACHARJGPVELAITS'IITLALGS'IAITHJEDAVYLYKNTICFP   IKRRILIMKSSAPTVVSVLCCFGIMIPRSLVLVENTITSFYANC   FILIMLWMEGFGGKEAVLERTLRDTENMVHTISPCCCCEPCCERL   LITEKKUQR'CMALSHTPS'* R**P** bWANCFSSTARMTQOTFL   RGAGLYGSTLSSA/CSTLIALINTIG'IISRQARLHGEONMGAKF   ALFQVILLITALOPSISTSVLANGGO'JACSPPYSSKTRSQVINCH   LILIETFIMTVLTRMYYRRKDIKVGVETFSSPIDLINLKALRNM   AMTHMGCCTH     AMTHMGCCTH     S911	1			LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE
LPRG\HTCLOPDMDLPTVSPRTPMLYEK\LLTA\VEETSTFOT		1		QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRFLP*KKWGKITS
S910   1526   WAEFAMEPGRTOIKLDPRYTADLLEVILKTBYGEPSCESOPT   AAQLLRAIGPUELALISITILLAKSIAPTEMPYLYKNTLOG   IKRRILLMKSSAPTVVSVLCCFGLMIPRSLULVEMTITSFYAVC   FYLLMLVWWEGFGKEAVLRTIRDTPMWVHTGPCCCCCPCRL   LITRKKLQ\R*-CWALSNTPS*1**R**PWWACPSSPTASMTQQTFL   RGAGLYGSTLSSA/CSTLLANTGIISRQARLHILGEOMMGKF   ALFQVULLITLALQPSIFSVLANGGIGCSPPYSSKTRSQVMRCH   LILLETFIMTVITRMYYRRKDIKVGYETFSSPDLDINLKALRMM   AMTMGCCTH   CCHRRGGAAFKYRPTPVVGPEQRPTGGKHMGGVSLLSPRLECS   GTISAHCNLELPSSSNSPAPAS*LAGITGVCHHAQLIFVFLUET   GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA   GTISAHCNLELPSSSNSPAPAS*LAGITGVCHHAQLIFVFLUET   GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA   SGOYSHBPGGDEPTYDLERKETVAGLPFFERERPPOPALTM   IAVLKHMINIVIKRSSTAATHEVVTVPSKSVPTLGQPNTLI   CLVDNIFPPVVNITWLSNCHSYTEGVSTRSSFKSDHFLQQD   VTSDSFPFF**DL*TAKVEGLGAMFEPLLKMGAETPTL   CLVDNIFPPVVNITWLSNCHSYTEGVSTRSSSFKSDHFLQQD   VTSDSFPFF**DL*TAKVEGLGAMFEPLLKMGAETPTL   CLVDNIFPPVVNITWLSNCHSYTEGVSTRSSSFKSDHFLQQD   VTSDSFPFF**DL*TAKVEGLGAMFEPLLKMGAETPTL   CLVDNIFPPVVNITWLSNCHSYTTOGPNTLI   CLVDNIFPPVVNITWLSNCHSYLDVLUEEDBELENEACAVLGGS   DSEKCSYSQSVKRQALVACSTCTPEGESPHGICLACSYECHGS   KKLFELTYRKNFERCDGGNSKFKINLECKLLPPAKAVNGGNKYNADN   FPGLYCLCKRYPDPPEDELTPDEMIQCVVCEDMFHGRHLGAIPPE   SGDPOENVCQACMKRCSFLMYAAQLAVTRIST\GMMDNCGTLM   E*/DDOENVCACMKRCSFLMYAAQLAVTRIST\GMMDNCGTLM   E*/DDOENVCACMKRCSFLMYAAQLAVTRIST\GMMDNCGTLM   AQATORSDPLMDTLSSMRWQQVELIC/GIQ*FED   CAGSSSSDLOTYFKNESLNAESKSGCKLQEKLAKQLIKKDTAT   YPELNMRSKLCTCLOPCMMYGGDLPYLTOFDYTLAYENKGKI   AQATORSDPLMDTLSSMRWQQVELIC/GIQ*FED   SGDPOENVCQACMKRCSFLMYAAQLAVTRIAGHSMCS:GDS   GDDYQIGPYKNILCYDHKTDVMEERRFMTTARGHNSMCS:GDS   GDDYQIGPYKNILCYDHKTDVMEERRFMTTARGHNSMCS:GDS   GDDYQIGPYKNILCYDHKTDVMEERRFMTTARGHNSMCS:GDS   GDSGSDDNIESMERFPDVLGVEAYSPCCOMTKVAPLILHANSE   SGVAVMSGRYTILGGSSMETPDVLGVEAYSPCCOMTKVAPLILHANSE   SGVAVMSGRYTILGGSSMETPDVLGVEAYSPCCOMTKVAPLILHANSE   SGVAVMSGRYTILGGSSMETPDVLGVEAYSPCCOMTKVAPLILHANSE   SGVAVMSGRYTILGGSSMETPDVLGVEAYSPCCOMTKAPLILHANSE   SGVAVMSGRYTILGGSSMETPDVLGVEAYSPCCOMTRAPPPPPCLVPPIS   KARGSGAPLAPH   SGGPOENCAPSCASMOH   PHRILPGLCRPAATS   SGGPCPPPCLVPPPIS   PREDEGESPALP				LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
IRRRILLINKSSAPTVUSULCCEGINIPRSIALIZEMITESPYANC   FILLINLINWEGEGKEAULRITPMINUTINGECCCCPC CRIL   LITRIKLQ\R*CWALSSTP\$* R*R*PMWACPSSPTASMTQQTFL   RGACLYGSTLSSA/CSTLLALWTLGI ISRQARLHLGEOMMGAKF   ALFQULLILITALQPS IFSULANGGQIACSPYSSKTRSCVINCH   LLILETFIMTVLTMYYRRKDIIKVGYETFSPPDLDLINKALRIM   ANTIMISCCTH	2910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSQPPT
FYLLMLWWEGFGKEAVLERTERTEMWITGFCCCCCCCCRL LLITRKLQRR - WALSNTPG* R** PWWAGFSSPTASMTQOTFL RGACLYGSTLSSA/CSTLLALWTLGI ISRQARLHLGEQNMGAKP ALFQVILLITALQPS IFSYLANGGG ILAGSPYSSKTRSQVMRCH LLILETFIMTVITAMYRRKDIIKVGYESFYSSKTRSQVMRCH AMTMRGCCH AMTMRGCCH  5911  109  595  Q.P.LAPCT QGRGLEMRSPKPQS FI IRSSHSGAGLLVKNPSTPVF CCHRRGGAFKYKPTPVVGPPQRPTGQKHMRGGVSLLSPRLECS GTISAHCHALRIPSSSNSPAPAS* LAGITGYCHHAQLIFVFLVET GFHHVQAGLELL/NVVIHLPFKVLGLQA  5912  974  277  MILNRALMIGALALTTVMSPCGGEDTVADHVASYGVNLYQSYGP SGOVYSHEPGDGEPTYVDLERKFRYDQD-PALTN IAVLKHNLINIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRFSSPKSDHFILQDQ VTSPSFPFE***DI** TAKVEQLGAWFEPLLKHMGAEIPTTL  5913  46  1198  QLRMAGAEGAAGRGSELEPVVSLVDVLEEDELEMEACAVLGGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKVNDN PFGLYCLGKRYPYDPEBEIPDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDPQEVVCQACMRGSFLAWAAQLAVTKIST/GMMDNCSTLM E*/DDQEVIKPENGEHDGSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSSEDLOTYKWESLNARSGCKLQBLKARQLIKKNTSK FYDDQEVIKPENGEHDGSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSSEDLOTYKWESLNARSGCKLQBLKARQLIKKNTSK SGDPQEVVCQACMRGGFLAWAAQLAVTKIST/GMMDNCSTLM E*/DDQEVIKPENGEHDGSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSSEDLOTYKWESLNARSGCKLQBLKARQLIKKNTSK SGDPQEVVCQACMRGSFLAWAAQLAVTKIST/GMMDNCSTLM E*/DDQEVIKPENGEHDGSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSSEDLOTYKWESLNARSGCKLQBLKARQLIKKNTSK SGDPQEVVCQACMRGSFLAWAAQLAVTKIST/GMMDNCSTLM E*/DDQEVIKPENGEHDGSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLOTYKWESLNARSGCKLQBLKARQLIKKNTSKINGNI SGRAVAWGRIYILGYHRWESKJCCTQDCMMYQDVLLQTQTVLAYENKGKI AQATORSDPLMDTLSSMNRVQQVELLGQTGVPTKVSSLAG GHDVQIGFYRKNLLCYNHRTDVUVPREADKWSGRVDFYTLASTEDMLVAI/GGRN ENGALSSVETSPRTDSWSVAGLPFTTGHAGTTYKDFVYISG GHDVQIGFYRKNLLCYNHRTDVUVPREADKWSGRVDDFYTLASTEDMLVAI/GGRN ENGALSSVETSPRTDSWSVAGLPFTTGHAGTTYKDFVYISG GHDVQIGFYRKNLLCYNHRTDVUVPREADKWSGRVDDF FRELPGICRPAPS-SLGQCTRRKKAKARGTRTGASDPCCASWDM FRHLPGICRPAATS SGVAVWEGRIYILGYBRATAFSKTVQVYDREADKWSGRVDDFPCT PQEDFFARLEGGPCPFRAPPSPGDFCCPFGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRFLDAPPCPCLVPPII KRILDFGACTAATAGQQCFTGPDCLRS PPGEPGSGLLDSPHPPVSGFFSAVVLLKGGLKPTAATAQQQCTGQQCPCA TVTGAVHRHLMHVAGL				AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
LUTRIKLO, R. CWALLSNITPS * R. * P. PWWACPSS PTASMYOOTFL RGACLYGSTLSS / CSTLALANTG II SROARLHLGEONMGAKF ALFQVLILITALOPS I FSVLANGGQIACS PPYSSKTRSQVNICH LLILETFIMTVITMYYRRKDIIKVGYETFSPPLDINLKALRIM AMTMIGCCTH AMTMIGCCTH  5911  109  595  G.PLAPCT GGKGLEMRSPKPOS FI IRSSHSGAGLLV KNPSTPVF CGHRRGGAFKYKPTPVVGPEQRPTGOKHMRGSVSLLSPRLECS GTISAHCRILPSSSNSPAPAS * LAGITGVCHHAQLIFVFLVET GPHHVGQAGLELL/NVV1HLPRPPKVLGLQA  5912  924  277  MILINKALMIGAIALTTWSPSGDTYADHVASYGVNLYQSYGP SQQYSHEPFOGDEFYYVDLERKETVWQLPLFRRFRFDPOFALTN IAVLKHNILNIVIKRSNSTAATNEVPBSVTFSKSPVTLAGPRTLID CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPSDHFILDIQ VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHMGAEIPTLI OLRMAGREGAAGRGSLEPVVSLUDVLEEBEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLPELYTKRNFRCDCGNSKFKMLECKLLDPDAKWNSGNKYNDN FFGLYCLCKRPYPDPBEEIEJENCVVPGQKGDVREVKVEQNSEP SGDFOEPVCQACMRGSFLANAAQLAVTRIST.CMMDNCGTLM B*/DOGEVIKPENGEHQDSTLKEUDVPGGKDDVREVKVEQNSEP SGDFOEPVCQACMRGSFLANAAQLAVTRIST.CMMDNCGTLM B*/DOGEVIKPENGEHQDSTLKEUDVPGGKDDVREVKVEQNSEP GAGSSSESDLOTVFKWESLNARSKSGCKLQELKARQLIKKNTAT YWPLNMRSKLCTCQDCMMYGDLDVLFTDEYDTVLAYENRGKI AQATOSEDPLMDTLSSNNRVQOLELC/GIQ+FED  5914  960  124  MLGGSELPPEEALFIQVSSNNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVAGLRRFTTGHAGTIYKDFVTISG GHDVQIGPYRKNLLCYDHRTDVWEERRFMTTARGHSNCS:GDS IYSIGGSDDNIESMERFDVLGVBAXSPQCNONTRVAPLILANNS GHDVQIGPYRKNLLCYDHRTDVWEERRFMTTARGHSNCS:GDS IYSIGGSDDNIESMERFDVLGVBAXSPQCNONTRVAPLILANNS SGVAVWEGRIYILGGSWBKTHASTVVQVDPBEADKWSRGVDLP KAIAGGSACPIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRILPGLCRPAATS  5915  1604  703  FPGRFTPPLKIGGSWBKTHASTVVQVDPBEADKWSRGVDLP PASRAEGPVAVVNNGHTEGPAPARSAPKBPPCLPRPLGSPPCPT PQEDFPALGGPCPPRMPPSPGFSAVVVLKGTPPPPPFCLVPPIG KPPPGFSGLLPSPHPPPSGKFRRPLIPAP/PCLPPP PASRAEGPVAVVNNGHTEGPAPARSAPKBPPCLPRPLGSPPCCPT PQEDFPALGBPCDARANAPANVLLKGTPPPPPFCLVPPIG KPPPGFSGLLPSPHPPPSGFFAVVLLKGTPPPPPFCLVPPIG SPRELPGEEPSAHPVHGGLPARRRGPLGROPGPLRVPGGPDLRS PVLOELPGPAGGFPFCL**AAGPAAH  5916  256  633  SPRMWEIWGPHRWESFSLEGEWPSRIPESPSDTKGTSGKGCR TVYGAVHRHINHVAGLIPWULNSQLKPTAATAQDQWTSQQYPDH	]			IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
RGACLYGSTLSSA/CSTLLALMTLGI ISRQARLHLGEONMGARE ALFQVLLILIADQSIFSVLANGGQIACSPPYSSKTRGVENNCH LLILETFLMTVLTRMYYRKDIKVGYETFSSPDLDLNIKALRMM ANTMISCCTH  SP11  109  595  Q-PLAPCTQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CCHRRGGAFKYKPTPVVGPEQRPTGOKHMRGGVSLLSPRILCS GTISAHCHLRJESSNSPAPAS-LAGITGVCHHAQLIFVFLVET GPHHVQQAGLELL/NVVIHLPRPPKVLGLQA  5912  924  277  MILNKALHGALAL-TVMSPCGEDIVADHVASYGVNL/VQSFG SQQVSHEPTGDEFYYVDLEFKRETVWQLPLFRFRFRFPDGFALTN LAVLKHILNIVIKRSNSTAATINEVBSVTVFSKSPVTLGQPNTLI CLVDNIFPPVVMITMLSNGHSVTGVSSETRPSSPKSDHFILQD VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHMGAEIPTLL  5913  46  1198  QLRMAGAEGAAGRGSELEPVVSLUVDLEEDEELRREACAVLGGS DSEKCSYSQSSVRQALVAGSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQBXVCQACMRRCSFLMAYAAQLAVTKIST\GMMDWCGTLM E*/DDQBVIKPENGEHQDSTLKEDVPEGKDDVSRVKVEQNSEP CAGSSSESDLOTVFKNESLNSKSGCKLQSLKAKQLIKKDTAT YWPLNWRSKLCTCQDCMMWYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQOVELLC/GIQ*FED  5914  960  124  NLGGSELPFPEEALFIQVASHWORRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGUPRFTYGHAGTIYKDFYVISG GHDDYGPYRKNLLCYDHRTDVBERRFMTTARGWHSMCS:GDS GHDXQGPSRNLLCYDRTKDVBERRFWTTARGWHSMCS:GDS GHDXGGSACFIAP*SLGQGTTKRKAKARGTTTGASDPSCASWDR KAIAGGSACFIAP*SLGQGTTKRKAKARGTTTGASDPSCASWDR PHRRLPGICRPAATS  5915  1604  703  FPGRFTRFLKLKJGRRKRARIIQAPHCISPRPRCCPFGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPPCT PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLDFSPHP\PVSRAPPPPPPPPPCLRYPLISPPCTP PQEDFPALGGPCPPRMPSPGFSAVVLKGTPPPPPPGLVPPIS KPPPGFSGLLDFSPHP\PVSRAPRPPPPPPPPCLRYPLISPPCLPPPIS PRELPGREPSSAHPUHQGLPAERRGPLQRVQEPLRSCGTGDDLRS PVLQELCGPAGGEPPECL**AACPAAH  5916  256  633  SPRNWEIWGWHRWESFSLEGEWFSRIPEPSPSTKGTSGKGCR TVTGAVHRHUNHVAGIIPWUHSGLKRTAATAQDQWTSQQYPDH PTKLLILC*NOATABKNNT*TTALLQPHGLLVYSPRMAEA	Ì	ļ		
ALFQULLILITALOPSIFSVLANGGILACSPYSSKTRSQVMNCH LLILEFTEMTVLTRMYYRKDIKVGYETFSSPDLDLNLKALRNM AWTMKGCCTH  5911  109  595  Q:PLAPCIQGKGLEMESPKPQSFIIRSSHSGAGLLVKNPSTPVF CHRRGGAPKYKPTPVVGPGRPTGOKHMRGGVSLLSPRIEGS GTISAHCNLRIPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GPHVVGQAGLELL/NVVIHLPPPKVLIGLQA  5912  924  277  MILNKALMIGALAL-TTWSPCGGEDIVADHVASYGVNLYQSYGP SGQYSHEFIGDEFYYDLERKETVWQLPLFRFRFRPDPGFALTN IAVLKHNLNIVIKRSNSTAMEVPSVTVPSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSXGHSVTEGVSETRPSSPKSDHFILQDQ VTSSFFPFE**PL*TAKVGQLGAMEPPLLKHMGABIPTTL CLVDNIFPPVVNITWLSXGHSVTEGVSETRPSSPKSDHFILQDQ VTSSFSPFE***PL*TAKVGQLGAMEPPLLKHMGABIPTTL GLWAMGABEGAARGGSELEPVSLUDVLEEDBELRNEACAVLGGS DSEKCSYSGSVKRQALVACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPRKAKVNSGNKYNDN PFGLYCLCKRPYPDPEDSIPDEMIQCVVCEDMFHGRHLGAIPPE SGDFQB*VVQACMKRCSFLMAYAAQLAVTKIST\GMMEMCGTLM E*/DDQEVIKPENGEHQDSTLEDVPEGGEDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNMRSKLCTQQMYMGDLDVLELTDSPDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQVELLC/G10*FED AQATORSDPLMDTLSSMNRVQVELLC/G10*FED  5914  960  124  NLGGSELPPEERLFIQVASNNQGRVDFYLASIEDMUVAL/GGRN AQATORSDPLMDTLSSMNRVQVELLC/G10*FED GDYQ1GPYRKNLLCYDHRTDVBERRRMTTARGWHEMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOMTRVAPILHANSE GHDYQ1GPYRKNLLCYDHRTDVBERRRMTTARGWHEMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOMTRVAPILHANSE SGVAWWEGRIVILGGYSBENTFSKKTQVTVDREADKWSRGVDLP KAIAGSSACFIAP*SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPFGALQAPEA PASAREGBVAVVVNGHTEGPAPARSAPKEPPGLPRPFPPPPFBLVPPIS KPPPGFSGLLDSHPP\PVSPAPPPPPPPRGVPPSPLPSBPPPPPLGSPPCPT PQEDFPALGGPCPPRMPPSPPFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLDSHPP\PVSPAPPPPPPPRCVPGALQAPEA PASAREGBVAVVVNGHTEGPAPARSAPKEPPGLRRDAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEDLRGVQTGPDLRS PVLQELPGPAGGFPECL**AAGPAAH  5916  256  633  SPRMWEINGPHRNWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVHSGLKETAATAQDQWTSQQYPDH PTKLILLO**NOATADKNN**TTALLQPHGLLVSPRMEAD	1			DCDCI VCCTI CCA (CCTI TA LITTI CALADONALITA
LILIETPIMTVLTRMYYRRKDIKVGYETFSSPDLDLNLKALRNM   AMTMRGCCH    5911   109   595   Q-PLAPCIQGKGLEMRSPKPQSFIIRSHSGAGLLVKNPSTPVF   CCHRRGGAAFKYKPTPVVGPEQRPTGCKHMRGGYSLLSPRIECS   GTISAHCHLRJESSSNSPADAS*LAGITGVCHHAQLIFVFLVET   GPHNVGQAGLELL/NVVIHLPRPPKVLGLQA     5912   924   277   MILNKALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP   SCQYSHEPJEQDEFYYDLERKETYWQL)FRFRRFRPPQFALTN   IAVLKHNLNIVIKGSNSTAATNEVPEVTVFSKSPVTLGQPNTLI   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSFKSDHFILQDQ   VTSPSFPFE**DL*TAKVECLGAWFFPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSFKSDHFILQDQ   VTSPSFPFE**DL*TAKVECLGAWFFPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSFKSDHFILQDQ   VTSPSFPFE**DL*TAKVECLGAWFFPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSFKSDHFILQDQ   VTSPSFPFE**DL*TAKVECLGAWFFPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSGEPAGICLACSYSCHGS   DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYSCHGS   DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYSCHGS   HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN   FFGLYCICKRPYPDEDEIPDCVVCEDWFHGRHLGAIPPE   SGDFOWAVQACMKRCSFLWAYAAQLAVTISTS\TGMDWCGTLM   E*/DDGEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEGNSEP   CAGSSSESDLCTVFKNSSKNRVQQVELIC/GIQ*FED   CAGSSSESDLCTVFKNSSKNRVQQVELIC/GIQ*FED   SGDFOWAVCQACMKRCSFLWAYAAQLAVTLIST\TGMDWCGTLM   E*/DDGEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEGNSEP   CAGSSSESDLCTVFKNSSKNRVQQVELIC/GIQ*FED   NLGGSELPPEAHTQVASMNRVQQVELIC/GIQ*FED   SGDFOWAVCGTCHVAYSHVANGAUSHANSE   SGNAVWEGRIYILGGYSWSVVAGLPRFTYGHAGTIYKDFVYISG   GHDYQIGPYRNILLCYDHRTDVWERRPRMTARGWHSMCSJGDS   IYSIGGSDDNIESMERFDVLGVBAYSPQCNQWTRVAPLLHANSE   SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREADKWSKGVDLP   PHRILPGICRPAATS   SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREADKWSKGVDLP   PHRILPGICRPAATS   SGVAVWEGRIYILGGYPRMPSSFSLEGGFRFTGSFPCTT   PQEDFPALGGPPCTAKTGSPPCTP   PQEDFPALGGPPCTMPSPGFPCTPPGALQAPEA   PASRAGGPVAVVNCHTEGPAPARSAPKEPPGLPRFLGSFPCTT   PQEDFPALGGPPCTMPSPGFPCTPT   PQEDFPALGGPPCTMPSPGFPCTPT   PGEDFPALGGPPCTMPSPGFPCTPT   PGEDFPALGGPPCTMPSPGFPCTPT   PGEDFPALGGPPCTMPSPGFPCTPT   PGEDFPALGGPPCTMPSPGFPCTPT   PREDFPGGFPCTMPIGGFPCTPT   PGEDFPALGGPPCTMPSPGFPCTPT   PGEDFPALGGPPC	1			ALFOYLLILTALOPSIESUL ANGCOLAGED NGCAKE
S911   109   595   Q.P.LAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF		]		LITTETFIMTULTEMYVDDVDIVVEVETECCDDIDINI VAT DEN
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CCHRRGGAFKYRPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS+LAGITGVCHHAQLIFVFLVET GFHHVQAGLELL/NVV1HLPRPPKVLGLQA  5912  924  277  MILNKALMIGALAL/TVMSPCGGEDIVADHVASYGVBLYQSYGP SGQYSHEPDGDEEFYVDLERKETVWQLPLFRFRRFDPQFALTIN LAVLKHILMIVIKRSNSTAATNEVEEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPF**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL  5913  46  1198  QLRMGAEGAAGRQSELEPVVSLVDVLEEDEELENERACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDMFHGRHLGALPPE SGDPQEMVCQACMKRCSFLWAYAAQLAVTKIST\CMMDMCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP SGDPQEMVCQACMKRCSFLWAYAAQLAVTKIST\CMMDMCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKWESLANESKSGCKLQELKAKQLIKKDTAT YWPLJWMRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQQVELIC/GIQ*FED CAGSSSESDLQTVFKWESLANESKSGCKLQELKAKQLIKKDTAT YWPLJWWRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQQVELIC/GIQ*FED GHDYQIGPYRKNLLCYDHRTDVWBERRPMTTARGWHSMCS-IGDS GHDYQIGPYRKNLLCYDHRTDVWBERRPMTTARGWHSMCS-IGDS GHDYQIGPYRKNLLCYDHRTDVWBERRPMTTARGWHSMCS-IGDS GHDYQIGPYRKNLLCYDHRTDVWBERRPMTTARGWHSMCS-IGDS GGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACPIAP*SIGQRTRKKAKARGTRTGASDPSCASWDH PHRILPGLCRPAATS SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACPIAP*SIGQRTRKKAKARGTRTGASDPSCASWDH PHRILPGLCRPAATS PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCCT PQCDFPALGGPCPPRMPSSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPFPPPPPRCLVPPIS KPPPGFSGLLPSPHPVPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPGLPAPARRAPAPEPPPPDKVRPPLBPPPPGLYPPIS KPPPGFSGLLPSPHPVPGLPAPARRAPQPURGQYPDLRS FRIMEIWGPHIRWESFSLEGEWSRIPEPSPBSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQOQWTSQYPDH PTRILICA*NQATAMKNN*TTALLQPLKYTAATAQOQWTSQCYPDH	5911	109	595	QLPLAPCIOGKGLEMRSPKPOSFIIRSSHSGAGLLVKNPSTDVP
GTISAHCNIRJESSNSFAPAS *LAGITGVCHHAQLIFVFLVET GPHHVQQGLELL/NVVIHLPRPPKVLGLQA  5912  924  277  MILNKALMIGALALTTWSFCGGEDIVADHVASYGVNLYQSYGP SQVSHEPDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN IAVLKHINLIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVNITIWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFF**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL  0D.RMAGAGGAAGRGSELPPVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLVCICKRPYPDPBEPDEIPDEMIQCVVCEDMFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWGSTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREUKVEQNSEP GCAGSSSESDLOTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATTDRSDPLMDTLSSMNRVQQVELLC/G1Q+FED  MLGGSELPPEEALFIQASMNQRRVPTYLASIEDMLWAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQ1GFPYRKNLLCVDHRTDVWEERREMTTARGWHSMCSLGDS GYAWWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACPIAP*SLGQRTRKRAKARGTRTGASDPSCASWDH PHRILPGLCRPAATS  5915  1604  703 FPGRPTRPLKLGGRRKRARITQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAFKEPPGLPRPLGSFPCTT PQGDFPALGGPCPPRMPSSFGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSSAPPPPPPQK/RPRLLPAP/PGLPS PRELPGFEPSAHPVHQGLPARRRRPLARQDWTSQCYPDH SKPPGFFSCLLPSPHPVPGSLPFARRRPLARQDWTSQCYPDH FTRLILC+NQATARKNN*TTALLQPHCNJCVPCYVPGCYCTGPDLRS PTRLILC+NQATARKNN*TTALLQPHCNJCVPCYVPGCYPGCYPDH SPRRILPGLPCAPATS	i .			CGHRRGGAAFKYKPTPVVGPEORPTGOKHMRGGVSLLSPRLECS
S912   924   277   MILNKALMLGALALTYWSPCGGEDLVADHVASYGVNLYQSYGP   SGQYSHEFDGDEEFYVDLERKETVWGLPLFREFRRFDPQFALTN   IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSPKSDHFILQD   VTSP5FPFF**DI**TAKVEQLGAWFEPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSPKSDHFILQD   VTSP5FPFF**TAKVEQLGAWFEPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSPKSDHFILQD   VTSP5FPFF**DI**TAKVEQLGAWFEPLLKHWGAEIPTTL   CLVDNIFPPVVNITWLSNGHSTTEGEEPAGICLAGSYECHGS   DSEKCSYSQGSVKRQALYACSTCTPBEGEEPAGICLAGSYECHGS   DSEKCSYSQGSVKRQALYACSTCTPBEGEPAGICLAGSYECHGS   HKLFELLYTKRNFRCDCGNSKFKNLECKILPDKAKVNSGNKYNDN   PFGLYCLCKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE   SGDFQEMVCQACMKRCSFLWAYAAQLAVKIST\cmmdmcGTLM   F*/DDQEVIKPENGEHQDSTLKEDVPFQKBUDVREVKVEGNSEP   CAGSSSESDLOTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT   YWPLNWRSKLCTCQDCHMYGDLDVLEHTDBYDTVLAYENKGKI   AQATORSDPLMDTLSMNRVQQVELLC/GIQ*FED   AQATORSDPLMDTLSMNRVQQVELLC/GIQ*FED   SGDFQEMVCQACMKCSFLWAYVAGLPRFTYGHAGTIYKDFVYISG   GHDYQIGPYKKNLLCYDHRTDWWBERRPMTTARGWHSMCSLGDS   IYSIGGSDDNIESMERFDVLGVEARSPQCNQWTRVAPLLHANSE   SGVAVWEGRIYILGSYSWENTAFSKTVQVYDREADKWSRGVDLP   KAJAGGSACPIAP*SLGQRTRKKAKARGTTGASDPSCASWDH   PHRHLPGLCRPAATS   FPGRPTRPLKLGRRRKRARIIQAPHCHISPRPR*CCPPGALQAPEA   PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT   PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPCLVPPIS   KPPPGFSGLLDSSPHP\PVSDAPPPPPPPCK/RPCLPPPIS   PPELPGEEPSAHVNQGLPAERRGPLQRVQEPLRGVQTGPDLRS   PVLQELPGPAGGEFPECL**AAGPAAH   SFRWWEI WGDWHRWESSELEGEWPSRIPEPSDDSTKGTGKGCR   TVTGAVHRHLNHVAGII PWVLHSQLKPTAATAQDQWTSQQYPDH   PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA   TVTGAVHRHLNHVAGII PWVLHSQLKPTAATAQDQWTSQQYPDH   PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA   TVTGAVHRHLNHVAGII PWVLHSQLKPTAATAQDQWTSQQYPDH   PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA   TVTGAVHRHLNHVAGII PWVLHSQLKPTAATAQDQWTSQQYPDH   TVTGAVHRHLNHQAII PWVLHSQLKPTAATAQDQWTSQQYPDH   TVTG	t			GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET
SGQYSHEPGGBEETYDLERKETVWQLPLFRFRRFDPQFALTM IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITHLISNGHSVTEGVSETRPSSPSKSDHFILDDQ VTSPSFPFF**EL*TAKVEQLGAMFEPLLKHWGABIPTTL  5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPFGGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQENVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E**/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLOTKRESLNAESKSGCKLQBLKARQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPR*CPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPFGLPRPLGSFPCFT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPCK/RPRLLPAP/PGLPS PASRAEGPVAVVVNGHTEGPAPARSAPKEPFGLPRVLGSFPCFT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPCK/RPRLLPAP/PGLPS PRELPFGEEPSAHPVHQGLPARRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWMEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA				GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
IAVLKHNINIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSFKSHFILQDQ VTSPSFFFF***PL*TAKVEQLGAWFEPLLKHWGAEIPTTL 5913 46 1198 QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGI CLACSYECHGS HKLFELYTKRNEPCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAVAAQLAVTKIST\GMMDNCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLOTVFKNESLNARSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATTRSDPLMDTLSSMNRVQQVELIC/GIQ*FED NLGGSLPPEEALFIQVASMNRVQQVELIC/GIQ*FED HGGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE GGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS FPGRPTPPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASKAEGPVAVVVNGHTEGPAPARSAPKEPPCLPRPLGSFPCPT PQEDFPALGGPCPPRNPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPAPPPPPPQK/RPRLLEAPP/PGLPS PRELPGGEEPSAHVVNGHTHEGPAPARSAPKEPPCLPRPLGSFPCPT PQEDFPALGGPCPPRNPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHPVPSPAPPPPPPQK/RPRLLEAPP/PGLPS PRELPGGEEPSAHVNGGLPABRRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAH  5916 256 633 SPRWWEIWGWHRWESFSLEGEWPSRIPEPSPSTKGTSGKGCR TVTGAVHRILNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ**NQATADKNN*TTALLQPHQRL\VSPRMAEA	5912	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
CLVDNI FPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL  OLRMAGAEGAAGROSELEPVVSIVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGI CLACGYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDENIQCVVCEDWFHGRHLGAIPPE SGDFOMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDNCGTLM E*/DQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLOTVFKWESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVVAGLPRFTYGHAGTIYKDFVY1SG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS GYAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTTPLKLGRRRKRARITQAPHCHSPRPKTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFFALGGPCPPRMPPSPGFSAVVLLKGTPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVGTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWEIWGFWHRWESFSLEGEWPSRIPEPSFDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA				
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S913   46   1198   QLRMAGAEGAAGRQSELEPVVSIVDVLEEDEELENEACAVLGGS   DSEKCSYSQSVKRQALYACSTCTPEGEEPAGICLACSYECHGS   HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN   PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE   SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDMCGTLM   E*/DDQEVIKPENGEHQDSTIKEDVPEQGKDDVREVKVEQNSEP   CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT   YWPLNWRSKLCTCQDCMKMYCDLDVLFLTDEYDTVLAYENKGKI   AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED   NLGSSLPPEEALFIQVASMNQRVDFYLASIEDMLVAI/GGRN   ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG   GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS   IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE   SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP   KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH   PHRHLPGLCRPAATS   FPGRPTRPLKLGRRRKRARIQAPHCHSPRPTCPFGALQAPEA   PASRAEGPVAVVNGHTEGPAPASAPKEPPGLPRPLGSFPCPT   PQEDFPALGGPCPPRMPPSPFGFSAVVLLKGTPPPPPPGLVPPIS   KPPPGFSGLPSPHP\PVSSAPPPPPPQK/RPRLLPAP/PGLPS   PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS   PVLQELPGPAGGEPPEGL**AAGPAAH   SPRWEIWGPWHRWESFSLEGWPSRTQPLGPSTGTSGKGCR   TVTGAVHRHLNHVAGIIPWULHSQLKPTAATAQDQWTSQQYPDH   PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA   PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA				CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFI.LQDQ
DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHOS  DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHOS  HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN  FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE  SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTIM  E*\PODGEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP  CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT  YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI  AQATDRSDPLMDTLSMMRVQQVELIC/GIQ*FED  NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN  ENGALSSVETYSPKTDSWSYVAGLPRFTTGHAGTIYKDFVYISG  GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS  IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE  SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP  KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH  PHRHLPGLCRPAATS  5915  1604  703  FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA  PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRFLGSFPCPT  PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS  KPPPGFSGLLPSPHP\PVSPAPPPPPPKKKGTPPPPPFGLVPPIS  KPPPGFSGLLPSPHP\PVSPAPPPPPPKKKGTPPPPPFGLVPF  PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS  PVLOELPGPAGGEFPEGL**AAGPAAH  5916  256  633  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR  TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH  PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA	5913	46	7100	VISPSFPFE**DL*TAKVEQLGAWFEPLLKHWGAEIPTTL
HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEWVCQACMKRCSFLWAYAAQLAVTKIST\GMMDNCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT QEDFFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGAGGEFPEGL*AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHQRL\SPRMAEA		1	1196	
FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMYCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTIM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEB CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFYVISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACPIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS FPGRPTRPLKLGRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPLPFPFDGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPECL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVNRHLINHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA				HKI.FEL.YTYPNEPCDCCNCVEVNI ECVI I DDVA KIRICONVENION
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SEQ	Predicted	Predicted end	
NO:	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
- }	I		FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGNP
l l			HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
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5919	1	4254	QKVLSHVNSGCQLLPQHQVPAY
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1	i	Ì	GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
1			GSRTAPKYGNAELMETGDGVPVSSRVSAKIOOLVNTLKRPKRPP
1			LREFFVDDFEELLEVQQPDPNQPKPEGAOMLAMRGEOLGVVTNW
	}		PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
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1			TIVNVLDFKKDVGLWHGILTSVMNMMHVISIPYSLMKVNPLSWT
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			ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRPDT
1			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVODVGLVMPG
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			PEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV
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1	l i		VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVML
1			MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
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1			TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
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i	[		SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL
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			LAAAPLHEOKOMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
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j			IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSOAGTKCOVD
	i i	1	RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
		ł	Q\GAAOOPO\*GALPDCOLOPDRSTGL*DDEWTGSVGLSDESKA
			Q\GAAQQPQ\*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG
5922	2475	495	Q\GAAQQPQ\*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG AAATHLIILRVIENRGAEGKRK SYSNWCLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T

			_
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ -	\=possible nucleotide insertion)
		<u> </u>	CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLGDT
ĺ			SKIITRTEEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
1			RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLOKGEAN
1	1		PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPOVVI
i		i	LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
		j	IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE
1	1		ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
			TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWTVPSGLY*IC
Į.			RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
1			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
1			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
1	1		DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
İ			IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
			PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE NSH
5923	137	638	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
			QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
í	ĺ		LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
L			QLELENKELRELLSISSESLQARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
i			PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
			SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTOD
1		1	HMKFWKNLPLHSHHLTPSVPQTV1PKKTGSPE1KLK1TKT1QNG
1			RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR
1			SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
1			ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYFWWPCMVSSDPQL
1			EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
			LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT
1			REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKKTRRPRSVL
1			NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG
			DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS
1			VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
			QVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
			QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHOWLRPE
			INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE
]			DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT
		j	QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
			ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
			PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
			GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
			IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
			CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ
			RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK
			\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP
			SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
	į		YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
	į		KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREOG
	i		WRWVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
	Í		MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
	ļ	Į	KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
	ļ	1	YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
j	.		RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
l	[		AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
ĺ	[		LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
	L		TO THE TOTAL MODERANISMS I DOVE TO THE TOTAL MODERAL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	I dord sequent containing eignal baseids
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	11410000	Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
}			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1	ł		AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
]		i	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
1			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
į	1	1	HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
ł			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
I			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
ı			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
	}		GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
5928	4146	1248	DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
1	i		KHFSKFGSQALYQLKRPASCQNSISVMPAQKITKPAAKYGIPLA
ı			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
1	i		KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
ł		İ	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
}	1		MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
J	}		YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
İ	}		RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1	<u> </u>		AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
ļ			SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
1			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
	i		LQLQTE_LENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
			AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
	1		GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1 7			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI EDENIKEGPSDSEDLUEBERTREIT
1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
1 1	]		GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5929	3	1558	LDFSMTTOLPAVVAILLEVUCDACGOODERS
.	i		LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
1 1	ŀ		WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
1 1	i		AKNNSTYWANICDKERCORGODOGODOGODOGO
1	ļ		AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
1 1	į.		LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
1			RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1 1	ŀ		QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
1 1	l l		LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLHTVE
1 1	1	1	GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMFSLSGTFGTQ
1	1	1	YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGR
			LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1 1	į.		KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1 1	ŀ	1	KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
[ ]		1	CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
ļ <u>i</u> .			LODREDOS IL CTCRECA CUMPANIA VILLE DE LA COMPANIA VI
1		İ	LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
1			TGYIVGANIETYLLEKSDAUDOAVDOODUSSRFGKFIRINFDV
¦			TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
		ļ,	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
	· ·	1	FSHEELLSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
1	1	j	CHILGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
1	1	į	KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEOLCINYTNEKLOOLENHEMBIL BORNEL
ĺ	l		SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
Í	f	1:	DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
1	1		GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
!			NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
ı			
		· [ ;	LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

SEQ	Predicted	Predicted end	
			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł		sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
1			LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
1	ĺ	į	NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
1			
	<u> </u>	i	EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM
	l .	4	RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ
i	l	Į.	DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
1	i	ļ	IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
1	ĺ	ĺ	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
ì			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
i			EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
ŀ	1		
1	1		QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
1	1		FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
1	1		QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
1	[	<u> </u>	FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
1	I	ł	EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
1	1		KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
1	1	1	HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
			KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG
ļ	1		KNVHELEKSKRALEQQV\EEMRTQLEELEDELOATEDAKLRLEV
l		Į	
1	ł	ĺ	NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
	Ļ	1	RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
l	1		DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
1	1	1	ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
1	1	l .	ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
1	Ī	l	QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1	1	į.	QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEOMEKA
i	ĺ		
1		i	NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
1			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
			TSDVNETQPPQSE
5931	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1			KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
i	i		KMNPPKFSKVEDMAELTCLNEASVLFNLKDRYYSGLIYTYSGLF
1	1		CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
l .		Ĭ	LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
1	ł	i	IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
ŧ	l		TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
l .	1		
1	1		KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
1	ł		FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
i	1		CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
1	1		KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
1			SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
ŀ	1	l	DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
1	i e	i	
1			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
ſ			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
İ			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
		·	GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDFLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGPMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNDPFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNDPFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKILHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEBKAKNLAKIRNKQEVMISDLEE
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKIQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRGELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPDFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPDFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEETTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEETRQGLEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
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			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPIND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEETTRGELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
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			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRGELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK

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Not   nucleotide				Amino acid segment containing signal peptide
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mmino acid residue of amino acid sequence  Sestine, T-Mireconine, V-Valine, amino acid sequence  W-Tryptophan, Y-Tyrosine, X-Unknown, *-stop codon, /-possible nucleotide deletion, (codon, /-possible nucleotide deletion, NEXULIDARAI COLOR (INSTITUTE OF CODON)  WEXTLIDAR COLOR (INSTITUTE OF CODON)  WEXTLIDAR COLOR (INSTITUTE OF CODON)  WEXTLIDAR COLOR (INSTITUTE OF CODON)  WEXTLIDAR COLOR (INSTITUTE OF CODON)  WEXTLIDAR COLOR (INSTITUTE OF CODO	ı	corresponding		La Leucine, Mamothionine Nanagarine
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mino acid sequence  mino a			residue of	S=Serine, T=Threonine, V=Valine
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NARMKOLKROLESAEERATRANSRRKLØRELDDATEANEGLER EVSTIKNRARGGETSFSSRSGRKORLDLEGASLELSDDDTESK TSDVNETOPPOSE  RILBEICFELFLÖKGKKIKLSGPRWEEGKPRGTGUAVKAERANM FGATLAVGUTITUCTCSCCCLYKTCRP PPVVAPP PROVIAPPOPP BEVPSYPE SYESVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROVIAPPOPP BEVPSYPE SYEVOUTHUPPOPGMPAAPY PROSSER FRENCHTURE SEED SEED SEED SEED SEED SEED SEED SE				QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGOLEEOLE
5932  33  572  RHLEETCFLFLOKGRKLKLSGPWEEGGFRGTGGLWYRAEANMG FGATLANGLTI FUND VIT LICETCSCCLYKTGREPRY VAPP PHP / PVVIAP PYOD PSUYPSY PGPSYGOYHTMPPQPGMPARY PHP / PVVIAP PYOD PSUYPSY PGPSYGOYHTMPPQPGMPARY PHOY PPPY AQPMGP AY HETLAGGAARY TPASOPY YAPP PHYP / PPVIAP PYOD PSUYPSY PGPSYGOYHTMPPQPGMPARY PAMAL  5933  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSDAHMDASGFSD SDMPSTTR KSPSRKHNYRNESARESLCDSPHONLSRPLLENKLK AFSIGKMSTAKRTUSKKEOEELKKKEDEKAABEI YEFFLAAFEG SDGNKVKTYRVGGVVNAAKEEHETDEKKI YKPSSRFADOKNP PNOSSNERPPSLLVIETKKEPLKKGEKKKKSNLELFKEELKQI OERDEENHTKKGRISRFEPPOSDSGGGRMADAPSRRNSSGVL DDVAPGSHDVGDPSTT NYFILENI NIPOMNLKKCCCOFFGREP LASVKTMMPRTDEERRAERNCCPVAFMBADARALIKKGKNI MSFEMKLGGKAKVPIPPHPIYIP PSMMEHTLPPPPSGLPPHAOP REEKLKMPANPMIPPPRMKEDPEKTLSQHTVVVI UPTERNILLALI HRMIEFVVREGPMEAMINNESINNPMRPLPENOTPAHVYKM KLYSILOGDS PTKWRTEDPFMPKNGS FWRP PELPHVILIGNSEG ETEAPVEEPSKKGALKEEGROKLEE LIAGUVKVI UPTERNILLALI HRMIEFVVREGPMEAMINNESINNPMRPLPENOTPAHVYKM KLYSILOGDS PTKWRTEDPFMPKNGS FWRP PELPHVILIGNSEG ETEAPVEEPSKKGALKEEGROKLEE LIAGUVKVI UPTERNILLALI HRMIEFVVREGPMEAMINNESINSPHGREPKHLOGHLOGHVIC LIANAEAAEEI VDCTTESLSILKTPLPKKIARIYLIVSDVLNNSA KVANASYYKFFFTKLCQI FSDLAATIGGHLOSPHKLOGDHLOGV PLLATEDSKKNED I FKVADSKWEAVDESELEAQAVTSKKELF GEVENVINDKLLQREKEKELEREREERIKLYSNPIKKEMTE SKFSKYSEMSEEKNAKLRSIELKVMKFOOELESGKRPKKPGOSF GEVENVINDKLLQREKEKELEREREERIKLYSNPIKKEMTE SKFSKYSEMSEEKRAKLRSIELKVMKFOOELESGKRPKKPGOSF GEVENVINDKLLQREKEKELEREREERIKGKRELLSSNEDKKEK DECTPTREERKRRSTSPSPSRSSGRPVKSSPSRSERSER SKHESSRSRSSHNISSPOWSKAKARSSTSOKKEKE DECTPTREERKRRSTSPSPSRSSGRPVKSSPSRSERSER SKHESSRSSSSHNISSPOWSKAKARSSTSOKKEKE DECTPTREERKRAKLRSIELKVMKFOOELESGKRPKKPGOSF OEGVENVATAKKRGELKKELEREREERICGPONKELESGRPKKPGOSF SONNKYTFVGGVVNAAAKEBETDEKKGKYTYBSGFPADOKNP PNOSSNERTSKRTSTKRTLSKKGCELKKKENDELFKELKOI GERERENCOPAMPRODAEDALKNINGKMI MSFPEKLGORGKAVTD I PHPIYIP PSMBHTLITPPPEGLFRINGE GERERRIKTKGRISSPSLOOFFRAMPRODAEDALKNINGKMI MSFPEKLGORGKAVTD I PHPIYIP SMBHTLITPPPEGLFRINGEEG ETEAPVEEPSKKGALKEEGREKKEELELELGLIPPRANGFORDERINGSGOU LINGAEAEET UVOLTESLSILKTPJEKKIARLIVISDULIVINSSA				QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
5932  572  RHEELCEFIFLOKGEKILKLSGPRWEEGKPRGTGLWVKAEANMG FGATLAVGITITULSVUTITICPTCSCCCLYKTCRPPPVAPP PGATLAVGITITULSVUTITICPTCSCCCLYKTCRPPPVAPP PHOP/PVULAPPOPD PSVPSYPGSVOTTMYPDOGMPAPY PHOPYPDVIAPPOPD PSVPSYPGSVOTTMYPDOGMPAPY PMOYPPPYPAQDMGPPAYHETLAGGAAAPYPASOPPYNPAYMDA PKAAL  5933  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVUSSGSSDAHMDASGPSD SOMPSTIPPKSPRKINYNNESARESLCDSPHONLSRPLLENKLK APSIGKMSTAKRTLSKKEOGELKKKEDEKAAAEIVEFLAAFGG SDOKKVKTPVRGGVWAAKEELETDEKRGGIYKPSGRFADOKNP PROSSNER PSLILUTETKKPPLKKEGEKKKKENSLELFKEELKOI QERDERHHTKGRISREPPOSDSDGORGRMDAPSRRNRSSGVL DDVAPGSHUVOPPSTT.NFYLINT\UNDKLKCCCCGEFGRPD LASVKIMMPRTDEERARENCOPVAPMINRDAERALKKLINGKNI MSFEMKLGGKGAVDIPPHIYIPPSMINKKCCCGEFFPADOP RERLKMPRAPHIPPPKKHSPFWINSSTWRPPPLINFYLHGMSEEO ETRAFVEEPSKKGALKEEGROKLEEILGTPRENDGOMAVPC LNAAEAAEEIVDCTTESLSILKTPLPKKLARIYLVSDVLVNSSA KVANASYYKFFFFKLGOTSDELIDGAVTTSKWELFD QHEESSEEPSKKGALKEEGROKLEEILGGHESTROKNGOMAVPC LNAAEAAEEIVDCTTESLSILKTPLPKKLARIYLVSDVLVNSSA KVANASYYKFFFFKLGOTSPONSKTERFENDODLDGV PLOATEDGKKMEPJFKVADSKGEAVDESELEDQAVTTSKWELFD QHEESSEEERMONDEESSEDEDETOSS KSTERFIKSPIKSPIKSENGOM TCRRWEDWAIYPPFHILKOMIFIGLUVIIIEKEKTEOVPDDLD GAPIEEELGAPLEDVORG Y DIAPHT DIAUPHTSKREMTE SKFSXYSEMSEEKRAKLREIELKWMK VQOELESKRPKKNGOF QEQVEHYNDKLLGREKKELERERERDKKOKKLEERSKOKKEK BEETTPTREERRRRHSTSFPSSSSTRFFKKSRSRSSSP KASGKKSRSSSSPHEKRKSKSKTTRSDVHSSGSSDAHMDASGFSD SOMPSTTEPKSPRKINYKNESARSSLCDSPHONISRFLLENKL LCPERSYP SKSKKSRSSSSSPHEKKSKSKTTRSDVHSSGSSDAHMDASGFSD SOMNVKTFVRGGVVNAAKEEHTDEKRGKTYKRSRFRRSRSP SKSKSKSRSSRSSHKSKSSSSSPHEKKSNLEJFKEELKOI OSERDERHKTKGLISRFEPPOSDSDGORRSMAPSRRNRSSGVL DDVARGSHOUNDSTT.NFVIJANI\NPAKAELTPLAPEG SCHNKVKTFVRGGVVNAAKEEHTDEKRGKTYKSSFPADOKNM MSFEMKLGMGKAVPTPPHIYTIPPSMHEHTLPPPSGLFFRAOP PROSSNER PPSLLVIETKPPINFLISHTMENFRPLIARILLAL INMIELSEGURDVARGSHOUNDSTT.NFVIJANI\NPATHTGAELGE SCHNKVKTPVRGGVVNAAKEEHTDEKRGKTYKSPSPPANDFROM KLYSILGGBOFTKMETEFFRNKNOSFPHNIPKLALLIL INMIELSEFTEDPROSPRSMATHRENGEGOFTHALDEI INMIELSFVNAAMMUPPTDEFRRENGFROFTHALDEI INMIELSFVNAAMMUPPTDEFRRENGFROFTHANTSTHIALLIL INMIELSFVNAAMMUPPTDEFRRENGFRONTOFTHALTYYN KLYSILGGBOFT	ı			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
5932  333  572  BHLEETCFIFLOKGRKILKLESGPRHEEGKPRGTGGLMVKAEANMG FCATLANGUTIPULSVVTIIICFTCSCCCYKTERPRYVAPP PHPP/PVVIIAPYPGPEVPESYPGSYGYKTHEPPGFRHPAPY PMYPPPYPAGPMGPPAYHETLAGGAAAPYPASOPPYPAPYMDA FAAAI  5933  1 3190  GTRKLKMADKTFGGSQKASSKTRSDVHSSGSSDAHMDASGFSD SDMPSSTRFKSFRKHNYNFESARESLCDSPHQNLSRPLLENKILK AFSIGKMSTAKRTLSKKEOEELKKKEDEKAABEIYEFLLANFEG SDGNKYKTRYBGSQVMAAKEEHETDEKGIYTYPSGPHDLENKILK AFSIGKMSTAKRTLSKKEOEELKKKEDEKAABEIYEFLENGIKNP PNQSSHERPSLLVIETKKEPLKGEKKKKSNLELFKEELKGI QERRDERHTKKGRISRFEPPOGSDSGGGMADAPSRRNESGVL DDVAPGSHDVGDPSTT.NFYLENI\NPOMMLKKCCCQEFGRFGP LASVKIMMPRTDEERRAERNCCGPVAPMADAFSRNESGVL DDVAPGSHDVGDPSTT.NFYLENI\NPOMMLKKCCCQEFGRFGP LASVKIMMPRTDEERRAERNCCGPVAPMADAFSRNESGVL DDVAPGSHDVGDPSTT.NFYLENI\NPOMMLKKCCCQEFGRFGP LASVKIMMPRTDEERRAERNCCGPVAPMADAFSRLENILGALI HRMIEFVVREOPMFRAMINNREINNPMFRFLEENOTDAHVYNEM KIJSILQGSSPIKWRTEDFRKHISGAIVKVVIDTERNILALI HRMIEFVVREOPMFRAMINNREINNPMFRFLEENOTDAHVYNEM KIJSILQGSSPIKWRTEDFRKHISGAIVKVVIDTERNILALI HRMIEFVVREOPMFRAMINNREINNPMFRLEENOTDAHVYNEM KIJSILQGSSPIKWRTEDFRKHISGAIVKVIDTERNILALI HRMIEFVVREOPMFRAMINNREINNPMFRLEENOTDAHWYNEM KIJSILQGSSPIKWRTEDFRKHISGAIVKVIDTERNILALI HRMIEFVREOPMATYPPFLIKIONIFIGLVNIIEKKETEDVEDDLDAW TCFRAMEDMATYPPFLIKIONIFIGLVNIIEKKETEDVEDDLDAW PLDATEDSKKMEPIFKVADSKMEAVDESELEAQAVTTSKHELPD QHEESSEEERNONGEESSEDEDTVOSSKKRELLSSNDIKKENDE SKRSSKYSEMESERNANLRSIELKVMKKODELESGGREKKREOGSF QEQVEHYNDRILLGDEREKERLEPRIERDKERKLISNDIKKENDE SKRSSKYSEMESERSSSSCREVVXSPSPKSERSRESS SKRSSKSSSSSSSSSSSSSSSSSSSSSDAHMDASGFSD SMPSRTTRPKSPKNINYNNESARESLCOSPHONLSKRLLENI DECTPTREERKRANLRSIELKVMKKOCHTERKFFKKOLTYMKCLOF LCPERSVF  5934  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGFSD SMMSTTARVISKSKCELKVINGERFRLENI DEVARGSHOUNDSTTINFYLIGHI\SPRAMETHLENI  DEVARGSHOUNDSTTINFYLIGHI\SPRAMETHLENI  DEVARGSHOUNDSTTINFYLIGHI\NPOMMLKCCCOCPETGREP  LASVKIMPRTDERRAERENCGPVAPMBRDAERALKMINGKMI  MSFEMKLGOKGAVYI PHPIYIPPSMMEHTLEPPPROTUPAHVYYNE  KLYSILQGSPTKMETEDFRIPKNINGSPRINGSCOLL  DEVARGSHOUNDSTTINFYLIGHINFRTINGHAMPFELERGU  LANNEAABEITUNCITESLISILKTPJEKKIALVINGDULIVINSSA  KVANASYYRKFFETKLCQ	1			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
FGATLANGUTIFVLEVVTILICTECCCLYXTCRERPV\APP EHPP/EVVIHPYEOPESVPESYEGESCCHYXTCRERPV\APP EHPP/EVVIHPYEOPESVPESYEGESCCHYXTCRERPV\APP EHPP/EVVIHPYEOPESVPESYEGESCCHYXTCRERPPV\APP EHPP/EVVIHPYEOPESVPESYEGESCCHYXTCRERPPV\APP EHPP/EVVIHPYEOPESVPESYEGESCCHYXTCRERPP\APP EHPP/EVVIHPYEOGESCHASSKTRSDVHSSGSDAHMDASGPED SDMFSTERESPEKINYRNESARESLCDSPHONDSRPLLENKLK APSIGKMSTAKTLSKKEODELKKELENGLYENGERCEKKSNLELEKEELKGI GERDARHITKGRISKFEPPESDSOGGRSMAPSFADQKNP PROSSNERPPSLLVIETKSKKEODELKEEKKSLELEKEELKGI GERDARHITKGRISKFEPPESDSOGGRSMAPSFARRSSGUL DDVAPGSHDVOGPSTT\NFVIGNI\APPONLEKCCCGEFGRED LASVKUMPRITDEERARERNGGYGARNDADERNRSSGUL DDVAPGSHDVOGPSTT\NFVIGNI\APPONLEKCCCGEFGRED LASVKUMPRITDEERARERNGGYGAVIVKVU PITERNILALI HRMIEFVVERGPMFEAMIMNEINNPMFREIDERPRIKALINAGKNI MSFEMELGKGKAVPIPPHPYIPPSMMEHTLPPPPSGLPFNAOP RELKMPNAPMIPPPBYNKEDPERKIPRINDEDPDATHYVTRW KLYSILOGDSPYKMFTBEFRMFNENFRIPPLHPRIVITHGMSEDG ETEAFVEEPSKKGALKEEORDKLEETLRGLTPRIVODIGDAMVFC LINAEAABEIVUCTIFELSISLIKTPLICUSISTIKTPLICMSEDG ETEAFVEEPSKKGALKEEORDKLEETLRGLTPRIVODIGDAMVFC LINAEAABEIVUCTIFELSISLIKTPLICUSTERITATETUSPEDDLD GAPIEEELGAPLEDVOGIPIDATYRTIGGHLQSENFRORW TCFRAMEDWAIYPEFFIKLOUFFDLINATYRTIGGHLQSENFRORW TCFRAMEDWAIYPEFFIKLOUFFDLINATYRTIGGHLQSENFRORW TCFRAMEDWAIYPEFFIKLOUFFDLINATYRTIGGHLQSENFRORW TCFRAMEDWAIYPEFFIKMPRIFTAGLWITFRCANVITSKWELFD QHEESEEENONQEESEGEDEDTOSS KSERHLIYSMPIREETT SKESKYSEMSEEKBAKLREIELVOKKFORELEGKRPKKPGGGF QECVEHYROKLICAREKKELEEREREDKKOKKEKLEERSIGDKKEK DECTFTREERKRRSTSFSFSRSSCRFKNSSPSKOKKK DECTFTREERKRRSTSFSFSRSSCRFKNSSPSKOKKK DECTFTREERKRRSTSFSPSRSSCRFKNSSPSKOKKKNSLELFTLAFEG SDONKVKTPVRGGVWANAKEEHETDEKRGKIYKPSSRFADOKNP PROSSNERPPSLLVITTKREPKKKEGDELKKKKSHLELFKEELKGI OERRERHIKTKGRLSRFEPPGDSSIGGRRSNADASRRNSSGVL DDYAFGSBTUVGHTST'INFILCHINGNIKKCCCCGPEGRED LASVKIMMPRTDEERARENCCFVAPMNRDABRALKNINGKMI MSFEMKLGWGAVDIPPHITYTPDEMILDHILDAMETLIPPHPOGDEPRAOP RELKNDNADMLPPFINKEDFREKKESRFELFROTPAHVYIRM KLYSILOGDSPTKMRTEDFREKKERSPFPLINKPILGMSEG ETEAFVEEPSKKGALEEGORDSTLEELIRGLTPRINDIGDAMVFC LINNEAAABETVOCTITSLISLIKTPLINGWEDEPHPOHDYDL	5932	33		
DHPP/PVVIAPYEOPPSVPBSYPGPSYCGYHMMPROGEMPARPY PMOYPPPYPAPAMDA PKAAL  STRLKMADKTPGGGKASSKTRSDVHSGSSDAHMDASGPSD SDMPSRTRPKSPRKINYRNESARESLCDSPHONISRPLLENKLK AFSIGKMSTAKKTLSKKEGELKKKEDEKAAABIYEEFLAAFEG SDGNKVKTPVRGGVVNAAKEHETDEKRGKIYKPSSFADQKNP PNOSSMERPPSLLVIETKKPPLKKGEKGEKKKSHLELFKEELKGI QEERDERHITKGRLSFEPPOGSDGGRSMDAPSRRSSGUL DDVAPGSHDVGDFSTT\PFYLGNI\PPOMILKKCCCGFGRPGP LASVKIMPRTDEEBERARENCGPVAPMNRDAEALICILINGKKI MSFEMKLGWGKAVPIPPHPYIPPSIMEHTLPPPPSGLPFNAQPH RELKMPNAPMIPPPKNKEDFENTLSQAIVKVIPTERNILALI HRNIEFVVREGPMERAMIMNEEINDMPFFLPENGTSHVYYKW KLNSILQGDSPTKWRTEDFRMFKNGSFWPPPLMPYLHGMNSEQ ETRAPVEBPSKKGALKEEGROKLERLGLFRFRUDGDAMVC LNNAEAAEEIVDCTTESISILKTPLPKKTARLIVISOVLYNSSA KVANASYYKKFFETKLCOIFSDLAATYRTIQGHLGSENFKORVM TCFRAWEDWAIYPRFFLIKLONIFLGLTVRINDIDALDGV GAPIEBELDGAPLEDVORJ PIDATPIDLIDGVIKSLDDDLDGV PLDATEDSKKWEPIFKVAPSKWEADVESELEAQAVTTSKWELFD QHEESSEEEMONGEESEDEDTOSSKSEEHLYSNPIKEHTE SKEKYKSKSKSKSKKKNENTENFKNKSFFKYSPSFKSGESRERE SKKSKSYSSSEKRAKLREIELKWKFODELESGKRPKKPGGSF QEQVBHYNDKLLQREKKELERERERDKKDKEKLESRSKDKKEK DETTPTREKRRRRISTSPSFRSSSFNKSPSFKSESERSRER SKKSSGKSRSSRSHKDSPROVSKKAKRSPSGSRTPKRSRSRSP KKSGKKSRSQSRSPHRSHKKNKGKTKTTGRFKKAVTYWKCDLF LOPERSVF SMSSKTTRYSPRKHNYRMESARESLCDSPHQNLSKPLLENKLK APSIGKMSTAKRTLSKKEOBELKKKBDEKAABIYEEFLAAPEG SONKVKYTYNGGVWAAKEEETEPOSDSGGRERADANDASGFSD CONKVKYTYNGGVWAAKEEETEPOSDSGGRERADANDASGFSD SONKVKYTYNGGVWAAKEEETEPOSDSGGRERADANDASGFSD SONKVKYTYNGGVWAAKEEETEPOSDSGGRERADANDASGFSD SONKVKYTYNGGVWAAKEEETEPREKGIYYPSSRPADOKNP PNOSSNERPPSLLVIETKKPPLKKGEKEKKKNILLFKELKQI DDYAPGSHUUDDSTT\NFYLANINGKKCCGPGFFGP LASVKIMPRTDEERARENCGFVAPMNRRDAREALKNINGKMI MSFEMKLGWGAVDITETKKRPPSDAMBHHTLPPPPSGLFPHAQP RERLKNPNAPMLPPPNINKEDFFKTLSQAIVGVVIPTERNILALI HMIEFYVRGOPMFERMINNRSINGFRFLFRKNITGDAWVFC LANAEAAEETVDCTTESLSLIKTTPLKRKIJVLINGDVVYRW KLYSILQGDSPTKWRTEDFRKNGSFWRPPLNYYIKW KLYSILQGDSPTKWRTEDFRKNGSFWRPPRNYYYRW KLYSILQGDSPTKWRTEDFLIKLONILGKEKTEDVUJNSSA KVANASYYRKFFETKLCQIFSUNATRTIQGGLAUSENFKORW TCFRAWEDBAALYYBEPFLIKLONILGKEETEDVPDDLD		33.	572	RHLEETCFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG
5933  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSGGSDAMMDASGPSD SDMPSTTPRKSPKHNYMRESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEFFLAAFG SDGNKVKTPVRGGVVMAAKEBETDEKRGKKKKSMLELFKEELKQI QEERDERHKTKGRLSKFEPPOSDSDGGRSMDAPSRNAKSSGVL DDVAPGSHDVGDPSTT\NFYLGLINI\NPQMALKKCCQEFGRFGP LASVKIMWPRTDEERARENCGFVAFMMRRDAERALKNINGKMI MSFFMKLGMGKAVPIPPHFIYLGLINI\NPQMALKKCCCGFGRFGP LASVKIMWPRTDEERARENCGFVAFMMRRDAERALKNINGKMI HRMIEFVVREGDWPFAMINNFBPRFLPFORTPAHVYYRW KLYSILQGDSPTKWRTEDFRFKNGSFWRPPLINFLHAMSEQ ETEAPVEEPSKKGALKEEQROKLEEILRGITPRKNDIGDAMVFC LNNABAABEIVDCITTESISILKTPLPKKIARILVISDULYNSSA KVANASYYRKFFETKLCQIFSDLMATTRTIGGHLQSENKORW TCFRAMEDMAIJPEFFLIKLCOHIFSLSILKFUNDSICHLEFE SKSKYSMSERKRAKIERIELGLUNTIEKSKETENDDDLD GAPIEEELGAPLEDVDGIPTDATPIDDLDCVPIKSLDDDLDGV PLDATTEDSKKNEPIFKVAPSKWRYDSELEGRYTKSMQSF QEQVBHYRDKLLOREKEKELERERDKKKDEKKEKENDVPGDL GAPIEEELKAPKRAKIERIELGLUNTIEKSKETENDYDL GERDERHKTRSTSPSPSSSGRYVKSPSPKSERSERSER SKSKSKSNSSSSSPHRSHKKSKGKTNTGRKFPKKANTYKKCDLF CECVBHYRDKLLOREKEKELERERDKKDREKLESRESIDKEKE DECTPTRKERKRRHSTSPSPSSSGSRYKSSPPKSERSERSER SKKGKKSRSQSRSPHRSHKKSKGKTNTGRFFYKKANTYKCDLF LCPERSVF  5934  1 3190  GTRKLKMADKTFGGSQKASSKTRSSDVHSSGSSDAHMDASGGPSD CMSSNERPPSLLVIETKKPLKKGKEKKKKNTSPSREADGKNP PROSSNERPPSLLVIETKKRPLKKGEELKKKENDERPLENKLK APSIGKMSTARKTLSKRGGELKKKEDEKAAAEIYEEPIAAPEG SDMNVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSPRFADQKNP PROSSNERPPSLLVIETKKRPLKKGEELKKKENDERPSLLFFEELKQI QEERDERHKTKGRLSRFEPPOSDSDGGRRBAPSRRMSSGVL DDYARGSHDVORDSTT\NFYLIGNI\NPQNNLKKCCQFFGRFGP LASVKIMPRTDEERARERNGFVAFMNRADERALKNINGKMI NSFEKKLEWGKAVUPPPHYLDGNEEFCL ETEAPVEPPSKKGALKEGREKKKSNLTPFENGTPHAVYRW KLYSILQGDSPTKWRTEDFRHKNGSFWPPPBCLPFRAAP RERLKNPAPMLPPPRKMEDFERMITNDFRFFENGTPHAVYRW KLYSILQGDSPTKWRTEDFRHKNGSFWPPPBLYLHGMSEEC ETEAPVEEPSKKGALKEEGROKLLEEILGRINGCHLGRWFC LINABAAEEIVOCTTESLSLLKTPLPKKIZGHLGSENFKGRW TCFRAMBERDHAITYPSFILKLQUITSGLAUNTLERERDUDDLD	1			FGATLAVGLT1=VLSVVTIIICFTCSCCCLYKTCRRPRPV\APP
1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSGGSDAMMDASGPD SDMPSRTRPKSPRKHNYNESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDKRAABIYEEFLAAFEG SDGNKVKTFVRGGVVMAAKEEHETDEKRGKIYPSSFFADQKNP PNOSSNERPPSLLVIETKKPPLKKGEKGKKKSNLELFKEELKQI DDVAPGSHDVGDPSTT\NFYLGNI \NPQMNLKKCCQEFGREDP LASVKIMPRTDEBERREKTKGLSFFEPPOSDGGRSRMDAPSRRNRSSGVL DDVAPGSHDVGDPSTT\NFYLGNI \NPQMNLKKCCQEFGREDP RERLKBNADAMPLDPPDKNKEDPEKTLSQAIVKVVI PTERRILLALI HRMIEFVVRGPMFEAMMINNER INNPMFRELFERNJFAHVYTRW KLISILQGDS PTKMRTEDFRMFKNGSFMFPPLNFYLHGMSEQ FERAFVEEPSKKGALKEECDRKALELINGTPRRNDIGDAMVFC LNNAEAAEEIVDCITESLS ILKTFILPKKIARILVLVSDVLYNSSA KVANASYYNKFFETKLCQI FSLAITTRIJCHGLGSENFKORVM TCFRAMEDMAIYPEFFLIKLQNI FICLUM I IEEKETEOVPDDLD GAPIEELGGAPLEDVOGG PIDAATTRITIGHLOSENFKORVM TCFRAMEDMAIYPEFFLIKLONI FICLUM I IEEKETEOVPDDLD GAPIEELGGAPLEDVOGG PIDAATTRITIGHCSENFKORVM TCFRAMEDMAIYPEFFLIKLONI FICLUM I IEEKETEOVPDDLD GAPIEELGGAPLEDVOGG PIDAATTRITIGHCSENFKORVM TCFRAMEDMAIYPEFFLIKLONI FICLUM I IEEKETEOVPDDLD GAPIEELGGAPLEEDVOGG PIDAATTRITIGHCSENFKORVM TCFRAMEDMAIYPEFFLIKLONI FICLUM I I IEEKETEOKKEK DECTPTPTKERKRKRHSTSPSPSSGRKVKSPSPSKEPKSRSGRS GEVENSPSPSKERSERSER SKKSKYSEMSEEKRALERIELKVMKFQDELESGKPKKRGQSF QEQUENTYROKLLQREKERLERERERKKOKEKLESRSSIGKKEK DECTPTTKERKRKRHSTSPSPSSGRKVKSPSPSKERSERSER SKKSSSRSSSSKNSSPSSGRTPKSSSGRTPKKSRSRSSS KKSKSKSSGSRSPHSHKSSGSSGSDAMMDASGFSD AKSGKKSRSGSRSPHSHKKSKGKTHTGRKFFKKAVTTWKCDLF LCPERSVF GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAMMDASGFSD SMMSRTPRSSFRKINSTNSSASSCSDAMMDASGRFDLENKLK APSIGKMSTARKTLSKKEGELKKKBGEKKKKSNLELFKEELKQI OERDERHKTKGRLSRFEPPQSDSDGGRRSMDAPSRRNSGVL DDYARGSHDVGDPSTT\NFYLGNI\NPQNNLKKCCQEFGRFGP LASVKIMPRTDEERABERNGGFVAFMNRADABRALKNLINGKMI MSFEKKLGWGKAVUP I PPDH YI 19PSMMEHTLDPPPSGLPFNAQP RERLENDNAPMLPPPKNKEDFEKTLLGALIVAVVI 1PTERNLIALI HMILEFVVRGGPMFEAMIMMER I NINPMFPLEFBOTPAHVYYRW KLYSILQGDSPTKWRTEDFRMKNGSFWRPPPLNPYLHGMSEEG ETEAFVEEPSKKGALKEEGRKKLEEILERRINGIGHANDFCGDAMVPC LNNABAABEUNDTTESLILKTPLPKKITGCHLQSENFKQRW TCFRAMEDWAATYPSFLILBLUITELJUWI ILEEKEREEDVPDDDLD	1			EMOVED DA ODMODDA VICTO A COLD DE DESTRO
5933  GTRKLKYADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRMESARESLCDSPHQMLSRPLLENKLK AFSIGKMSTAKRILSKKEGELKKKEDENADALTYEFILAAPEG SDGNKVKTPVGGVVNAAAREBETDEKRGKIYKPSSRFADQKNP PNQSSNERPSPSLVIETKKPPLKKGEKKKKENBLEFKEELKQI QERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDVAPGSHDVGDPSTV\NPYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMMPRTDEERARENCGPVAFMNRRDABEALKNINGKNI MSFEMKLGGKGKAVPIPPHPIYIPSMMEHTLPPPPGGLPFNAQP REPLKAMPNAPMLPPPPKNKEDPFTAKSGAVKVVIYPTERNILALI HRMIEFVVREGPMPEAMINNEINNPMFRIPFNCNDIGDAMVPC LNNAEAABEIVDCITESLSILKTPLPKKIARLVIVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLAATTRIQGHGSENFKORVM TCFRAMEDWAIYPEFFLIKLQNIFLGUNNIIBEKETEUPVDDLD GAPIEEELLGGALEDVDGIPIDALGVITISKELPD QHEESEEENONGVEESEDBEDTJGSKSEEHADAVTTSKWELPD QHEESEEENSKNSPIFKVAAPSKWEAVBSSELEAOAVTTSKWELPD QHEESEEENSKNSPIFKVAAPSKWEAVBSSELEAOAVTTSKWELPD QHEESEEENSKNSPIFKVAAPSKWEAVBSSELEAOAVTTSKWELPD QHEESEEENSKNSPIFKVAAPSKWEAVBSSELEAOAVTTSKWELPD GEVBHYRDKLLQREEKEKELERERERKOKEKLESRSIOKKEK SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGRPKKPGQSF QEQVBHYRDKLLQREEKEKELERERERKOKEKLESRSIOKKEK SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGREPKKPGQSF QEQVBHYRDKLLQREKEKELERERERERKOKEKLESRSIOKKEK SKRKSKSSGSRSPHRSIKKKSKSKTNTGRKFPKKAVTYWKCDLF LCPERSVF  5934  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGFSD SDMPSRTRPKSPRRINKTNESARESLCDSBHQNLSRPILLENKLK AFSIGKMSTARRTLSKKEQELLKKKBBEKAAEITEFILAAFEG SCHNKVATYVRGVVNAAKEEHETDERRGIYKNSPRADAVND PROSSNERPPSLLVIETKKPPLKKGEKKKSNLLFREELKQI DDYAPGSHUVGDPSTT\NFYLGNI\NPQNNLKKCCCQEFGRFGP LASVKIMMPRTDEBRABERNGGVVAPMNARDABRRNKSGVL DDYAPGSHUVGDPSTT\NPYLGNI\NPQNNLKKCCCQEFGRFGP LASVKIMMPRTDEBRABERNGGVVAPMNENDABRRNRSGVL DDYAPGSHUVGDPSTT\NPYLGNI\NPQNNLKKCCQEFFGRFGP LASVKIMMPRTDEBRABERNGGFVAPMNRADABRALKHLIAKI HMILEFVVREGPMFAMIMMREIINPMPRPLEBNOLDAMVPC LINNAEAAEIVUVGIPFBAMILANGEI HMILEFVVREGPREAMIMMREIINPMPRPLEBOLDAMVPC LINNAEAAEIVUVGIPFBAMILANGEI HMILEFVVREGPREAMIMMREIINPMPRPLEBOLDAMVPC LINNAEAAEIVUVGIPFBLILLALIITERNBUIGDAMVPC LINNAEAAEEIVOCITESLSILKTPLPKKIACHCHANDVLINNSSA KVANASYYRKFFETKLCQITSSLINATYCIGCHLQSENFKQRW				PKANI.
SDMPSRTPRKSPREHNYRESARESLOSHOMUSPLENKLK APSIGKMSTAKRTLSKKEGELKKKEDEKAABIYEEPILAPEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRPADQKNP PNOSSNERPPSLJVIETKKPPLKKGEKCKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPOSDSDGRRSMDAPSRRNRSSGVL DDVAPGSHDVGDPSTT\NFYLGNI\POPMILKKCCCGEGREGP LASVKIMWPRTDEERARERNGCFVAPMHRIDABRALKKINGKMI MSFEMKLIGGKGAVPIPPHTYIPPSMHHTLPPPPSGLPFNAQP REKLKMPNAPMLPPPKNKEDFEKTLSQATVKVVIPPERNILALI HRMIEFVVREGDMPEAMIMMREINDMFRPLPENOTDAHVYVRW KLYSILQGDSPTWRTEDFRMFKNGSFWPPPLNYVLKM KLYSILQGDSPTWRTEDFRMFKNGSFWPPPLNYLKGMSEEQ ETEAPVEEPSKKGALKEEGROKLEELLRGLTPRKODIGDAMVFC LNNABAABEIVDCITESLSILKTPLKALIVLWSDVLYNSSA KVANASYYRKFFFTKLCQIFSLLKTPLKADILTSKROWN TCFRAMEDWAIYPEPFLIKLQNIFLGLUSHIKKETEDVPDDLD GAPIEEELCGAPLEDUDGIPSLONATYRTIQGHLGSENFKORW TCFRAMEDWAIYPEPFLIKLQNIFLSLUNILEKETEDVPDDLD GAPIEEELCGAPLEDUDGIPSLESKERENDILSENT SKFSKYSEMSEEKRAKLRRIELKVWKFQDELESGRFKKNEGSF QEQUBHYROKLLQREKKELERERERDKKOKKKLESRSKDKKEK SKFSKYSEMSEEKRAKLRRIELKVWKFQDELESGRFKKNEGSF QEQUBHYROKLLQREKKELERERERDKKOKKKLESRSKDKKEK DECTFTRKERKRHSTSSPSPSSGRFKVSSPSFSERSERSER SHKESSRSSHKDSFRDVSKKAKRSPSGSRTYKSSPKSERSESER SKKSSRSSSHKDSFRDVSKKAKRSPSGSRTYKKSPSKDSSKSK KKSKRSSCSSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  SOMPSRTREKSPRKINYRNESARSELCDSPHQNLSRPLLENKLK APSIGKMSTAKKTLSKKEGELKKEBDERAAAEITEEFLAAFEG SCHNKKTFVRGGVVNAAAEEBTERERDKKKYKSSRVLLEFKEELKQI DDYAPGSHDVGDPSTT\NFYLGNI\NPOPMILKKCCCGEFGFGP LASVKIMWPRTDERARERNCGFVAFMRRADERALNILNGKMI MSFEMKLEWGKAVPIPPHIYIPPSGLFPRNAOP RERLKNPNAPHLPPPSKLFPTNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP RERLKNPNAPHLPPPSKLFPRNAOP LANGKERPSKCGLKEEGDRKKELLIKGLTPRKNDIGDAMVPC LNNAGASYTREFETLACCITSDLNATYRTIGGHLQSENFKQRW TCFRAMEDWAITYBEFTLIKCPILGUNTIRGERDIDANDRIC LNNAGASYTREFETLACCITSDLNATYRTIGGHLQSENFKQRW TCFRAMEDWAITYBEFTLIKCPILGUNTIRGLBUNDL	5933	1	3190	
AFSIGKNSTAKRILSKREQEELKKKEDEKAAABIYEEFILAAFEG SDONKVKTYPURGGVVNAAKEEPTDEKRGKIYAPSSRFADQKNP PNOSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGGRSMDAPSFRRNESSGVL DDYAPGSHDVGDPSTT\NPYLGNI\NPQNNLKKCCQEEGREGP LASVKIMWPRTDEERARERNCGFVAPMIRDAERALKNINGKMI MSFEMKLIGMGKAVPIPPHPIYIPSMEHTLIPPPSGLPPHAQP REKLKMPAPMIPPPKNKEDPEKTLSQATVKVVIPPERNILALI HRMIEFVVREGDPFEAMIMNETINPMFRFLPENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGITPRKNDIGDAWFC LNNAEAAEELVDCITESLSITFLEKVATKJUNSDALVINSSA KVANASYYRKFFETKLCQIFSDLINATYRTIQGHLGSENFKORVM TCFRAMEDWAIJPEPFLIKUPITLGLUWI IEKETEUVPDLDLD GAPIEEELCGAPLEDUGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESSLERAQAVTTSKWELFD QHEESSEEENQNQEEESEDEETQSSKSEHLYSNPIKKEMTE SKESKYSEMSEEKRAALREIELKVMKFQDELESGKRPKKPGQSF QEQVBHYRNKLJCREKKELERERERDKKOKEKLESNSKOKKEK DECTPTRKERKRHSTSPSPSRSSGRRVKSPSPKSERSSRS SHKESSRSSKSPSPHRSHKKSGKTNTGRKEPFKKAVTVWKCDLF LCPERSVF SKESKYSEMSEEKRAALREIELKVMKFQDELESGKEPKKPGGSF KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKEPFKKAVTVWKCDLF LCPERSVF GTKKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SJMPSRTRRKSPRKINNYNNESARESLCOSPHQNILSRPLLENKLK AFSIGKMSTAKRTLSKEQEELKKKEDBKAAEITEEFLAAFEG SDGNKVKTFVRGGVVNAAKEBELETDEKKGKKYRSSRFADRINP PROSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKELKQI GEERBHTKTKGRLSFREPPGSGGGRGSRSDABPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMMRRDAERALKNLINGKMI MSFENKLGWGRAVDIPPHIYIPDSMMEHTLIPPPSCLPTRAQP RERLKNPNAAPHLPPPKNREDFRKNASPRRPPPLAVYYRW KLYSILQGGSPTKWRTEDFRRPKNGSFRRPPPLNYYLHGMSEEQ ETEAFVEEPSKKGALKEEGRIKLEELILGGLTPRKNDIGDAMVPC LNNAEABEUUDCITESLSILKTPLPKKIARLYLVSDVLINNSSA KVANASYYRKFFETKLCQIFSDLMATYRTIQGHLQSENFRQRW TCFRAMEDWALTPBEFFILGUFGDLMATYRTIQGHLQSENFRQRW TCFRAMEDWALTPBEFFILGUFGLDLAGUFGDLDL	ļ.	1		SDMPSRTRPKSPRKHNYRNESARESI.CDSDUONI CDDI I DAVE V
SDONKVKTFVRGGVUNAKEBETDERGKIYKPSSRFADQKNP PNGSSNERPBSLJVIETKKPPLKKGEKEKKSNLELFKELKOI  QEREDERHKTKGRISRFEPPOSDSDGQRRSMDAPSRNRSSGVL  DDYAPGSHDVGDPSTT\NFYLGNI\PPOMILKKCCCQEFGRRGP LASVKIMWPRTDEERARERKGFVAFMMHTLDPPBGLPFNAQP REKLKMPNAPMLPPPKNKEDPERTLEGATVKVVIPPERNILALI HRMIEFVVREGDMFEAMIMMREINNPMFRFLPPNTGPHNVYYRW KLYSILQGDSPTKMRTEDFRMFKNGSFWRPPPLNYFYHGMSEQ ETEAFVEEPSKKGALKEEGRKLEELIRGLTPRKDIGDAMVPC LNNAEAABEIVDCITESLSILKTPLPKKTARIYLVSDVLYNSSA KVANASYYRKFFFTKLCQIFSLNATYRTIGGHQSENFKORVM TCFRAMEDWAIYPPFFTKLCQIFSLNATYRTIGGHQSENFKORVM TCFRAMEDWAIYPPFFTKLCQIFSLSALATKTUSDVLJONLDGV PLDATEDSKKNEPIFFVALPSKEADUDGSLEAQAVTTSKWELFD QHEESEEELOAPLEDUDGIPIDATDIDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFFVALPSKWEAVDESSLEAQAVTTSKWELFD QHEESEEERNONGEESEDEEDTOSSKSEEHLLYSNPIKEEMTE SKFSKYSEMSEKRALKREIKVMKFQDELESGKRPKQPGSF QEQVBHYROKLLQREKEKELERERERDKKOKEKLESGKRPKKPGOSF QEQVBHYROKLLQREKEKELERERERDKKOKEKLESGKRPKKPGOSF QEQVBHYROKLLQREKEKELERERERDKKOKEKLESGKRPKKPG SKKSSKSSSSSSPHRSHKKSKGKTNTGKFPFKKAAVTYWKCDLF LCPERSVF SKKESSRSSSKNSPHRSHKKSKGKTNTGKFPFKKAAVTYWKCDLF LCPERSVF SCHCMSTAKRTLSKKEGELEKKEDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELKKKBDEKAAAETYBEFLAAFEG SCHMSTAKRTLSKKEGELGAETYBEFRAAFFRORDAM PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKELKQI GEERDERHKTKGRLSRFEPPGDSDGGGRSMDAPSRRNSSGVL DDYAAGSHDVGDPSTT\NFYLGNIYNPGFFLFFRONTAHVYYRW KLYSILQGGSPTKMRTEDFRHFKNASFWRPPPLHPTLHAMSEG FTEAFVERPSKKGALKEGORAAAETALVNLVSDVLINNSSA KVANASYYRKFFETKLCQIFSDLMATTATIQGHLQSBNFKQRVM TCFRAMEDWALTYBEFTLKLQIFSDLMATTATIQGHLQSBNFKQRVM	j	<u>'</u>		AFSIGKMSTAKRTLSKKEOEELKKKEDEKAAARIVEERIAARG
PNOSSNERPPSLLVIETKKPELKKESKEKKKSNLELFKEELKOI  QEERDERHKTKGRILSFEPPOSDSDGGRSMDAPSRRNSSGVL  DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRREGP  LASVKIMWPRTDEERARERNCGPVAFMMREDAERALKNINGKMI  MSFEMKLGWGKAVPIPPHI'IPIPSMMEHTLPPPSGLEJFNAQP  RERLKMPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI  HRMIEFVVRECPMFEAMIMNEINNPMFRFLFENQTPAHVYYRW  KLYSILQGDSPTKWRTEDFRWFKNGSFWRPPPLMPYLHGMSEGQ  ETEAFVEEPSKKGALKEEQROKKLEEILGGLTPRKNDIGDAWFC  LNNAEAAEEIVDCITESLSLIKTPLPKKTARILYLVSDVJLYNSSA  KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM  TCFRAMEDWAIYPEPFLIKLQNIFIGGWNIIBEKETEUVPDOLD  GAPIEEELDGAPLEDVDGI PIDATPIDDLOEVPIKSLDDDLDGV  PLDATEDSKKNEPIFKVAPSKMEAVDESELEAQAVTTSKWELFD  QHESEBEERONQEEESBEEDTQSSKSEEHHLYSNPIKEMTE  SKFSKYSEMSEEKRAKLREIELKVMKYQDELESGKRPKKPGQSF  QECVBHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKKEK  DECTPTRKERKRHSTSPSPSRSSGRVKSPSPKSSERSERSER  SHKESSRSSSHKDSPDVSKKAKRSPSGSSDAHMDASGPSD  SKKSKKSRSORSPHRSHKKSKKTNTGRKFFKKAVTYWKCDLF  LCPERSVF  5934  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD  SMPSTRPKSPRKHNYNESARSELCDSPHQNLSRPLLENKLK  APSIGKMSTAKRTLSKKEQEELKKBDEKAAAEIYEEFLAAFEG  SDCNKVKTFVRGGVVAMAKEEHTDEKGKIYKPSSRFADOKNP  PNQSSNERPPSLLVIETKKPPLKGKEKKKKSNLEJF KEELKQI  DEKPOSHRHTKKGLSRFEPPQSDSDGQRRSMDAPSRRNSSGVI  DDYAPGSHDVORGSHVANAKEEHTDERAGRIYKPSSRFADOKNP  PROSSNERPPSLLVIETKRPLEKRERNGGFVAFMINRDARAFRINGKMI  MSFEMKLGWGKAVP IPPHIYIPPSGLPFNAOP  RERLKNPNAPMLPPPKKNEDFEKTLSQAIVKVVIPPERBILLALI  HRMIEFVVREGFMFEMAINNEINNPRFLEFNOTPAHVYYKW  KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLIPVIHGMSEED  ETEAFVEEPSKKGALKEEGROKLEETLERGLTPRKNIGDAMVFC  LNNAEAAEEIVDCITESLSILKTPLPKKIARLVLVSDVLYNSSA  KVANASYYRKFFETELLCQIFFSLINATYRTIQCHLOSENFKORVM  TCFRAWEDWAITYBEPSLIKJIETKLOUTIELGENFERORVM  TCFRAWEDWAITYBEPSLIKJIETKLOUTIELGENFERORVM  TCFRAWEDWAITYBEPSLIKJIETKLOUTIELGENFEROPDDD	1			SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADOKNP
QEERDERHKTTGRISTFEPPQSBGQRRSMDAPSRRNRSSGVL DDYAPGSHDVDGPSTT\NFYLGNI\NPOMNLKKCCQEFGFPGP LASVKIMWPRTDEERARERNCGFVAFMMRRDAERALKVLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKUBNDAMPLPPPKKREDFEKTLSQAIVKVVIPFENLLALI HRMIEFVVREGPMFEAMIMNEINNPMFRFLFENGTPAHVYYRW KLYSILQGGS DFTKMRTBDFKNGSFWRPPPLNYPLHGMSEQ ETEAFVEEPSKKGALKEQRDKLEEILRGLTPRNDIGDANVFC LNNAEAABEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFFTKLCJTSDLMATYRTIGGHLGSENFKORVM TCFRAMEDMAIYPBFFLIKLONIFLGLWNIIBEKETEDVPDDLD GAPIEBELDGAPLEDVORIPDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVDAFKWEAVDESELEAQAVTTSKWELFD QHEESEEENQNQEESSEDEDTGYSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEERRAKLREILKVMKFQDELEGSKRFKKPGQSF QEQVBHYRDKLLQREKELELRCHENDKKOKEKLESRSKDKKEK DECTPTRKERKRRSTSPSPSRSSGRVKSSPSKSERSERS KKSGKKSSGSSSPHSHSRKKSKGKTNTGRRFFKKAVTYWKCDLF LCPERSVF  SHKESSRSSRSSHNDSFRDVSKKAKRSPSGSSTPKRSRSRSRS KXSGKKSSGSSSPSHSSHKKSKGKTNTGRRFFKKAVTYWKCDLF LCPERSVF  SJMPSRTRFKSPKKHNYRNESARESLCDSPHQNISRPLLENKLK AFSICKMSTAKRTLSKKGCELKKKBDEKKARAEITEEFLAFEG SCONKVKTFVRGGVVNAAKBEHETDEKRGLYKPSSRFADOKNP PMOSSNERPPSLLVIETKRPPLKKGEKEKKKNLELFKEELKGI QEERDERHKTKGRLSRFEPPQSDSDGGRRSMDAPSRRNRSSGVL DDYAPGSHDVOGPSTT\NFYLGNI\NPQMMLKKCCQEFGRFGP LASVKIMWPRTDEERARERGVFAMMNRDARAERJLKNIKGMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLGAIVKVVIPTERNILALI HRMIEFVVREGGPMFEAMINNREINNPMFRPLFENOTPHAVYYKW KLYSILQGDSPTKWRTEDERRRERDFENOTPHAVYNE KLYSILGGDSPTKWRTEDERRFRNSSFWPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEGDKLEETLRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKTARLVLVSDVLYNSSA KVANASYYRKFFETELCQTFSDLANTYRTIQCHLQSENFKQRVM TCFRAWEDWAITYBEFLIKIQNIFFLGLUNIIEEKETEEDVPDDLD				PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKOT
DDYAPGSHDVGDPSTT\NFYLRI\KRCCCGEFGREGP LASVKINMPRTDEERARERNCGPVAFNRRDABEALKNINGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSCLFPHAQP RELKMPNAPMLPPPKNKEDFERTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMINNREINNPMFRFLFENDTPAHVYYRW KLYSILGGDSPTKWRTEDPRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAPVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAWFC LNNAEAAEEIVDCITESLSILKTPLPKKLARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIGGHQSENFKQRVM TCRAWEDMATYPPEFILKQMIFLGAUNIIEKEFTEDVPDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEERNQNQEEESEDEEDTQSSKSEEHLLYSMPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPQGSF QEQVEHYRDKLLQREKEKELEREREDKKDKEKEKSKKEK DECTPTRKERKRRESTSSPSRSSSGRVKSSPSPKSERSERSER SKHESSRSSRSCHKNSPRDVSKKAKKSPSGSTPKRSRSRSESP KKSGKKSRSSSSSPFRFSPRSSSGRVKSPSPKSERSERSER SKKSEKSSSSSSPFRFFSPRSHSKSGRFVKSPSPKSETKSER SKKSKKSENSSPFRFSPKSHKKKSKGKTNTGRKPPKKAVTYWKCDLF LCPERSVF  3190 GTRKLKMADKTPGGGGKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSTTRPKSPRKHNYNNESARESLCDSPHONLSFPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVNAAKEEHETDEKGKIYKPSSFADQKNP PRQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKELKQI GEEDBERHKTKGRISRFEPPOSDEGGRRSMDAPSRRNRSSGVL DDYAPGSHDVOGDPSTT\NFYLGNI\NPOMNLKKCCCQEFGRFGP LASVKIMPFRIBERARERNGGFVAFMNRRDAERALKNINGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLEPFNAQP RERLKNPNAPMLPPPKMGFFKFTLSQAIVKVUPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPRFFLFENOTPAHVYYKW KLYSILQGDSPTKWRTEDFRHKNGSFRRPPPLIPPIHHEMSERO ETEAPVEEPSKKGALKEEGROKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIJCBAURVSCR	ı	·		QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVI.
LASVKIMMPRTDEERARERNCGFVAFMINRRDAERALKNILNGKMI MSFEMKLGWGKAVDIPTENTIJPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMINNEEINNPMFRELFENOTPAHVYTRW KLYSILQGDSFTKWRTEDPRMFKNGSFWFPPDLMPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDANVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARIYLVSDVLYNSSA KVANASYYRKFFETELLCGIFSDLNATTATIQGHLGSENFKGRVM TCFRAMEDWAIYPEFFLIKLQNIFLGLVNIIBEKETEDVPDDLD GAPIEELDGAPLEDVDGITJATITDGLIGGVIKSLDDDLDGV PLDATEDSKKNEPJFKVAPSKWEAVDESSLEAQAVTISKWELFD QHEESEEERNONQEEESEDEDTOGS KSEEHHLYSNPIKBEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKEEGOSF QEQVBHYRDKLLQREKEKELERERERDKKDKELKESRKDKKEK DECTPTRKERKRRSTSPSPSRSSGCRVKSPSPKERSRSRSP KKSGKKSRSSSHKDSPRVSKKAKRSPSGSRTYKSPSPKERSRSRSP KKSGKKSRSSSHKDSPRVSKKAKRSPSGSRTYKSPSPKERSRSRSP KKSGKKSRSSSHKDSPRVSKKAKRSPSGSRTYKSPSPKERSRSRSP KKSGKKSRSSSHKDSPRVSKKAKRSPSGSTAMMADASGPSD SJMPSRTRPKSPRKHNYRNESARESLCDSPHONLSRPLLENKLK AFSICKMSTAKRTLSKKEQEELKKEDEKAKLIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKKKKNLLFKEELKQI GEERDERHTKKGRLSREFSPOSDGGGRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT,VNFYLGNI,VNPOMNLKKCCCQEPGRPGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLINGKNI MSFEMKLGWGKAVVIPPHPIYIPPSMMEHTLPPPBGLFFRNAQP RERLKNPNADMLPPPKNKEDFEKTLSQAIVKVVIPPERNILALII HRMIEFVVREGPMFEAMIMRREINNPMFRFLFENOTPAHVYYKW KLYSILQGDSPTKWRTEDFRIKTNGSFWRPPPLNPYLHGMSERQ ETEAFVEEPSKKGALKEEGGRKLEEILEGLTPRKNDIGDAMVPC LINNAEABEIVDCITESLSILKTPLKNDIGDAMVPC LINNAEABEIVDCITESLSILKTPLKNDIGDAMVPC LINNAEABEIVDCITESLSILKTPLKNDIGDAMPC LINNAEABEIVDCITESLSILKTPLKNDIGDAMPC				DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCCEFGRFGP
REELKNPNAPMLPPPKNEIDFEKTLSQATUKUVIPTERNILALI HRMIEFVUREGMPKAMINREINNDMFRFLPENQTPAHVYYRW KLYSILQGDSPTKWRTEDFEMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNAMAABEIVDCITESISILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLGSENFKQRVM TCFRAMEDWAIYPEPFLIKLQNIFLGLVNIIEKENTEUVEDDLD GAPIEEELDGAPLEDDIDGIPIDATUPIDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESEDEDTQSSKSEHHLYSNPIKEMTE SKFSKYSEMSEEKRAKIEELEKVWKFODELESGKRPKKWEQGSF QEQVBHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSFSPSRSSSGRVKSPSPKSERSERSER SKHESSRSSSHKDSFRDVSKAKKSPSPKSERSERSER KKSGKSRSSSHKDSFRDVSKAKKSPSSPKSERSERSER SKHESSRSSSKSSHSSFRDVSKAKSPSPKSERSERSER KKSGKSRSSSHNSSFRDVSKAKKSPSSDAHMDASGPSD SMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKQEELKKKEDEKAAAEITEEFLAAFEG SSMRKVFTVRGGVVNAAKEEHETDERRGKIYKPSSFRADGNAP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI OEERDERHKTKGRLSRFEFPGDSDGGRRSNDAPSRRNRSSGVI DDYAPGSHDVGDPSTTVNFYLGNIVNPOMIKKCCQEFGREGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIJTPSMMEHTLPPPPSG_FFRAQP REGLKNPNAFMLPPP PKIKEDFEKTLSQAIVKVVJTERNILALI HRMIEFVVREGPMFEAMIMNREINNPMFRPLFENOTPAHVYYRW KLYSILQGDSPTKWRTEDFRWFKNGSFWRPPLMPYLHGMSEEQ ETEAFVEEPSKKGALKECORDKLEETLIGGLTPRANDFC LNAMBAAEEIVDCITESLSILKTPLPKKIARLYJVSDVLYNSSA KVANASYYKKFETKLCQIFSELLKUTIPFKKIARLYJVSDVLYNSSA KVANASYYKFFETKLCQIFSELLKUTIPFKKIARLYJVSDVLYNSSA KVANASYYKFFETKLCQIFSLLKNITIGCHIQSENFKQRVM				LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNINGKMT
HRMIEFVVREGPMFEAMIMMELINNPMFRLFENQTPAHVYYRW KLYSILQGSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKTARIYLVSBOVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVW TCFRAMEDWAIYPEPFLIKLQNIFLGLWNI IBEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKKELFD QHEESEEEENONQEEESEDEEDTQSSKSEEHHLYSNPIKEMTE SKFSKYSEMSEBKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKKEKLERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRSTSPSPSRSSGRVKSSPSKSERSER SHKESSRSSSHKDSPRDVSKKAKRSPSGSRTVKSPSPKSESERSER SHKESSRSSSHKDSPRDVSKKAKRSPSGSRTYKRSFSSEN KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFPKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SJMPSRTRPKSPRKHNYRNESAESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQBELKKLBDEKAAEIVEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PRQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKELKQI OBENDERHXYKGRISRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMLKKCCCQEFGRFGP LASVKIMWPRTDEERAREENCGFVAFMNRRDAERALKNINGKMI MSFENKLGWGKAVPIPPPHIYIPPSMCHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI HRMIEFVVREGPMFEAMTMNREINNPMFRLFENOTPAHVYYRW KLYSILQGDSPTKWRTEDFFRFKNGSFFRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGAKECQNDKLEEILRGLTPRNDIGGDAWFC LNNABAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEFFLLKQNIFIGLUNTIEEKERTEDVDDLD	1			MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
KLYSILQGDSPTKNRTEBFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQROKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLEKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIGGHLQSENFKQRVM TCFRAMEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDDLD GAPIEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKMEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVBHYRDKLLQREKELERERERDKKKKEKELSRSKDKKEK DECTPTPRKERKRRSTSPSPSSSGRRVKSPSPKSERSERS SHKESSRSSSHKDSPRDVSKKAKRSPSGSTPKRSRSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  SHESSYF  SHKESSRSSHKDSPRDVSKKAKRSPSGSTPKRSRSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  SHKESSRSSHKDSPRDVSKKAKRSPSGSDAHMDASGPSD SDMPSTTPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEBFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFPPPQSDSDGQRRSMDAPSRNNRSSGVL DDYAPGSHDVGDDST\NFYLGNI\NPQNNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPPPIYIPPSMMEHTLPPPPSGLFFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLALI HRMIEFVVRSGPMFEAMINNREINNPMFFFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFFRKFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEGRBKLEEILRGLTPRKNDIGDAWFC LNNABAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCJTSDLNATYRTIQCHIQSENFKQRVM				RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
ETEAPVEEPSKKGALKEEQRDKLEEILRGJTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDULYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKORVM TCFRAWEDWAIYPBFFLIKLQOIFIDATYRTIQGHLQSENFKORVM TCFRAWEDWAIYPBFFLIKLQOIFIDATYPIDLLDGVPIKSLDDDLDGV PDLDATEDSKKNEPIFKVAPSKWEAVDESSELEQAVTTSKWELFD QHEESEEEENQNQEEESEDEEDTOSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLEEILELKVMKFQDELESGKRPKKPGQSF QEQVBHYRDKLLQREKKELEERERDKOKKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSGRRVKSPSPKSERSERER SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP KKSGKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SJMPSRTPRKSPRKHNYRNESARESLCDSPHQNLSRPLLEHRLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSREPPPGSDSDGGRSMDAPSRRNRSSCVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFNNRRDAERALKNLNGKMI MSFEMKLIGWGRAVPIPPHPIYIPPSMHEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGFMFEAMIMNREINNPMFFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEQ ETEAFVEEPSKKGALKEEQRDKLEETLRGLTPRKNIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIGGHLQSENFKQRVM	1			HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW
LINNAEAAEEIVDCITESLSILKTPLPKKIARLYIJVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFIGLVNIIBEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKMEAVDESELEAQAVTTSKWELFD QHEESEEEENQNGEESEDEEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSGDKKEK DECTPTRKERKRHSTSPSPSRSSGRRVKSPSPKSERSERSER SHKESSRSRSSHNDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPPKKAVTYWKCDLF LCPERSVF  1 3190 GTRKLKMAADKTPGGSQKASSKTRSDVHSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEBEHTDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGREGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGRAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMINNBEINNPMFFFFENOTPAHVYYRW KLYSILQGDSFTKWRTEDFRRFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYMSSA KVANASYYRKFFETKLCQIFFGLUNTITEEKETEDVPDDLD	1			REISTLOGDSPIKWRIEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
KVANASYYRKFFETKLCQIFSDLNATTRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDULD GAPIEEELDGAPLEDVDGIPTDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELPD QHEESEEEENQNQEEESEDEEDTOSSKSEEHHLYSNPIKEEMTE SKKSKYSEMSEKRARKIREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKKDKKEKLESRSKDKKEK DECTPTREKERKRRESTSPSPSRSSGERVKSPSPKSERSERSER SKKSSKSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRRFFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSGCSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPGLKGKEKKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGFMFEAMIMNREINPMFRFLFENDTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRNDIGDAMVFC LNNAEABEIUDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAITYPEPFIIKLQNIFIGLWNIIEEKETEDVPDDLD				LANAFAAFETUDGITTEGI GILVETTE DIVINI DANAFAAFETUDGITTEGI GILVETT
TCFRAWEDWAITYEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEENTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGGSF QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRHSTSPSPSRSSGRRVKSPSPKSERSERSER SKKESSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAETYEEFLAAFEG SDGNKVKTPVRGGVVNAAKEEHETDEKRGKIYKPSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKKSNLELFKEELKQI QEENDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPSGLFPNAQP RERLKNPNAPMFEDFERKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWPPPLNPYLHGMSEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGBMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFFRAWEDWAIYPEPFLIKLQNIIFGLSUNIIEEKETEDVPDDLD	1			KVANASYYPKEFETKI.COLEGOLNATYDTIOGU GUTTUURISA
GAPIEEELDCAPLEDURGIPIDATPIDATPIDATPIJCHGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEERQNQEEESEDEEDTOGSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRHSTSFSPSRSSGRRVKSPSPSRSERSER SHKESSRSSSHKDSPRDVSKKAKRSPSGRTPKRSRRSRSPS KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  5934  1 3190  GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAETYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSMERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEPGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPFKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFFFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSEPFKQRVM TCFFRAWEDWAIYPEPFLIKLQNIIEEKETEDVPDDLD	}			TCFRAWEDWATYPEPFLIKLONIELCLINII DEVENEROURDALD
PLDATEDSKKNEP I FKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESEDTQSSKSEEHHLYSNPIKEEMTE SKPSKYSEMSEEKRAKLREIELKVMKPQDELESGKPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSGGRVKSPSPKSERSERSER SHKESSRSSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  1 3190 GTRKLKMADKTPGGSQKASSKTRSDVHSSGSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNINGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI HRMIEFVVREGPMFEAMIMNREINNPMFRPLFENQTPAHVYYRW KLYSTLQGDSPTKWRTEDFRMFKNGSFWRPPPLNYYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD				GAPIEEELDGAPLEDVDGIPIDATPIDALDGVPIVELDDDIDGV
OHEESEEEENONGEEESEDEEDTOSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEKRAKLREIELKVMKKFQDELESGKRPKKPGQSF QEQVEHYPDKLLQREKEKELERERERDKKDKEKLESRSVDKKEK DECTPTRKERRRHSTSPSPSRSSGRRVKSPSPKSERSERSER SHKESSRSSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSPSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF LCPERSVF  STRLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTTVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMINNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNFYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLUVNIIEEKETEDVPDDLD	1			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAOAVTTSKWELED
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AFSIGKMSTARRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKELKQI QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD		*	3730	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
SDENKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMPPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	f f			A POLICIA MORTA WHITE CHARLES A POLI
PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHHTKGRLSRFEPPQSDSDGQRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRNKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSUVINSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1 1			ALDIGHTSTAKKIPSKKEGEFFKKKEDEKAVAEIAEELTAEEG
QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMHEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRKKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSUDLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	j J	ļ		PNOSCHED DOG! I VIETKYDDI KARAKEHETDEKRGKIYKPSSRFADQKNP
DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHYIPPSMMEHTLPPPPSGLPFNAQP RERLKMPNAPMLPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1 1	1		OFFIDERHATACHT SEE BENDOCHUS SON SON SON SON SON SON SON SON SON SO
LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD			l	DDYADGSHDYGDDGTT\ NDVI CNT\ YDDYAY WYGAGATT
MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	, , ,		•	LASUKIMWPRTDEEPAPPDNCCDUA DNNDDDAADA
RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	]		j	MSFEMKLGWGKAVPIPPHDIVIDDOMMEUTI DDDDGG DTGG
HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	1	1	1	RERLKNPNAPMLPPPKNKEDFEKTT.COATUKIRIT DERDATT TOTAL
KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRIKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSOVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	!!	}	ļ	HRMIEFVVREGPMFEAMTMNREINNDMFDFI.FEMOTDALITAVEN
ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD		İ	1	KLYSILOGDSPTKWRTEDFRMFKNGSFWPDDDINDVI DOMORDO
LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD	]			ETEAFVEEPSKKGALKEEORDKLEETI.RGI.TPPKNDTGDAMURG
KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD			•	LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLVNGGA
TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD		1		KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLOSENFKORVM
GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV	. [			TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD
				GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

		····	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Farhenylaianine, Gadiyethe,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide defector,
	sequence		\=possible nucleotide insertion)
	<del> </del>		PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
	ł	Ì	QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
	i	1	SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
	[	ł	QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
	I	1	QEQVEHYRDKLDQREKERELERAKERDKADKERDESKSKDKKKK
		ł	DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
	1	1	SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
	1	l .	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
	1	l	
	1		LCPERSVF
5935	3	4493	SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
	1		SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF
	i	(	TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
	1	ł	LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
	1	1	DEPUMENDE CONCET COLLOS EMPEROTED DE IMPERO
	1	1	GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
	1	1	IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
	1		DDVOVESTEEEOESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
	1	1	KESEPAEEVKOEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
	1	1	VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
	I	I	GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
	Ĭ	1	GKVWIESAETHVSCCVIIV KNIEKTHITHIRKHIKIDHVI EETDDIDEKE
	1	1	PISMKDVYEEFDEKIATKYKIMKFKSKPVEKNYAFEIPDVPEKS
	1	i	EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
	I.	1	GPCWLEVKKSTALNOPVSWCKVEAMALKPDLVNVIKDVSPPPLV
	1	į.	VMAFSMKTMQNAKNHQNEIIAMAALVHHSFALDKAAPKPPFQSH
	1	Į.	FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTLLGFFLAKV
1	1	1	FCAARANCILLIAM KEATEKWAKARAMININGALCHI KDCWW
l		1	HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKRSNM
			PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
		ł	ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC
		I	ELNVLPLALQITNIAGNIMSRTLMGGRSERNEFLLLHAFYENNY
1	1	İ	IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
l .	1	1	TVPDKQTFKKPQQKLGDEDEELDGDTKKTKGKKGKGCCTTVODVACRAOKV
1		ł	DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASEAQKV
Į.	1		TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
1	1	1	LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
1	ì	1	YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEBVFKL
1	Ì	1	GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
	· I	l .	GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
l	<b>!</b>	i i	GWAALKOEPKGPDIAKKDMCDTWKDIGMAALOGTDDDG2KD11A
l	•	1.	ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
	t	l'	HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
1	1	1	LOKODNLTIDTOYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
1	1 .	l l	\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
1	1		TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
l	1	l l	TOT DAT IDNATIONS TO THE PARTY OF THE LAND.
1	1	i	KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
1	1	1	ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
1		Į.	LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV
1	1	I	KS
		<del></del>	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
5936	1124	139	ROLEUT DADERRE MUDGEGER DUGGEGER DURANTE DE CONTRA DE CO
į.	ŀ	1	RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS
1	1	l l	NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
1	i	ı	PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
1	l	1 .	SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
l .	Į.	1	SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
1	1	<b>{</b>	PUN / LTA LAVAMACIMIA A ANGUS CALLES ANGUS CALLES CONTRACTOR CALLE
1	l	l l	SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
1	1		QEQASSGWGSRIRGDGSGFSL
	31	1600	PTSLLKSTVOLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
5037		1	YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
5937	1		A COLOG TOWN THE PROPERTY OF THE PARTY OF TH
5937		i e	
5937			LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK
5937			LVKNAODKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSOLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSOLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLEELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPOVVTDLLPSLOKLSLDNEGSKLVVLNNLKKMVNLKS
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS LFLISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ
5937			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLEELIPEVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL KSSISRIPOVVTDLLPSLOKLSLDNEGSKLVVLNNLKKMVNLKS

SEC	Predicted	T = 37	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
- [	í		LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
5938	395	1865	PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
1		1000	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
1	į.	1	MTVWILLLESLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
-		ŀ	TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
1			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQI,QLHNFP
1	j		MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF
1	1		VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
			VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
1	1	1	YVTAMOLFVSVCF1FVFSALVEYG\TLHYFVSNRKPSKDKDKKK
l l	1		KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF
ı			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
			VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
l	i		LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
i			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
	l	İ	SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
			LGCGIGYGYLHRIPTRPFEEGKKISLPGOMAGTPITPLKDGFTE
			VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
1		Į	PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLNPFTROGI,PNI.PO
			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
ł	ĺ		APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
j.			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
5940	145	717	VDANASESP
	1	71,	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
1	1		LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
	1		QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
1	1 :		LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT LA\VYLVQMVVLILI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
1	1		WGQCNAJEW\LPFARPTNLTDEFEFFIGTYLNYECRPGYSGRPF
ŀ	ì		SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
1	l		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
1	1 1		TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
1			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
1	1		NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
·}	1		VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDW
1	1		SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
	· .	i	QLKGSSASYCVLAGMESLWNSSVPVCEOIFCPSPPVIPNGRHTG
1			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPOGNG
	1		VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
i		,	CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNCMVH
		J	VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHNSTKPPI
	1		CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
	i I	•	FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
	1	j	VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
j	1	l.	CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAA
í	1	į	SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
1	ĺ		KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
l		İ	PVIPNGRHTGKFLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
l	'		RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD FPIGTSLKYECRPBYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
1	1	1	PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
1	]	1	TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
			CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
	] [		TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
	1		LNKWEPBLPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
		!	EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
		1	LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP
	L		VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

Deginning cortion of location corresponding to first amino acid amino acid an	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notestion   Corresponding to first amino acid residue of anino acid residue of anino acid residue of anino acid sedue of acid sedue				
Cocresponding   to first   amino acid   to first   amino acid   to first   amino acid   to first   amino acid   to first   to firs				
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence  Perfoline, Gedlutamine, R-Argaine, S-Sexine, T-Threonine, V-Valine, Geduence  Tryptoplan, Y-Tyrcone, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide deletion,	1.0.	§		
to first amino acid residue of amino acid sequence  sequence  #TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop sequence  #TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop sequence  #TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-Stop TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, *-STOP TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, Y-TYPTOPHDAIN, Y-TYPTOSHE, X-UNKNOWN, Y-TYPTOPHDAIN, Y-TYPTOPHO,	i	3		
amino acid residue of amino acid sequence  Sequence  Sequence  Feyrptophan, Y-Tyrosine, K-Wukknown, **stop Codon, /=possible nucleotide deletion, /=possible n				
residue of amino acid sequence  amino acid sequence    Vapossible nucleotide deletion,    Vapossible nucleotide insertion   Vapossible nucleotide insertion   Vapossible nucleotide insertion   Vapossible nucleotide insertion   Vapossible nucleotide insertion   Vapossible nucleotide insertion   Vapossible nucleotide	1		ř	
amino acid	l	•	residue of	S=Serine, T=Threonine, V=Valine,
Sequence    A-possible nucleotide insertion	į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence    A-possible mucleotide insertion	ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
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VARELAI FRVPMKYPTSKAVYIAPLKALVÆRENDDWKVRI LEEKL GKKVIELTGDVTPDMKSIAKADLIVTTPEKWEGVSRSWQNRNYV QQVTILI IDEIHLLGEBERGFVLEVIVSRTMFISSHTEKPVRIVG LSTALANARDLADWLMIKQMGLENFRPSVRPVPLEVHOGFPGQ HYCPMASMIKPAFQAIRSHSPAKPVLI FVSSRRQTRLTALELI AFLATEEDPKÖWLINDERBEMEN I ATVRDSNILKLTLAFGIGMHH AGLHERDRKTVERLFVNCKVQLIATSTLAWGVNFPAHLUJIKG TEYYDGKTRATVDFILFVNCKVQULIATSTLAWGVNFPAHLUJIKG TEYYDGKTRATVDFILFVNCKVQULIATSTLAWGVNFPAHLUJIKG TEYYDGKTRATVDFILFVNCKVQULIATSTLAWGVNFPAHLUJIKG TEYYDGKTRATVDFPTVCKVQULIATSTLAWGVNFPAHLUJIKG TEYYDGKTRATVDFPTVCKVQULIATSTLAWGVNFPAHLUJIKG VANDKFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKQDALD YITMTYFFRRLTMIPSYYNLGDVSHDSVNKFLSKQTALD KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKQDALD YITMTYFFRRLTMIPSYYNLGDVSHDSVNKFLKHTOKDRAKEL LSYCIBIGBDINSI BEILKGTAIASYVLKFICTWORFVNFRFLE STEELLSILSIDABETYDLPVRINEDHMISELAKCLP I ESNPHSP BSPHTKAHLLLQAHLSRAMIPGENIANGVUKGKUKDSSLLTLENIENHHL HLFKKWKPIMKGGHAARGRTSIECLPELIHACGGKDHVPSSWVES ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQEVVLQVSLQRVHFGFHKGKPESCAVT PRFPSKNDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSPYT PEILPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ GL  5943  1 2274 DKPTRHKTYLSSSWAKMAABAGGPVGDGELWQTWLPNHVVFLRL GLKNQSPTEASKPASSLDSSPPPOLLTRNVVEGLGGELFLWD GEDSSFLVVRLRGPSGGS\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELFRRWGKNESFEGGKSTVNCSTTP VAERFFTSSTLTLKHAAWYPSSILDPHVVLLTSDMVIRITUSL EPQTPTNVIILSEABEESSLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNKGKDAVAYPSLYLLYENGETFLITTISLLHSEGN/I WKAVGSIAHAS\AABHNYGYDACAVLCLPCYPNILVIATESGM/I WKAVGSIAHAS\AABHNYGYDACAVLCLPCYPNILVIATESGM/I HKLHFLGSDEEDDKSLGPLKSKWGRSTPLGCYPRHILTTREPN/I HKLHKFLGSDEEDDKSLGPLSTERQKCPVEHILCTKPLPCRQPAP IRGWUVPDILGPTMICITSTYBCLWPLAFGAVHSVGLITWI HKLHFLGSDEEDKNSLGPLSTERQKCFVEHILCTKPLPCRQPAP IRGWUVPDILGPTMICITSTYBCLWPLAFGAVHSVGLITWI HKLHFLGSDEEDKNSLGPLSTERQKCFVEHILCTKRPLPCRQPAP IRGWUVPDILGPTMICITSTYBCLWPLAFGAVHAGEKG LAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCD	į.	į.		1
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TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVILVHDI KKDFYKKFLYEPFPVESSLLGVLSDHLMAEIAGGTITSKQDALD YITWTYFFRRLIMPSYYNLGDVSHDSVNKFLSHLIEKSLIELE LSYCIEIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC STEELLSILSDAEEYTDLPVRINEDHNNSELAKCLPIESNPHSP DSPHTKAHLLLQAHLSRAMLPEPDYDTDTKTVLDQALRVCQAML DVAANGGWLVTVLNITMLIQMVIQGRMLKDSSLLTLPNIENHHL HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVES ELHAAKTKQANNFLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQEYVLQVSLQRVHFGFHKGKPESCAVT PRFPKSKDEGGMFLILGEVDKRELIALKRVGYIRNHHVASLSFYT PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ GL  5943  1 2274 DKPTRHKTYLSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLPEIYQVL LSPTCHHVALIGIKGLMVLELPKRWGKNSEFEGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTFTNVIILSEABEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AABDNYGYDACAVLCLPCVENILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVPECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWLVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTK EDVEVAESPLERVLAETPDSFEKHIRSILQRSVANPAPLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDO	}	1	i	•
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YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE LSYCIBIGEDNRSIEPLTYGRIASYYYLKHOTVKMFKORLKPEC STEELLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF DSPHTKAHLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNIENHHL HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVPSSMVES ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQEYVLQVSLQRVHFGFHKGKFESCAVT PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASLSPYT PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ GL  5943  1 2274 DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR EGLKNQSPTEAEKPASSSLPSSPPPPQLLTRNVVFGLGGELFLWD GEDSSFLVVRLRGPSGGG EEPALSQYQRLLCINPPLPEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGKSTVNCSTTP VAERFFTSSTSLTLKHAAMYPSEILDPHVVLLITSDNYIRIYSLR EPQTPTNVIILSEAEEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILVENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRTDLIPSLVVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHTLCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYBCLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHTRSILQRSVANPAFIKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1	Į.		
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DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSEAEEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLVVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILGRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ		1		
EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSEAEEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGR/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPPA IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ		L	<u> </u>	<u> </u>
GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSEAEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGR/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPPA IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	5943	1	2274	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR
GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVIILSEAEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGR/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPPA IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1	i	1	EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD
LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR EPQTPTNVILISEAEEESLVINKGRAYTASLGETAVAFDFGFLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESCML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESFLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	i	1	1	
VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSIR EPQTPTNVIILSEAEEESLVINKGRAYTASIGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESCML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPPDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1			, , , , , ,
EPQTPTNVIILSEAEEESLVLNKGRAYTASLGETAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1	ł	l	
AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	ł	Į.	1	
WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGML YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDFFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1	1	Į·	
YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1	Į.	1	1
ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	I	1	ļ	· • · · · · · · · · · · · · · · · · · ·
HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	I	1	1	YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVELELALKL
HKLHKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLPCRQPAP IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	į.		1	ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWI
IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLLCTR EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1			1
EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLKASEKD IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	I	1	<b>!</b> .	
IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ	1		· ·	1
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	ì	1	ļ	Land to the second seco
TOTAL TOTAL	t			I KKKALEDI. EVPDEEDKEI DEMARDI ADKVEEAVEKARDIMIOMV

SEQ	Predicted	Predicted end	I have a second and a second an
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion.
	sequence	<del> </del>	\=possible nucleotide insertion)
	1	į	KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
1	1		KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
5944	167	3428	KQINDIRNHVNF
Í		3420	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
	İ		ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
1	ŀ		KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
ł			GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
1	i		SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
1			TRQATQLINALIKDPDKEIDELIPKNRLKSSSANSKIGSSAPTT
İ		,	TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
1		}	VN\NVRPGFPVSFP\LAYPPPOFAHALLAAOTFOOIRPPRI.PMT
	,	1	HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNONSS
1	1		GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRROLF
1		]	VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSS₽
		1	SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
1		ĺ	TNTRPPNSSSSGSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
1	1	·	EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
1			PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
	ļ	ļ.	SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
i		ĺ	FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
1			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
1			GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIROTG
`	}		TSAPSVIGSNLSTSVGHSGIWSFEGIGGNODKVDWCNPGMGNPM
1			IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHOHVPAGYMDFPK
			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
5945	1461	197	MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
	2102	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
l i			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
]			KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
1 1			AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
1 .1			GETRSPENRSPTPSLQYCENCDTHFODSNHRTSTAELLSLSOGP
	•		QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
1 1	,		LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
5946	541		REERRREE\KDRAWERDLRTYMNLEF
1 220	247	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
] [			SEGSPORVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
j	1		YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
[ ]	1		YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
1	i	i	KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF
<b> </b>	ł		SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
	1		DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVI:
] 1		1	
			DENSYPLOQDFSLLDFYPDIVKHGANARL
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEOGFGAPCLKCKEK
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK  CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT  KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA  PPVQNQALARQYMCMLPKEKOPVAGSEGAOYRKKOLAKOLPAHD
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMCMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGYGDVKLPCEMDAOG
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTOYSCYCYKLSMKEG
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PYVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDI KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENONWHLKHFCCFDCDSI
5947	3		DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDI KYTTLIAKLKSDGIFMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMOMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDBLIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCOGCHNAIDPEVORVTYN
5947			DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMCMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NFSWHASTECFLCSCCSKCLIGQKFMPVEGWVFCSVECKKRMS
	39	3370	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMCMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDBLIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NPSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGDTDO
		3370	DENSYPLOQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVONQALARQYMOMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG RHYCDSEKPRCAGCDBLIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NPSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAOAODM
		3370	DENSYPLQQDFSLLDFYPDIVKHGANARL  RGIPDRRRRGPIGRVMMDLENKVKKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA PPVQNQALARQYMCMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG RHYCDSEKPRCAGCDBLIFSNEYTQAENQNWHLKHFCCFDCDSI LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN NPSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGDTDO

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location		
	D .	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding		L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
Į.			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1	1		VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
1	i		RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
İ		ļ	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
ł		Í	OCHKANCYTAFHVTCAOKAGLYMKMEPVKELTGGGTTFSVRKTA
ŀ	<b>[</b>		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
i	ļ	ĺ	
ł	1		KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
	1		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
ł		į.	KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
l	1	]	MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
	l		KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1		1	FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
ļ.	1		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
l	1	ļ	SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1	1	l	GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
I	1	J	TNGFGGARSEOEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
1			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAAR!AAEV
1	}	]	CQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
l .	ì	i	PGHHNGVTIPAPPLDVLKIGEHMOTKSDEKLFLVLFFDNKRSWO
1		1	WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
1	1		
5949	39	3370	SRVHGEPTSDLSDID
1 2949	""	33/0	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
1	i		GNHYQMRRKGRCHRGSAARHPSSPCSVXHSPTRETLTYAQAQRM
j		İ	VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
1	1	ļ	PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY
1	1	]	SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
1			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1	1	<b>!</b>	VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
1		Ì	RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
l		ļ	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1		}	QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
1	1	1	YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1			KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
I	(	j	FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1	1	1	KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA
1			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1	1 .		KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1	(		FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
1			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
ı	1	[	SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
I	l		GPEAGEEVLPRLETLLOPRKRSRSTCGDSEVEEESPGKRLDAGL
1	1		
1			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
J.		1	FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
I	1.	<b>!</b>	GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
ł	1	İ	PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
1	1	ļ	WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
			SRVHGEPTSDLSDID
5950	1166	373	ESRS_TMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
J	i	ł	CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
1			DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
		1	SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
1		f	KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
1	1	l	LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
5951	143	5449	
7,5,5	1 143	3449	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
1	1	l	VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
1	1		GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGYCEDA
1	I	]	ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDQNSK
I	1	1	QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
1	1	1	VIHSKONMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
ı	i	]	QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ
	1		L XXIII INI A VAVIVINA TO STATE IN TAGE A DO A LOS AND A

SEQ	Predicted	Predicted end	1200
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	l .	\=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
		ĺ	QCHKPQQQAPAMKTNSHVKEELEHPGVEHFKEEDKLKLKKPEKN
- 1	1		LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
1	1		WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
ŀ	1		GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
į			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
- 1		į	NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGFK
1			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADOTPOSVP
- 1	ł	}	HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFFDTDAK
	1		YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
			KELAAWRRRENRHTIEMIEKEOREVERRPITKTTHKGETETESD
J	1	Ì	APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
	1		QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
	1		AESIADALSSTSNILASEFFEEEKOESPKSTFSDADDDDDDDCTV
-	Í	ļ	EVESTFLARLNFIWKGFINMPSVAKFVTKAY?VSGSPEYLTEDL
1	i		PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
1	1		SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
	J		PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
1			NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
i			ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSABIETSVVG
1			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
J			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
1	i j	•	LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
ł	1		HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
			PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
	1 1		VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
	]		SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\ONDM
1	1	J	VPWPPVV\HLP\GQPQRMMGPLSOASRYIGPONFYOVKD7PPDF (
İ			RRHSDPWGRQDQQQLDRPFNRGKGDRORFYSDSHHLKRFRHEKE
			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHCDRGTD
1			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
5952	3226		KDRDHTDRTKSKR
	3220	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
ſ	ŀ	ľ	ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
			QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
		· ·	QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
1 1			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR EQYESFEILAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET
1 1	ľ	I	YTFTIFENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS
1 1		ļ	PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL
1	}		QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
1 . 1			DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1	· i		NIERQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVRDODR
1 1		i i	GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGTRYKKI.
j 1	ł	1	TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDOG
1 1	į.		GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAETVAVDD
1 1	1	i i	DEPIHGPPFDFSLESSTSEVORMWRLKAINDTAARI.SYONDDDR
] [	ļ	1	GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
		j i	GGVQLGKWAILAILLGIALFFCILFTLVCGASGTSKOPKVIPDD
] [		ļ.,	LAQQNLIVSNTEAPGDDKVYSANGFTTOTVGASAOGVCCTVGSG
1 1		. 1	I KNGGQETI EMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
5953	330		RYTYSEWHSFTQPRLGEESIRGHTLIKN
	550	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
1 1	İ	] ;	LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
]		1 ;	KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
5954	32	2130	VSNDLWGDFSTASSSVPNQAPQPSNWVQF
			PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE
LI		1;	AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH

Predicted   Pred				
Notestide   Corresponding to first mainto acid residue of amino acid residue of amino acid residue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of amino acid sedue of the acid of acid of acid of the acid of th	SEQ	Predicted	Predicted end	Amino acid segment containing signal pertide
corresponding to first amino acid residue of amino acid amino acid residue of amino acid sequence sequ				
to first amino acid residue of amino acid residue of amino acid sequence  P-PTOLINE, V-Valiane, V-Valiane, sequence  P-PTOLINE, V-Valiane, S-Serine, T-Threonine, V-Valiane, sequence  PFSKQAVENCEHERSKUP TO-VIVOSINE, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide insertions: ADTOGNOWANCIANER REPORTED THE SERVE OF THE SERVE O	NO:			, · · · · · · · · · · · · · · · · · · ·
to first and acid residue of amino acid and acid residue of amino acid and acid sequences sequences s	l .			
amino acid residue of amino acid sequence  ### Septime, T=Threonine, V=Valine, amino acid sequence  ### Septime, V=Prysosine, X=Unknown, *=Stop Codom, V=possible nucleotide deletion, V=possible nucleotide insertion)  ### SERVETTEROMETRICAL SERVETTION OF THE SERVET	ļ		1	
residue of amino acid sequence (Oddon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion)  PFSKOMPROGRAMENTHINDEFSWIRITGRGGFGEVYGCRK  ### PFSKOMPROGRAMENTHINDEFSWIRITGRGGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGFGEVYGCRK ### PFSKOMPROGRAMENTHINDEFSWIRITGRGFGEVYGCRK ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVYRADAPPTIGFSPEDTMSTIRIDGTOGFTSFELDGGLL ### RGSVGRADAPPTIGFSPEDTMSTIRIDGTAMPTIGGTGGTGGTGTDOGFTSFELDGGLL ### RGSVGRADAPPTIGFSPEDTMSTIRIDGTAMPTIGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	ł			
amino acid sequence  Codon, /-possible nucleotide insertion)  PFSKQAVEHYQSHLSKKQVISTLFQPYIELICSLRKGDIFOKEM ESDKETHFCQMKNUELNIHLIMMESPURE ICESLRKGDIFOKEM ESDKETHFCQMKNUELNIHLIMMESPURE ICESLRKGDIFOKEM ESDKETHFCQMKNUELNIHLIMMESPURE ICESLRKGDIFOKEM ADTGONVANKCLNKKRIKKKGETLALIRER HILLUSTENDEPJ  VCMTTAFHTPDELCFILDLMMEGGIHTMILGHENGESKENEFYA TEILIGLEHMHHRFVVYRDLEFANILLDEHGRANIS VDLGLACH FRKKRHASVGTHOWARPEVLQKOTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGISFFRGHYRTKDHREIDRUTAVISSADMYSELKGMLEKUL RGYMKELCHINGREFYLYPELAVRELARGESPALKELKE RGYMBLLENDHLIMME REFERRIAVELARFANDENLERGKGGGFRAUKELKE TYKKAQRILLERAPKINKPRSGTVELEPSELCHRENDLIMME LILVSETDIJEDRUTAVISTATERSEKVETBWKTASGAVLALGE WASSLEGILPHLAINFULDVILOTITOPHLENGEGGLKSGOFRADVIS VKRICHNINBDVGLFGVLBETANSEREVERWKTASGAVLALGE WASSLEGILPHLAINFULDVILOTITOPHLENGEGGLKSGOFRADVISTA VLAVACOSCILLITUTATDTSLETTRESGCAVULSHPGHTPVTSLA WASSGGLLASPOVANISTIVELKHRIDGUTAVISLAMPHYSA VLAVACOSCILLITUTATDTSLETTRESGCAVULSHPGHTPVTSLA WASSGGRLEARVICEPLITSLSFPRECESKIK ALEVOSOQULMQICL RQOTREMOMRACHERICH DET SLETTRESGCAVULSHPGHTPVTSLA WASSGGRLEARVICEPLITSLSFPRECESKIK ALEVOSOQULMQICL RQOTREMOMRACHERICH DET SLETTRESGCAVULSHPGHTPVTSLA WASSGGRLEARVICEPLITSLSFPRECESKIK ALEVOSOQULMQICL LYVKSSILITUTATOOPEVAKRRIBLEKENDCHOCHUS SANDVITSLA SPORSKLATTUSAVRIVAVARAVINERGENKEN SALELDAMBALSHKRANDEVAKURENDEVAKUPATAVINERGENKEN LYVKSSILITUTATOOPEVAKRRIBLEKENDCHOCHUS SANDVITSL SALELDAMBALSHKRANDEVAKURENDEVAKUPATAVINERGENKEN RAILEDAMBALSKARERKULLGOPTAVINERGENKANTAVINERGENKANT RAINKAMPHYSTATUTATOOPEVAKRRIBLEKENDEVASSADMANTAVINERGENKANTAVINERGENKANTAVINERGENKANTAVINERGENKANTAVINERGENKANTAVINERGENGANTAVINERGENGANTAVINERGENGANTENTAVINERGENGANTENTAVINERGENGANTENTAVINERGENGANTAVINERGENGANTENTAVINERGENGANTENTAVINERGENGANTAVINERGENGANTENTAVINERGENGANTAVINERGENGAN	ļ	amino acid		
Sequence   Sequence	i	residue of	amino acid	
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ROQYRHOWERGLEERLTPWSGTPVGNVNLCL  SYSTEM 1705  139  GVGVVRGARAMATVQEKAAALNLSALHSPAHEPPGFSVAQKPFGA TYWKSIINTLQTQVEVKKRHELKRENDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVYGKDKKPT PEDSSCSLYRPTTIPNDQSLGENKILYSPARYADALFKSSDIR SASLEDLWENISLKAPANSPHYNISATISPQVINEVWGEFIGRL LQLVDLPLLDSLLKQQEAVPKIPQPKVGETMVNSSNYLDRGILK AYSDSQEDEMLSAAIDCSSYLPDQMVVEISRSFPEQPDKTDLVK ELLFDAIGRYYSSREPLINHLSDVHNGIAELLVNGKTEIALEAT QLLLKLLDFQNREFFRELLYFMAVAANPSSFKLQKESDNRVVK RIFSKAIVDNKNISKGKTDLLVLFL\NDHQKDVFKIPGTT\HKI VS\VK\LMAIQNGDPNRDAGYIYCQRIDQRDYSNNYTEKTKDB LLNLLKTLDEDSKLSAKEKKK\LLGGFYKCHPDIFIEHFGD  S957  1479  451  ELQVAVAMDTLDRVVRFKTRRAKRFLEFKEPKLNENIKNAMLIK GNNANTVTKVLKDVYALKKYVGYVKKNITRPFEDDTSLEFF SKKSDCSLFMEGSHNKKRPNILVIGRMYDVHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDLYLLSKMPKALKKKKNISHD TFGTTYGRIHMQKQDLSKLGYRM\KGLKKRPAERTIPDEKKS KRIKKKLMELSQPLLFHCVLLKRIIKNGSIGSFL  5958  1  3138  AAALGMLLWFPACQAFNLDVEKLTVYSGFKGSYFGYAVDFHIPD ARTASVLVGAPKANTSCPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSOWFFG,ATVKA\HKGKSCCFVAP LLFFMRFILKPTERGENGTVAVAJEFSPCGNSNADP EGGGYCQAGFSLDFYNGDLIVGGGGSFYWQGQVITASVADIIA NYSFKOLIRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGVYSIINSYDMTFIQNTTGEQMASYFGYTVV VSDNNSDGLDDVLWGAPLFMEREFESSPREVGGIYLYLQVSSLU FRDPQILLGTBTFGFGSMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPPFKFCGGWASHAVPSGFGFTLRCD SDIKNNYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENNKTCQVPDSMTSAACFSIRVACYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSIRVACYRARPVTVTVAQLLHPMIIN LENKTCQVDSMTSAACFSIRVACYRARPVTVTVAGCLDFNILMEVGLD SLKKGGAIKRTLFLDNHQAHRVPFLVKRQKGGGCCQDFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRTLFLDNHQAHRVPFLVKRQKGGCCCOPFILYYLAD SLKKGCGAIKRALEFAUDESTFKEGLEVKPLINYTRENIVSE CAHILVCCCGEDNLCVPDLKLSARPDKHQVIIGGENHLMLIINAR NGGGGAVEALERLEFAUDESTFKGLGEKVPLINYTRENIVSE CAHILVCCCCOMPUNSCTNYSLEADVGLERNKGFRPLSCEYMBSNTV		ļ	1	
S956  1705  139  GVGVRGRARMATVQEKARALNICSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRHRIKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDVKVFEAVPTKVFGKDKKPT FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARVADALFKSSDIR SASLEDLWENISLKPANSPHINSTATLSPQVINEVMOEBTIGKL LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQBEMLSAAIDCSEYLPQGMVVLSRSFFFRGPORTDLVK ELLEDAIGRYYSSREPLLINHLSDVHNGIABLLVNGKTETALEAT QLLLKLLDFQNREEFRILLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIUDNKNLSKGKTDLLVJEIJMDHGKOWFKIPGTI-HKI VS\VK\LMAIQNGRDPNRDAGYTYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGGPYKCHPDIFTEHFGD  S957  1479  451  ELQVAVAMDTLDRVVKPKFKKRFLEKKREPKLNENIKNNMLIK GGNANATVTKVLKDVYALKKPYGGVYKCHPDIFTEHFGD SKKSDCSLFMFGSHNKKRPLNKLYGRMYDYHVLDMIELGIENFV SLKDIKNSKCPEGTKPMLIFADDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKYYFRSYKLLKKSGCRTPRIE LEEMSPSLDLVLRTHLASDTVLKSKMKKLKSGCRTPRIE LEEMSPSLDLVLRTHLASDTVLKSKMKKKLKSGSFF TYGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHGSIGSFI  5958  1 3138  AAALGMLLWFPACOAFHLUDVEKLTVYSGFKSSYFGTAVDFHIPD ARTASVLVGAPKANTSQPLVEKGAVYCPWPAEGSAQCRQIPF DITNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFFWRIFLKFTEPSKGPVGTYVANGSFYFGQQVITASVADIIA NYSFKDLIRKILAGEKQTEVAPSVDSYLGYVAAGEFTGDSQQ ELVGIPRGQNFGYVSIINSYDMTFIQNFTGDQMASYFGYTVV VSDNNSDCLDDVLVGAPETFREFEENFRVGGIYTALVGVSLL FRDPGILTGTETFTGRFGSAMHLGDLNQDGYNDIAIGVPRAGKD GRGWLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD GRGWLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD GRGWLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD GRGWLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD SDJDKNDYPDLIVGAPGTGKVAVYRARPVVTVAQCLLLHMININ LENNTCQVPDSMTSACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLUKRQKSGJQCQDFIVYILAD BLENKTCQVPDSMTSACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLUKRQKSGJQCQDFIVYILAD BLENKTCQVPDSMTSACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLUKRQKSGJCCQDFIVYILAD REFERDKLSP INISLNYSLDESTFKKGLEVKPLINYYREMIVSE QAHILVDCGEDNLCVPDLKLSRRAKFGLEKVRLINYREMIVSE PARDRULSPINISLNYSLDESTFKKGLEVKPLINYTREMIVSE QAHILVDCGEDNLCVPDLKLSRRAKFRLSINKGFRPLSCETKMENVT RMVCDLCHNWVSGTNVSLGLRRAVPPLESTNNSINFDLQIRSS		1	1	GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
TYWKSSINTLOTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKKKPT PEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR SASLEDLWERILSLKRANSPHVNISATLSPQVINEWQEETIGRL LQLVDLPLLDSLLKQQASVPKIPQEKRQSTWNSSNYLDGRILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT QLLKKLLDFQNREEPFRILYMAVANNPSFFKLQKESDNRMVK RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYQRTDQRDYSNNTEKTTKDE LLNLKTLDEDSKLSAKEKK\LLGQFYKCHPDIFIEHFGD  5957 1479 451 ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEQGTSLEFF SKKSDCSLFMRGSHNKKPPNNLVIGRMYDYHVLDNIELGIENFV SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFGSYKLLKKSGCTPPHF SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFGSYKLLKKSGCTPPHF LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKNISHD TFGTTYGRIHMQKQDLSKLQTIKMYKGLKKRPAERITJDHEKKS KRIKKKLMELSGPLLFHCVLLKRIIKHGSOSFL  AAALGMLLNFFACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGABKANTSQPDIVESGAVYCPWEAEGSAQCRQIFF DITNNRKIRVNGTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSCGPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSGCPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGKSGCPVAP LLFTMRNFLKURSTKEPIEFKSNQWFG\ATVAK\HKGLLIFMIN NYSFKDLIKKLAGERGTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELWAGIPRGAQNFGYSINSTNYBTQNFTGEGMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPEVGQIVITASVADIIA NYSFKDLIKRLAGERGTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELWAGIPRGAQNFGYSINSTNYBTQQVITASVADIIA LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVPPLVIKRQKSGCQDFTVYLED ETEPRDKLSPINISINYSLDESTFKKGLEVKPILNYTRENIVSE QAHILVDCGEDMLCVPDLKLSARPDKHQVIIGGENHLMLIINAR NEGGGAVRAELFVMIPPEGDTVYSLGLERFAVELEKTMMSINFDLQIESS	1	1		RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
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TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL  5958  1  3138  AAALGMILWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	l	1	1	•
KRIKKLMELSQPLLFHCVLLKRITKHQSIQSFL  5958  1  3138  AAALGMLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTEFFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPLLNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCETKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			
AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGGQYQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQPFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPLNYYPRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYBAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1		1 "
ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTCTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	5959	<del></del>	3128	
DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP  LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP  EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWGQVITASVADIIA  NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ  ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV  VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL  FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD  QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFFTLRGD  SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHHPMIIN  LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD  SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD  ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE  QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR  NEGEGAYEAELFVMIPEEADYVGIERNKGFRPLSCEYKMENVT  RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1 ' 1	2130	
LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			
EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYUQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYMGNKDGLNTXPFPKFCQGWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYBAELFVMIPEEADYVGIERNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	I .			
NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPPFKFCQGWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			
ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLFMEREFESSPREVGQIYLYLQVSSLL FRDPQLITGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1		
VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKKDGLNTKPFPKFCQGVMASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	ı			
FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKTLFLDNHQAHRVPPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLINAR NEGEGAYBAELFVMIPEEADYVGIERNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			
QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYBAELFVMIPEEADYVGIERNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1		1	
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	ı			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	ļ		
LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYERNIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1		
SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	l	1		
ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	i			
QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1	1		
NEGEGAYEAELFVMIPEEADYVGIERRNKGFRPLSCEYKMENVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS				
RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS	1			
		1		
NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE	1	1		
	L	<u> </u>	<u></u>	MYDWADSULASTOTULLAAAOAETKGASHAAOTATHWEAEE

SEQ	Predicted	Predicted end	1 Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
[	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
			LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
		Í	TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
		i	GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
·	1	1	AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
	<u> </u>		TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
į	1		NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
- [	İ		LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
l	1	ĺ	AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
i	1		DIPKEDINPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
F			NVKSVCSRERGSGIRSVSFYEHIITVGTGOGSLLFYDIRAORFI.
1			EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
5960			FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
3360	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
1			LDWASINGFCEQLNEDFEGPPLATRLLAHKIOSPOEWEATOALT
	1 1		VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
	!		NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
			TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
1	1		MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
1	1		SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
	i 1		NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
1	ļ i		PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
1	1 1		PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRFPAQTSLP ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
ļ	ĺ		NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
			LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
	[ ]		LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
	ĺ		ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
-		·	WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
			GLEVAIKMIDKKAMYKAGMVQRVONEVKIHCOLKHPSILELVNV
1 1			FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHOTIT
	ľ		GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATOLKMPHE
1 1	į		KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
1 1	j		FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
1 1			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
1			STS1SGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1	1	İ	FYTOWGNOETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1 1	1	}	SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
1 1		j	NFFKEKTSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE
]	1	ł	TVQQWFGNLQINAHLRKTTEYDSISPNRDFQCHPDLQKDTSKNA
	f		WIDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
	1		KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
		}	PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
1 1			SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
1	Į.		HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
j 1			ICLALES I ISEEERKTRSAPFFPI I IGRKPGSTSSPKALSPPPS
] }		1	VDSNYPTRDRASFNRMVMHSAASPTOAPILNPSMVTNEGIGI.TT
] [		1	TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATO\LTSGAVW
1	İ	1	VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKO
5000			KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFORAOFAEATORLSER
	j		NCIEIVNKLIAQKQLEVVHTLDGKEYITPAOISKEMRDELHVRG
	1	1	GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVOLVLGOLIDEN
		1	YLDRLAEEVNDKLQESGOVTISELCKTYDLPGNFLTOALTORIG
1		1 -	RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSI.
	İ	j.	LSKYGFQEQLLYSVLEELVNSGRLRGTVVGGRODKAVFVPDTYS
<u> </u>	<del></del>		RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL

CEO	Drodiatod	D. 32 - 2 - 2 - 2	1
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine,
Į.	residue of		S=Serine, T=Threonine, V=Valine,
į.	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Í		sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	<u></u>	\=possible nucleotide insertion)
1	•	1	PLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
1	ļ.		AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
ł	Ī	1	QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
1	<b>[</b>		TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
1	ŀ	İ	KKPEISFMFQDEIEDFLRKHIQDAPEEFISELAEYLIKPLNKTY
1	1	İ	LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
1			MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
1	i		AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
1	1	1	AEACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT
1	1		SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
į			LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
			SIKDLVLKSRKSSVTEE
5963	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
ł	1	İ	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
1		.	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
1			AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
ļ	1	ł	GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
i	1 -		CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
1	1		GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEG
1	]		PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
			RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRPGGMEEACQVQTTK
1	1	1	RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
1		1	PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
1			FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
1		i	KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
1		ł	MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
		ļ	ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
į.			LADLYNASGRLTLADIERIAPLAEGALPYNLAELQRQQSPGLGR
1	1		PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
1		1	SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI
			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI
1	1		VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
1			FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
1	1		TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\KEEGPSAFWKG TAARVFRSSPQFG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK
1	1	1	SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
ì		1	VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
1	1	14,76	CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
ì	1	1	SOWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
			EVOVOAPPVVAATPSPTAVPEVASGETADVVOTAAEOSFAELGL
1		1	GSYTPVGLIONLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
1		1	
		1	TGQREAARIINHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL YQXKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
1		1	GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
1	1		MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
1	1		AVRTVLKI PORVVHDLDKLPPREGFLES FKKGWKNAEMTROLRE
		1	REQRMRNQLELAARGPLRQTPTHNPLLQPGKDNPPN1PSS\SS
I		1	SSKPKSKYPWHDTIG
5966	102	1026	RSKQVMARLTKRRQADTKAIOHLWAAIEIIRNOKQIANIDRITK
3300	102	1925	
1		1	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
1		1	GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
1	1	1	SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
1		}	RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
1		1	PKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
J	1	1	KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
			DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
i .			
			QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF

<u></u>	EQ	1 Dua 32 - h - 1		_
	ID	Predicted beginning	Predicted end	
- 1	Ю:	nucleotide	nucleotide _	M-Aidning, C=CVSteine D-Assessin Amid n
-	•	location	location	Glucamic Acid, F=Phenvialanine G-Clusine
i		corresponding	corresponding	n=n1stidine, l=Isoleucine, K-Jucine
ľ		to first	to first	L=Leucine, M=Methionine, N=Asparagine
-		amino acid	amino acid residue of	Parcoline, QaGlutamine, Rahrginine
- 1		residue of	amino acid	S=Serine, T=Threonine, V=Valine
- [		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ		sequence	sequence	Codon, /=possible nucleotide deletion
			<del></del>	\=possible nucleotide insertion)
- 1				KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
			,	EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
59	67	102	1925	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
ĺ			-525	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
1				YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
]				GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
1	- 1		İ	SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
- 1			l .	RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
	ĺ		1	FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
1	i		l	KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKB
1	- 1			DNQVDVRFFGHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1	- 1			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV
1	- 1		ı	SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
i	- 1			KDRNKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
	- 1		ŀ	EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
596			1	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
390	۱ ۳۰	81	1288	VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP
1	i	•		RPVGV51SAQAQVQPPAMHRRRLALGLGFCT.LACTCLCVT.tutur
1				ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLOPVZMGOVPODVI
				LEHRPTQLLTLTPWLAPIVSEGTFNPFI.IOHIVODINI TICIPMI
	- 1		i	FAVON/HELESAEEFFMRGYRVHYYTFTDNPAAVPGVDICDUDI
1	- 1		1	LSSIPIQGHSHWEETSMRRMETISOHIAKRAHDEUDVIRCEDUD
1	i		ì	MVFRNPWGPETLGDLVAAIHPSYYAVPROOFPVEDDDUCTA EVA
1	- 1		•	DSEGDF I IGGAVFGGOVARVYEFTRGCHMAILADKANCINA AND
	- 1		į .	ESHLINKHFISHKPSKVLSPEYLWDDRKPQPPSLKLIRFSTIDK
596	9	1126	503	DISCURS
1	J	- <del>-</del>	303	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
i	- 1.			TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
1	- 1			FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
				GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
597	0	316	4712	SODNIGHBLLOWHOUNT COOL GYOY CORD
İ	- 1	İ		SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
ì	- 1	İ	i	KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK
ł	- 1			QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP
1	-			MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
į				GPFTAVQ1TNTTGLAQAPGLASOGISFG1KNNIGTPLOKICUSE
l	- 1		ŀ	SPARKAPVKLESIASVFKDHAEEGTSEDGTKPDFKSSDOGLOVK
i	- 1	1		GDSDGSSNLDGKKEDEDPODGGSLASTLSKLKPMKDFFCACATE
1		i		PEI IHII PPAHCKVKPNFPFLLFMRASEOMDGDNTTHDVNADER
	- 1	ļ		KKGSSPKPKSCIKAAASOGAEKTVSEVSEODVETCMTEDOEDOG
	- 1	· j	. ]	RAEARKALGGDVSDQSLESHSOKVSETOMCESNSSKETSLATDA
	ł	į	l	GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS
	- 1	i	İ	YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE
		Ţ.		PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE
	- 1	ľ		TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTEEK
	- 1	}	, 1	SSKAESGEKSKKRKKRKKKKKKSSAPADSERGPKPEPPGSGSPA
	- 1	i	Ī	PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ
	i	1		KSPSQYSEEEEEEDSGSEHSRSRSRSRSRSRSSSSSSSSSSSSSSSSSSSSSSS
				DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS
	- 1	·	- I	SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS
	ı		1.	SSCSKSKSKRSRSTTAHSWORSRSYSRDRSDSTDSDSODSCSD
				RESWGHESPEERHSGRRDFIRSKTYRSOSDUVEDCCDCDCDCDC
	1	ļ	1.	DUGRGDDSKATGPPSONSNIGTGRGSEGDCSDPDVNGUPD VI I
		)	1.4	EXIOSKKVEKKPSVSEEVOATPNKACPKI.KDDDOGVECDVI DDG
		ļ	[ ·	GNKPVLPLIGKLPATRKPNKKCEESGLEDGEPOPOOPTERODD
		· }	1,4	SSUALFGHOFP (SEETIGPLI,DPPPFFSKSCFVTADUDVAD)
	-		1 2	PAHFDCYLGDPTISHNYI.PDPSDGNTI.FSI.DSccopeDypogt
		———— <u> </u>	1	PIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEQ	Predicted	Predicted end	Lamino poid pogment contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid ·	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	_	\=possible nucleotide insertion)
			TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFPASAALAPATPAL
		•	QPIHIQQPATASATSITTVQHAILQHHAAAAAAIGIHPHPHPQ
1	i		PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
I	1		SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
1	i	İ	FSGQDLQHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
Ì			PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
1			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
l l	l		FDR3SPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
)	j		SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP
			PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
į.			FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
1			LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
1			CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYG
1			YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV
[			EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFIN
1	i		SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
			PROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHP
<b>j</b>			KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHY
1 1			VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
			KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ
1			EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
1			SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
1 - 1			PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
			NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGSMS
1			DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV
i i			SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIAISSL
1 1			TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLV
1 1			LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
			GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
1			NP
5973	65	-2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
!			GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
i i			NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
1 3			HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
j	Į.		KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
1	İ		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
1 1	l l		LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
1	i		KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV
1 1	ļ		NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
1 1			LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTOPR
] [			GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD
1			IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
1			PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSK
1	•		GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
			DTAPQGNKDLKEHVLQSSLSQEHKDPKATPP
5974	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1	İ		LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
] [			TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1 1	1	1	DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
<b>1</b>	i		EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1 /	]		VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
f l	i		ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
į j	i		QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
1	İ	İ	LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLOE
1 1		į	REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
{			KGKLHGKFSLIDLAGNERGADTSSADROTRLEGAEINKSLLALK
ţ j	Í	İ	ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1 1	ł	ł	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
L			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Water technic value, value,
J.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
i	sequence	Doguerice	\
		<del></del>	\=possible nucleotide insertion)
1			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
5975	4293	2200	AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
33.5	1233	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1	į.		LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
Į.	1		TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1			DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
1			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
	I		VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
i	ł		ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
ľ			QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
	1		LELQVYATFFEIYSGKVFDLINRKTKLRVLEDGKQQVQVVGLOE
1	ĺ		REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFOIILRR
	i		KGKLHGKFSLIDLAGNERGADTSSADROTRLEGAEINKSLLALK
1	l i		ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
}			MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNOI\DD
			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
1			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATOLE
<u> </u>			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5976	20	2949	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF
1	į		PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
1			FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
			ECIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE.
1			TGYTKRLRKQLPSPPPPIPPPRPLIQRNLOPLMRSPISROODPL
			MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
			ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
		•	LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
I i			RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
			CGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPP
j j			GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
1	l		APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ
1 1	!		KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
			RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
	Í		RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
1			KAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAQPR
1			PSANRENFSPERFI, PLNIRNSPFTRGRREDYVGGQSHRSRNIGS
1 1	l		NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR
1 1	Į.		KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
1 1	1		PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
1 1	1		SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
			TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
			EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
1 !	İ		PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWOWATGFFLKVK
1 1	ļ		AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV
			DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG
1	ļ	ļ	EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ
[	f	ſ	TRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH
!!	1	1	VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
L /	·	ì	GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
1 1	j	1	RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC
j ľ	. 1	. 1	FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ
1 1		i	LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
1	·	l	GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV
1		ļ	EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
		İ	OFTELLES LOWUFUOL DECEMBER TOWNS TOWNS OF THE TOWNS OF THE TOWNS OF THE TOWNS OF THE TOWN
]			QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM
1		i	ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
			LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR VEMVHQSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
			YLNPQNDTVILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
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		<del></del>	INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

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L-Leucine, M-Methionine, N-Asparagine, ensidue of tesidue of amino acid residue of amino acid sequence   Sescrine, T-Threonine, V-Valine, Sescrine, T-Threonine, V-Valine, Sescrine, T-Threonine, V-Valine, M-Methionine, N-Valine, M-Methionine, Methionine, M-Methionine, Methio	NO:	1		
to first amino acid residue of amino acid residue of amino acid sequence  sequence  ##TYPTOPDHAN, Y=Tyrcosine, X=Unknown, *=stop codon, /=possible nuclectide deletion, Codon, /=possible nuclectide deletion, Codon, /=possible nuclectide insertion)    CSDMLLER(GPYSAS VICEARCEBEEKIONEDYHHELSDGDL   CSDMLLER(GPYSAS VICEARCEBEEKIONEDYHHELSDGDL   DLDLVYEDEVHOLDGSSSSASSTATSHTEENDIDEETHSGENDV   EYNNMEREGELHER/SYVESASSHISHTELGSIGDLOHER   FYNNMEREGELHER/SYVESASSHISHTELGSIGDLOHER   FYNNMEREGELHER/SYVESASSHISHTELGSIGDLOHER   LIARSYNANCY IRRORRYESDLOHER/SEVGSASSHISHTELGSIGDLOHER   LIARSYNANCY IRRORRYESDLOHER/SEVGSASSHISHTALGSIGDLOHER   LIARSYNANCY IRRORRYESDLOHER/SEVGASSHISHTALGSIGDLOHER   DROCKALDSDAVVAVSCOLEPARER/SYVESASSHISHTALINGSIGDLOHER/SEVGHDSSYNANTSHIRKHSSKENSSSSASSISHTANDOCE   NSRSKODCOTLESGSSGSSGSSGSSSSSSDSDICCOTLESGS   SPENSTSCHOLDFOLDER/STRUTCHSSSTODLOHER/SEVGHDSSYNANTSHIRKHSSKENSSSSSSSIDLECOTLESGS   GEEHTSVOGFHDSSTWINTOPPDICTISTSPOCKOLOFINST   DROCKALDSDAVVAVSCOLLARESSPOCKOLOFINSTSHIRKHSSKENSSSPOLLINGSIGN   CSDMLLINGSGR    SEVENTY STATES		1 '		
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amino acid sequence  Codon, /=possible nuclectide insertion) CEDRILER (GPYSAS VVERAKEDEREET (ONEDVHHELEDGGL DLDLVYEDEWNG) (LDGGSSAS STATS)**TERRED ID DEEMSGENDY FEYNMELEGGEL**REDAAAACPAGSSHGY VGSSSRISRRTHLCSA ATSSLIDITOPILIHLLDLKDESS IENN.MGQDFPSLQDTA SYSKENDORKOQAMMEVPSDLKRHLKTUMAEVRCMKTDVKAN TLSSISSASASGMOTSJESSADQAALAACCTERSCHQLMEM LLAKSSVANCYIRNSTMKKSNSPKPARSSVAGSLSIRRAWDOF SHSREKOCOTLSESS PSGSSGSGSFRSPRALIGIGAD LEME LLAKSSVANCYIRNSTMKKSNSPKPARSSVAGSLSIRRAWDOF BRACKALDSDAVVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELQFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELQFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELQFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELQFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELQFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI QMTDLENNSETGELGFVLPEGASAPEEMSSBIGGOILPFETE DRQCKALDSDAVVAVFSGLPAVEKRRKKYTLGANAKGGLLEGI TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TITLSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSGANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE TELSCANGVITTUMAESTERDEVICTORSPETDOILTVANSE T		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
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OMTOLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE GEBITSVEGGTHDSFMVTQPPDEDTHSSFPDGEOLGPEDLSFNT DENSGR 1-PEMIWILMILLALARGFAFLDTEVPTYGGSFPBPTDAYLANGS TTTLSPSGSAVISTTIATTPSKPTCDEKYANITVDYLYNKETK LFTAKLNVAENVECQNNTCTINEVINLTECKANAVSISHINSCTA POPKTLLIUDPFOVEKVEVPHCCS\QVPGDSTIMLKKNISTESTG DTQNITYRQCGOMMIFDNKSIKLEMLEPEHSYKCDSEILYNSHK FTNASKIKITDTGSSFGEQIIFCRSEAAHGQVITWRPPGRSFHN FTLCYIKETEKDCLALDKNLIKYDLQNLKPYTKVUSLHAYIIA KVQRNGSAAMCHFTIKASPPSQVMMWTVSMTSONSHIVKCRPPR DENGGHERYHLEVEAGNTLVRNESHKNCDFFVKULQYSTDTTFK AYFINGSYDGEPFILHHSTSNISKLIAPLIIVTSIALIVV LIKIYDLHKKRSCNLDEQGELVERDDEKQLANVEPHADILLET YKRIKLADEGREPLAEFGSIFWFSKFK LERREFFKONKNEYVD LIVPUYNRVELSEINDAGSNYINASYLOGFKEPRIYIAAGGPR DETVODDEWMI HEQNATUTIVWAVTRCENRYKCCEVPREMEEGT RAFGECCCKDLTKHKRCP\DYIIOKLNIVVKKEKATGREVTHIO FTSMPDHGVPGETEVNLSELHPYLHMMKKRPPSEPSDLEAE FQRLSSYRSWRTQHIGNGE\ENKINGVYTLVKNQVEAQYT LIHQALVENQVEGETEVNLSELHPYLHMMKKRPPSEPSDLEAE FQRLSSYRSWRTQHIGNGE\ENKINGVYTLVKNQVEAQYT LIHQALVENQVEQETEVNLSELHPYLHMMKKRPPSEPSDLEAE FQRLSSYRSWRTQHIGNGE\ENKINGVYTLYVVLKRCRCLAWQVEAQYT LIHQALVENQVEQETEVNLSELHPYLHMKKRNSNIPPDINNVELKHE LEMEKESEEBDSDSSDDDSDEFFERYINASFINSWRF\ENKINGVYTLYVQ YTNNSVEQLDAEFKELISMIQVVKAKNHOEBKIEFECQYMG GOKQTYGDLEVDLKDTDESSTYTLAVFELRHISKRDSRTVYQYQ YTNNSVEQLDAEFKELISMIQVVKAKNHOEBKIEFEDBEVD KVKQDARCVAPLGAPFKLPEAKEQAEGSEPTSGTEGFBEHSVNGD ASPALNGGS OAMGCKLRELRFTYGTGYRVSLALDEQOVELVHTLVAHQGOMBTI LIHCHCLSDIFINGVAGAHANINGVAKSEGKINHKESTPL LHCHCLDIFINGAPDMGRDLQITPRRESTYRHAPVETTHSESSYTR MIJBGIKQIIQRITMSNLSTYRANGEFALUFVAHQGOMBTI LERCLGSLEKGODVSVHITSNIKGULLGYJSSSSTANLANGSSTANLANGSSVG MIJBRICGSSTRUNGSFERAFALGLQEGGIGGEIRKYESSFY MIJBRICGIRGIGELISRINGVAANINESSVTR MIJBRICKICIRGIQELITSRINGVAANINESTHAPVEVTYBESSSYTR MIJBRICKITGIQELITSRINGVAANINESCHIKTSSSTTR MIJBRICKITGITSTRINGVARAVEVTYTHSGSSYTR MIJBRICKITGITGITSTRINGVARAVEVTYTHSGSSYTR MIJBRICKITGITGITSTRINGVARAVEVTYTHSGSSYTR MIJBRICKITGITGITSTRINGVARAVETYTHSGSSYTR MIJBRICKITGITGITSTRINGVARAVETYTHSGSSYTR MIJBRICKITGITGITSTRINGVARANITUSTRINGULDULGSSVE DHARPHARLSLESSRSLQDVLLHERPRLEVPORGELGVALLAGUNDLAGUNG UVESIFFLENGGLAVHNOVARGABEELLOVA		}	į.	
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5979  212  3665  LEDWINKLILARGERFLDTEVFVTGGSFTESPTDAYLINESE TTTLSPSGSAVISTTIATPSSYPTGKYANITYOYLVIKETK LFTAKLNVNENVECGNINTCTNNEVINLTECKNASVSISHNSCTA PDKTLILDVPSCVEKVPVHCCS)QVEGDESTIHLKKNITETSTC TOTQNITYRYPCGOMIPTOMIKEILKEBLEVKCDSELIVNSHK FTNASKLIKTDFGSFGEPQIIFCRSEAAHGQVITWMPFGRSFHN FTLCYIKETEKDCLALUKDRILKTUGHKYTKVUSLIVATIA KVQNRGSAMCHFTTKSAPPSQVWNNTVSWTSONSHIVKCRPPR DRINGHBERVHLEVERGANTUKNESKHKNCDFRVDLQVSTDYTFK AVFINGDYPGEPPILHISTSYNSKALDAFLAPLIIVTSIALIVV LVKIYDLHKRSSCNLDEQOELVERDEGANIVEPPHADILLET YKRKIADEGRLEPLAFEGSIPRVSKFPKVEARKPFNONNRYVD ILFYDYNRVELSEINGDAGSNYINASYIDFKEPRONNRYVD ILFYDYNRVELSEINGDAGSNYINASYIDFKEPRONNRYVD ILFYDYNRVELSEINGDAGSNYINASYIDFKEPRONNRYVD FTSWPDDWEMINEQGATVIVWTRCEGSNRKCAEVWPSMEEGT RAFGECCCKDLITKHRCP\DYIIQKLNIVNENKERAGREVTHIQ FTSWPDDWEMINEQGLERERKVDVGYVVVLRRQRCLMVQDVQAQYI LIHQALDVENNGGESTEVALSLERPYNRAFSPFSGEIVVHCSAGVGR TSTYIGIDAMLBGLERERKVDVGYVVVLRRQRCLMVQDVQAQYI LIHQALDVENNGGESTEVALSLERPYNTAFTMYNDYNRVPLKHE LEMKSESEHDSDSSDDDSDSDESKYNNAFSINSNYNTYDYNRVPLKHE LEMKSESEHDSDSSDDDSDSDESKYNNAFSINSVYNYQ YTNNSVRQLPABPKELISHIQVVXQKLPQNSSSEGNRHKKSTPL GROTYGOLIFVALNATURSSTYTIAREINSKRNSRSTVYQYQ YTNNSVRQLPABPKELISHIQVVXQKLPQNSSSEGNRHKKSTPL LIHCALDVSTIFQATGTFGALLINLESATTEEVVDICTVVXALRRARP GWYSTFEQQTGFJFQUIASTYPALARGGSEPTSGTEGFRHSVNGP YTNNSVRQLPABPKELISHIQVVXQKLPQNSSSEGNRHKKSTPL LIHCALDVSTIFQATGTFTVSLALPCQVELVHTLVAHQCNINET BEBOLEQVGNNEDAAHDLTELEVTHHALLGEUDVVVAPCQGLR PTVDVLGDLVNDFLPVTYALHKDELSGREDGEIRTRYFSFP VSFKVEVKLSSEI IDSSTRMESESFRYQTQQTELVTHLVAHQCNINET PEBOLEQVGNNEDAAHDLTELEVTHHALLGEUDVVVAPCQGLR PTVDVLGDLVNDFLPVTYALHKDELSGREDGEIRTRYSFFP VSFKVEVKLSSEI IDSSTRMESESFRYANTVEVTHYSSSSVTR MIMBQISQIIQRITWSLFSRYNDAANANLSSVDYLRESFYGTL ERCCGSLEKSQDVVSHTINSNYLEQIIAANAVEVTHYSSSSVTR MIMBQISQIIQRITWSSPATILEMKRKVAQEAIESLSSAKIAK SICSGFRTRINSSHERAFAASLGLGEGGERETEDULRUNDL DHARPLARISLESRSLQOVLLHKRKPLQGEIGSSVRUNDLUNDR DHARPLARISLESRSLQOVLHKRYNSGLEKETDLUNDLUNDR DHARPLARISLESRSLQOVLHREFRALLUNDREGUNDAALTILDTECQUE VOTREIKCCITGIQELITSRINDLONAANTUSTHASSSVTR MIMBQISQIITGTPIMBELGUNDAATTILDGTCAL DVESIFFERALSVOHERDERLINDSLEVALLEGUND		1.	1	I "
TTTLSPSGSAVISTTTIATTSKPTCDEKVANTVUDYLYNKETK LFTAKLEWENVECGNITONEVHINLTECKNASVSISHNSCTA PDRTILLDVPPGVEKVPVICCS\(C)VORDPDSTIALKKRIETSTC DTQRITTRFCGGMMIPDNELKLENLEPEHEYKCDSELLYRSHK FTNASKLIKTDFGSGPEPQIIFCSEAAHGGVITNNPPQRSFIN FTLCYIKETEKDCLINLDKNLIKYDLONLEPYTRYVLSLHAYIIA KVORNSGAANCHFTTKSAPPSOVNMTVSMTSUNSMHVACRPPB DENGPHERYHLEVEAGNTLURNESHSNCUPTVSVLJUGYSTDTTPK AVFHNGDYPGEP FILHHSTSNASKALTAPLAPLITVSIALAV LYKIYDLHKKRS CNLDEQQELVERDDEKQLMVEPIHADILLET YKRKIADEGRIFLAEFQSIPRVFSKFFIKERRPFNQKRNRYVD LYKIYDLHKKRS CNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFLAEFQSIPRVFSKFFIKERRPFNQKRNRYVD LILPVDYNNVELSEINIGDAGSNYIHASYIDGFKEPRKYITAGGPR DETVDDSWRNIWEQCATVIVMVTRCEEGINNKCAEFWPSMEEGT RAFGECCCKDLTKHKRCP\DYIIOKASIVINKKEKAFREVPHIG FTSWPDHGVPEDPHLLIKLRRRVNAFSHFFSGFIVVHCSAGVGR TGTYIGIDAALEGLEAENKVOVYVKLERGRCLMOVORAQYI LIHQALVENYOFGETEVNLSELHPYLHIMKKRPPPSEPSPLEAE FQRLPSYRSWRTQHIGNQS\ENKSKINRSNVIPDYNRVPLKHE LEMBKESEEHDSDESSDDDSDESEPSKYINASFIMSYHKP\EVMI AAQGPLKETIGDFWQMIFQRKKVIVNLITELHSHGDQBICAQYMG BOKGTYGDLSVDLKAUCTURSSTYTIXVFELHSKRKDSRTVYQYQ YTNNSVRQLFAEFKELISHIQVVKOKLPOKNSSEGNKHHKSTPL LIHCRDSQQTGIFCALLALLESETEVVDIFQVVKALRKARP GWSTFFRQYQFLYDVIASTYPAONGOVKKNHHGDKIEFDREVD KVKQDANCVAPLGAPEKLPEAKQAEGSEFTSGTEGPEHSVNNGP ASPALNQGS  DAMGCKLRFLRFTYGTOTRVSLAELGQQYELVHTLVAHQGNWBTI PEEDLEVQENNEDBAHDLITELEVTMHHALLQEVDVVVAPCQGLE PTVDVLGDLVNDFLPVITYALHKDELSERDGELQEIRKYFSFP VFFFKVPKLAGSEIIDSTSRRMSERSPLYRQLDLGYLSSSHMN CGAPGODTKAQSMLVEQSEKLHHLSTSSHQULQTRLVDAKAKLN LHCHCLDIFINGAPMORDLOIPKRELYTERKENLYSESIM CGAPGODTKAQSMLVEQSEKLHHLSTSSHQULQTRLVDAKAKLN LHCHCLDIFINGAPMORDLOIPKRELYTRKENELYSESIM LANKQEBMKOMIVEGEKLHLSTSSHQVLARSSYVT MIMSQIKQITQRITMVSPPAITLEMKKVAQBAIESLSASKLAK SICSQFTRINNSHEAFAASLRQANKLISSTYNLERSPVOTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHBGSSVTR MIMSQIKQITQRITMVSPPAITLEMKKVAQBAIESLSASKLAK SICSGFTRINNSHEAFAASLRQARGGREEKETEDMLEVRK DHAPRLARLSLESSRSLQOVLHERKPKLGGELGGGGYGVVYLCON MGGHFPCALKSVVPDPDEKHWINLAKRIGGELGGGGGGGGGGGAGACHOA DVWGSIFPCALKSVVPDPDEKHWINLAKRGRERGEREKTERUMLEGR SVIDYNYGGGSSIAVILLIBERHRINDLTGLKARGLITERRULDIAG DVWGSIFPLIGGGIVHPDIKENHLANGVR			<u>                                     </u>	DENSGR
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DENTILIDVEPGUEKVEVICCS\QVGEODETIALKMKNIETSTC DIQNITYREPQGEMINEPINERILELBILEBEHEKKOSETLIYMSHK FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN FTLCYTKETEKDCLNLDKRLIKYDLQNLKFYTKYULSLHAYITA KQRRSGAAACHETTKSAP PSQUVMNTVSMTSDNSMHVCKEPPB DRNGPHERYHLEVEAGNTLVKNESHKRUCDFYKDLQYSTDYTFK AYFHNGSYPGEPP ILHHSTSYNSKALIAFLAPLITYSIALLVY LYKLYDLHKKRSCNLDEQQELVERDDEKQIMVEPIHADILLET YRKLADEGRIFLALEPGSIPRVFSH IKEARRPHOKNENYVO LILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYLDAGOPR DETVDDFWRMI MEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT RAFGECCCKDLTHERRCP\DYIGVAVKKEKAFGREVTHIQ FTSWPDHGVEDPHLLLLKLRRVANFSNFFSGIVVHCSAGVGR TGTYIGIDAAHLEGLEAENKUDVYGVVVKLRGRCLMVOVEAQYI LIHQALVEXNOFGETEVNLSELHFYLHIMKKRDPPSEPSPLEAE FORLDSYNSWRTQHIGKGS\ENKINSNIVIPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVYRPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVYRPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVYRPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSDESDDBSDEEPSKYINASTIMSVRYPYDNRVPLKHE LEMBKESEHDSGRODDSGEEPSKYTOKROBELCELOOPTURG GROTYGDIEVDLKDTDKSTYTLRVFELRHSKRKDSRTVYQYQ YTNNSVRQLPAEP KELISHIQVVXQKUKDONSSEGNKHHKSTPL LIHCRDSGOTGIFCALLALLESBETEVUTIFQVVALRKARPP GWSTFFQYQFLYDVIASTYPAQNGQVKKNHGENKIEFDDREVD KVKQDANCVAPLGAPEKLPEAKGADESSETSGTEDEHSUNGP ASPALNQGS  DAMGCKLERLRPTYGTOTRVSLALDEGGYELVHTLVAHQGNWETI PEDDLEVQENNEDAAHDLTELEVTRHALLQEDVVVALRKARP GROTYKAQSMLVSQSKKRHLSTSHQVLQTRLVDAAAALN LUHCCLDIFINGAPMQBDLGTHRLYRSLPKHKELYSELMN LANRQEEMKOMTVETLNTMKEELLDDATMBEKDUTVERGEP VOTREIKCCTRQ 10ELIISBLANAVANKLISSDVJTRESPYOTL ECCLOSLEKSQDVSVHITSNYLKQILNAAYHVSVTHSGSSVTR MIMSQIKQITGRTHWYSPATHEENTRUKERLYBELMULKOR DHAPRLARLSLESRSLQHPDLKENKLEGELGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1		
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FTSWPDHGVPEDPHLLKLERRVNAFSNFFSGPIVVHCSAGVGR TSTYIGIDAMLEGLEAENKVDVGYVVKLRKQRCLMVQVEAQVI LHQALVEYNQFGETEVNLSELHPYLHIMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDESEPSXYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPAEPKELISHIQVVKQKLPQKNSSEGNKHHKSTFIL LHRCRGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQVGFLYDVIASTYPAQNGQVKKNHQEDKIEFDNEVD KVKQDANCVMPLGAPEKLPPAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVAPCQGLR PTVDVLIGDLVNDFLPVITYALHKDELSERDEQELGIRKYFSFF VFFFKYPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPRKLEYTRKESNELVESLMN IANRKGEMKDMIVETLNTMKEELLDDATNMEFKDVIVPBNGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYMVEVTFHSGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRVAQEAIESLSASKLAK SICSGPRTELNSSHEAFAASLQLEAGHGSGELEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRKRVAQEAIESLSASKLAK SICSGPRTELNSSHEAFAASLQLEAGHGSGELEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRKRVAQEAIESLSASKLAK SICSGPRTELNSSHEAFAASLAQLEAGHGSGELEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRKRVAQEAIESLSASKLAK SUCSGPRTELNSSHEAFAASLRQLEAGHGSGELEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRKRVALDERGLRGGGVGVVYLCON WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLIG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFFGKYDNSVDVYARGILEWYICSGSVK LPPAFFERCASKDHLWMNVVRGGAB PERLPVPTDEECMQLMERCNDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST	ł		ł	1
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DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA  MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST	l	1		1
MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST	l	1		•
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SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histiding, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ctop
i	amino acid	sequence	Codon, /=possible nucleotide deletion
<b></b>	sequence		\=possible nucleotide insertion)
1			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD
			LPFHPLTQMMYSPQNSDYLLALSTENGI WVSKNFGGKWEETUKA
			VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
ı	1	l	GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
ľ			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
			KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
1			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
	Ì	}	EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
1			RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
1		1	LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
ŀ	l e		GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
1			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLTVXKVVC
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1 3302	36	2316	ATR?PRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
1	1		GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR
1			FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILINS
1			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
1			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
1			LGTTGRGNDMQVGTY1EKMFMSELSGNIIDICPVGALTSKPYAF TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE
I i			VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
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1 1			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAOKIRM
			TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPDKVI.F
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAVT
[ ]			EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSPIAGMTL
1 1			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
1 1			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA VEEPSIC
5983	248	1763	
] [		2.03	EARGDGGRRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG RQ\YSAAIALLEPAGSBIADDLSILYSNRAACYLKEGNCSGCIQ
			DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
1 1	1		GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
1 1			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
1 1		1	DALSKYSECLKINNKECAIYTNRALCYLKLCOFFEAKODCDOAL
	1		QLADGNVKAFYRRALAHKGLKNYOKSLIDLNKVILLDPSITEAK
	ĺ		MELEEVTRLLNLKDKTAPFNKEKERRKIEIOEVNEGKEFPGRDA
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	}		SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVPTMY FHHSLRSISRFSSG
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		í	HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNOTRSVGOVDDGGEG
•			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITOGF
			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNGEVEIARCHVRGQVE
			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM

C 070		r = - 32 3 3 3	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
<b>i</b> i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
]	sequence		\=possible nucleotide insertion)
5986	1806	184	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPOOGGATPOVP
1	ĺ	1	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1	ł	1	GLRWTPKSPLDPDSGLLSCTLPNGFGGOSGPEGERSLAPPDASI
		1	LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
	ĺ		EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
ł l	ļ	1	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
		1	QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
			, , , , , , , , , , , , , , , , , , , ,
1 1	ł	1	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
]	]		RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
	Į.		DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
		L	TV
5987	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1		İ	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
	1	1	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
}	l	1	LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
1	1	Ī	EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
		1	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
]			CNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
1	1		VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
	[		RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
		1	DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKBLCHCKL
}	•	j	TV
5988	1292	410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFO
3,00	1232	410	
	E		RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG
		[	LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
		i	FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
ļ		į.	PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
1	}	į	ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE
			KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA
	ł	1	ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE
1		İ	NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNAEALAT
1		1	EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
	ł	t	SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALSESS
	1	<b>J</b>	EQEMEVEPARKGEEEQKEQEEQEEEGAGPAEVKEEGSQLENGEA
!	i	i	PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH
1 .	1	ł	KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
1			AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED
			CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
1		-	THOTOKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ
	<u> </u>		FTTSGNLKRHLRIHSGEKPYVCIHCORQFADPGALORHVRIHTG
	1	1	EKPCQCVMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS
[ ·	{	1	SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLSKHIIIHTGEKPY
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	1		LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
]		1	VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
ł			VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
1	ł	Į.	FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE
			ТЅРТАРЕСРРРАЕ
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
	İ	1	SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASL1S
[			LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
i			PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
l i	I	Ī	MHLACPEEEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
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			LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVPOVSPGPPPVLLDDSLFTSSALOLLMPTLFSFTFAAVRVTL
			VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
			VVROVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP
			VVROVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS
			VVROVSPGPR PVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
		·	VVROVSPGPR PVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
		·	VVROVSPGPR PVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN

Degianing   nucleotide   location   corresponding   correspo	SEQ	Predicted	D	
No:   nucleotide		1	Predicted end	dord segment containing signal beneficial
Cocresponding			1	A=Alanine, C=Cysteine, D=Aspartic Acid, E=
COTTESPONDING to first amino acid residue of amino acid residue of amino acid sequence control of acid sequence control of amino rol of acid sequence control of acid sequence c	1			Glutamic Acid, F=Phenylalanine, G=Glycine,
to fixet amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid anino acid anino acid acquence of sequence of codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion)  DPVPNDLTPUPPULVENEVEVENESTSATUHEAR PRILISISTERER ROOKOAGETERES(DPYTROMES) PERFECT PRICE AND ACCOUNTY OF THE PRICE	i			h=histidine, l=lsoleucine, K=Lysine,
maino acid residue of amino acid sequence  S-Serine, T-Threonine, V-Valiae, amino acid sequence  Sequence  Sequence  Dovanine, V-Vpossible nucleotide deletion, V-possible nucleotide deletion	1			Paperoline, Mamethionine, Nasparagine,
maino acid amino acid anino acid				S-Soring Tombus anime, R-Arginine,
Sequence  Codon, /-possible nuclectide deletion,			l e	W-Truntonhan W-Truncius Waline,
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DVVQAFISEIGIEASDLSSLLEGFEKSEAKKECPPPAPADSLAV GNSGGVID PQEKREDLENQAPELANVELTPPATPPHOLIWFILA AVSLLAKAKSP KSTAQEGTLKEPGTEAKHIPAAVRIQEGVIGPS RVHVGSGDBHDYC\VSRTPPKK\MPALLIPPASTRAVIQEGVIGPS RVHVGSGDBHDYC\VSRTPPKK\MPALLIPPASTRAVIQEGVIGPS SLLSPEASPCRIDMNTRIPPEPSAGNETYKRENGDI TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS SLLSPEASPCRIDMNTRIPPEPSAGNETYKREQDYSAGNERSPESG GWOGRGRNSRSVSGSMRTSBASSSSSSSSSSSSRBGRERIGIPD HKRWRSSCSSGSAGSRESSSSSSSSSSSSSSSRBGRERIGIPD HKRWRSSCSSGSAGSRESSSSSSSSSSSSSSSRBGRERIGIPD HKRWRSSCSSGSAGSRESSSSSSSSSSSSSSSSRBGRERIGIPD PSPRRSDRRRYSSYRSHDPVORORVLQKERAIEERVVPIGK IPGEMTRSELKORPSVFGIEBECTIHPRVCGDNVGFVTYRYAEE AFAAIESGIKLROADEOPPLOFGGROGFCKRSYSDLDSNREDP DPAPVASKEDSLDEPTLLKQAGKNIRR RLSSHIFGOCSPSITC\TKPFKKGGNTSFERKKTELYQELGIQAR BLRCHWMSITVRNNRIINEMPLKAVITTPECLILIDVRNINIK, GWEPSELPSOLGSGGG/UTVTPLPFEFRAIEALLQWINTLOGKL SILOPLILETLDALGDPKHSSVDRSKLHILLONGKSLSELETDI KIPKESI ERILDEEELLEGLCVSKRSDVPEKSSAGIDHAEM ELLLEMYYRIAADDLSNAARELEVLIDDSQSITFILDSHRINVEN RLMIQLIMATFISLEFGLGWAFGGNINLESSLEEDHRIFWLITGI WFMOSGLIURRILLSFILGR/LARSSILSYGMKMWVINGIVEGI SILOPLILETLDALGDPKHSSVDRSKLHILLONGKSLSELETDI AFANTAMTYSLLAGVINGTWEGSILSPATRILWFALCFVC GVFSILGRIM-PSGGROGOATENELPPINGAMEKLERVI SGQDDEGQLITAODSQINI,/SEVLIDASSLSFNTRILWFALCFVC GVFSILGRIGHLMPGGGRIKAPVYTIGALALASTCPLAMPVX GLKKMPEATRILLATIVALLCPITFICAALMWKKGLAVLPCILQ FLEMTWYSLSYIPYANDAVIKCCSSLLS SQADBEQGLITAODSQINI,/SEVLIDASSLSFNTRILWFALCFVC GVFSILGRIGHLMPGGGRIKAPAVYTIGALALASTCPLAMPVX GLKKMPEATRILLATIVALLCPITFICAALMWHKKGLAVLPCILQ FLEMTWYSLSYIPYANDAVIKCCSSLLS SVAMDMFQKVEKIGETTYGVVYKARMETGGUVALKKIRLDLEM GVPSTAAREISLIKELHENPUNKLLDVYNDRRKLYLVPFLSQ DLKKYMDSTFOSEIPHLILKSYLGULQGVSCRIKRRVHRDLK FORLILIBGAIKLADFDGARGFOWPTTACHALHAUPHTENAC	1	1		KDDI-DATKANDTODOCTUDVI DAMIDADI DVI GDI DEDDE COL
GNSGGVDI POEKRPLDRIAGAPELARVAGLIFPATTPHOLMKPLA AVSILLAKAKS PISTAGGETLKEPGUTSEPANGAVELGEVINGES RVHVGSGDHDYC\VRSRTPPKK\MPALLI PEVGSRRNVKRHQDI TITKPULSLEPANAPP PECIAASREPLIDHETSSEQADPSAPCLAPS SILLSPEASPCRNDNTTRTPPEPSAKORSMRCYEKAGRSASPESG GWGGRGGRGNSRSVSGSGNFTSBASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	ı			DVVOAFTSRIGIFACDI.CCI I POEPVCEAVKDODDANADO
AVSILAKAKSPISTAQEGTI-KREUT-AKHIPAAVRIQEGVIGPS RUHMGSGIDHDYOLVARSTPPKK/MPALLI PSVGSRMNYKRRIQDI TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQAPSAPCILAPS SLISPEASPCRNDMTRITPEEPSARQSMMCYRKACRSASPSG GWQRIGGRISRSRVSGSNRTISEASSSSSSSSSSSRSREGREISP HKRWRISSCSSGSRSRCSSGSSSSSSSSSSSSSSSRSREGREISP PSPBRISDRRRYSSYSSHDHYQROWLQKRALEERRVVFICK IPGMTMSSLKORPSVFGELEECTH WOODNIGFVTYRKAES AFAALEEGHLLROADBOPPDLCFGGRQFCKRSYSDLDSNNEEP DPADVSKSKPSLDPDTTLLKQAKMIRR  RISSHFSQCSFSITVLYKFDKGGNTSFERKKTELYQELGIQAR DLRRQHYMSITYRNRRI IMEMEYLKAVITFECLLLDYRNINLK GWLFFSLESPSLSGSGGLVTYPLPFFFRAIBALQWINTLOGKL SILDPLILETLDALGOPKHSSVDRSKLHILLONGKSLSELETDI KIFKESILETILDEELLELCVSKWSPVERKSAGTIGHAEM ELLLENYYRLADDLSNAARELEVLIDDSQSITFINLSHRIVM RIANGZITMATTFSLSLFGLMCVAFGMMLESSLEEDHRIFWHITGI  AGPOPRIKUNGVSGSGFFGGGGGAGTAFLPPROMARKERFUL SGQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GVFFSILGTGLIM-FGGGGGGGATERPPROMARKERFUL SGQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GVFFSILGTGLIM-FGGGGGGGATERPPROMARKERFUL SGQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GVFFSILGTGLIM-FGGGGGGGGATERPPROMARKERFUL SGQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GVFFSILGTGLIM-FGGGGGGGATERPPROMARKERFUL SGQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GLKKMFEATRILATIVMLICPIFTICAALAWHKKGLAVLFCILQ FLISTMYSLSYIPYARDAVIKCGSLUS  SQDDEEQCITADDSQINL/SEVLDASSLSFNTRIKWFAICFVC GLKKMFEATRILATIVMLICPIFTICAALAWHKKGLAVLFCILQ FLISTMYSLSYIPYARDAVIKCGSLUS GEVPSTAREISLIKELKHPHIVELLDVVINKRKLIVLPFIGG DLKKYMDSTOSSEPHLILIKSYLOLLGGVSGCKLFSAFCFFGS SVAMMMPGVKKIGGGTYGWYRKNRETGGUVALKKIRLDLEM EGVPSTAREISLIKELGHIPHIVERULDVVINKRKLIVLPFIGG DLKKYMDSTOSSEPHLILIKSYLOLLGGVSGCKLFSAFCFFGS RDLLMQLLQYDPSGRTTAKTALAHPYTSSPEPSPARAGVYLQRF RH FRILGTSEDWFGVVQLDPWKGSFRYNTRKLEELEVPRLEEPBG RDLLMQLLQYDPSGRTTAKTALAHPYTSSPEPSPARAGVYLQRF RH LAATEFYTIADDINSIGGIFAEMVTRKALEELEVPRLEEPBG RDLLMQLLQYDPSGRTAKTGCLEGETGFTLUPSELPBPAGG PQFGILGAVTOPKKGGSRNAMGNGSVABLISQAIESAPFRICHT FRRSSSNASSVSTRISPLRFESEVLAESIPASSSSAGGVPT LUNGLELDIANITSSHLLGRBSSKLARGNSSRCHPREADMTT FRRSSSNASSVSTRISPLRFESEVLAESIPASSSSAGGVPT LUNGLELDIANITSSHLLGDFSSKLARGVCLCKREERAPARAAAAAA PKKKESGDPAPPGAGMUTTARA	İ	1		GNSGGUDT POFENDEL ON DEL ANTIA CE MADA MADALIAN
RVHVGSGDHDYG\VSRTPPKK\MPAILIPEVGSRMNVKRHQDI TIKPVLSLGPAAPPPCTLASRE\MPAILIPEVGSRMNVKRHQDI TIKPVLSLGPAAPPPCTLASRE\MPAILIPESCAPCLAPE SILSPEASPCRNDMNTRTPPEPSAKORSMCTRKACGRASPSSQ GWGGRGNRSRSVSGSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1	1	İ	AVSLLAKAKSPKSTAOEGTI.KDEGUTDA VUDA AUTT ODGE
TIKPVLSLGPAPPPCTAASREPLDHRTSSOADPSAPCLAPS SLLSPEASPCRNDMTRTPPEPSASSRSMENGLYPARCASASPSSO GWGGRGRNSRSVSGSNRTSEASSSSSSSSSSSSSSSRSRSLSPD HKRWRSSCSSSGERGCSSSSSSSSSSSSSSSSSRSRSRS PSPRRSSDRRRYSSYRSHDHYQRQRVLQKERAIEBERVVFIGK IPGRMTRSELKQRFSVFGEIBECTIHERVGGDNYGFVTYRYABE AFAAIEBGHKLRQADEQPFDLCFGGRQFCKERSYSDLDSNREDP DPAPVKSKPDSLDFTTLKKQAQKNLER RLSSHFSGCSPSIVCTVFFDFGGRQFCKERSYSDLDSNREDP DPAPVKSKPDSLDFTTLKKQAQKNLER RLSSHFSGCSPSIVCTVFFDFGGRQFCKERSYSDLDSNREDP DPAPVKSKPDSLDFTTLKKQAQKNLER RLSSHFSGCSPSIVCTVFFDFGGRAFCKERSYSDLDSNREDP DPAPVKSKPDSLDFTTLKKQAQKNLER RLSLDFLUGLEGGGULTVFLDFFATEALLQVFWINTLQGKL SILQPLILERIDALGDPKHSSVDRSKLHTLLQDKSSLSELETDI KIFKESLEILDEBELLEELCVSKATEALQVFWINTLQGKL SILQPLILERIDALGDPKHSSVDRSKLHTLLQDKSSLSELETDI KIFKESLEILDEBELLEELCVSKATEALQVFWINTLQGSL SILQPLILERIDALGDPKHSSVDRSKLHTLLDDKSSLSELEDHRIFMILTGI MFMGSGLIWRALDSFLGRVAARGWRENSELEDHRIFMILTGI MFMGSGLIWRALDSFLGRVAARGWRENSELEDHRIFMILTGI MFMGSGLIWRALDSFLGRVAARGWRENSELEDHRIFMILTGI MFMGSGLIWRALDSFLGRVAARGWRENSELEDHRIFMILTGI MFMGSGLIWRALDSFLGRVAARGWRENSELEDHRIFMILTGI  SGQDDBEQGLTAQDSJOINL/SEVLOALMWRKKGLAVLPCILQ GVFFSILGTGLLMLPGGIKLPAVPTYTCANLAMRKKGLAVLPCILQ FLSMTWYSLSYIPVANDAVIKCCSSLLS AEGISWAWAGLGKAGGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFQXVEKIGGGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHRIVIRLLDVYHRERIJVTVFFFISQ DLKKYMDSTPGSELPJELLIKSVLFQLLQGVSFCKSHVYHRALK PQMLLINELGAIKLADFGLARAFGVVLKKTRILDVEFFISQ DLKKYMDSTPGSELPJELLIKSVLFPGDS\EDD\LTFT FRNLGTPSEDTWFGVTQLPDYKGSPFKMTRKGLEVPFLEFEG RDLKMQLLQYPDSGTTAKTALAHPYTSPSPFSPAARGVVLQRF RH  AGSVQLHVWIRGMRIQPG/KAAAITDLDPDFEPQSRFRSCTWPL PREIANQPSKPPVEVPDLGEKVHTEGRSEPILLPSRLPERDAWHT FRPRSSNASSVSTRLSPLRPSSEVLABEIPRAVSSYAGGVPPT LAGIGLLDGINLTSSHLLSSGLSGSCRPRRAASMBSSKLLERGRKA PKKKPSGLPAPFGGATTSSVCHFAKGSFCNNENSIRINILLHSKFIKV HWBATGKSSWMMINPPGGKSGRAPRRAASMBSSRNLINGRSKA PKKKPSGLPAPFGGATTSSVCHFAKGSFCNNENSIRININILLHSKFIKV HWBATGKSSWMSLTHVALGHPAPHTTSPCHARGSGFCNDHGTVTGPHTTYSS SLPSPAEGPLAAGGGGCSSOALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSKLLARGSGRCFREERGAAAAAAA ABMEELHSLIDPIRGELBERTYTGLGGKSCPPHFPFPERGGARARAAAAAA ABMEELHSLIDPIRGELBERTVLOGLG	1	1	Í	RVHVGSGDHDYC\VRSRTPPKK\MDAI.I.T DEUGGBLDEUT
SILSPEASPCRIDMITRIPPEPSAKORSHRICTRACKSASPSSO GWOGRAGNRSWSGSSMSTENSESSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	ŀ	Ì		TIKPVLSIGPAAPPPPCIAASPEDI.DUDTSSEOADBSA.DCI.A.SS
GWGGRGRINSSUSGSBRISSSSSSSSSSRSRESSLSPP HKRWRSSCSSSGSRESRCSSSSSSSSSSSSSSSSRSRESS PSPRRSDRRRYSSYRSHDHYDRORVLOKERA IEERRVYFICK IFGRITTSBLKORFSYTGEHEET/HPVQGDWYGFVTYRYABE AFAAIEGHKRQADEQPFDLCFGGRQFCRSYSDLDSWREDF DPAPVKSKPDSLDFPTLKKAQKONLER RLSSHFSQCSFSIYC\TKFDKQGWYSFFRKKTELYQELGLQAR DLRQHYMSITVRNNRIIMKMEYLKAVITPSECLLILDYRHLNIK, OWLFRZIPSQLSGEGGUTVTELPFATEALLQYWINTLQGKL SILQPLILETLOALGDFKHSSVDRSKLHILLONGKSLSELETDI KIFKESILEILDEBELLEELCEVSRTEATEALLQYWINTLQGKL SILQPLILETLOALGDFKHSSVDRSKLHILLONGKSLSELETDI KIFKESILEILDEBELLEELCEVSRDFQVFKKSSAGIDHAEEM ELLLENYYRLADDLSNARELRVLIDDSGSIFTINLDSHRWOM ELLLLENYYRLADDLSNARELRVLIDDSGSIFTINLDSHRWOM ELLLENYYRLADDLSNARELRVLIDDSGSIFTINLDSHRWOM ELLLENYYRLADDLSNARERRVLIDDSGSIFTINLDSHRWOM ELLLENYYRLADDLSNARERRVLIDDSGSIFTINLDSHRWOM ELLLENYYRLADDLSNARERRVLIDDSGSIFTINLSHRWIGH ELLLENYYRLADDLSNARERRVLIDDSGSIFTINLSHRWIGHEKERVL SQDDDEEQGITAQDSGINL/SEVLDASSLSENTELKWHAICTEV GVFFSILGTGLLWLEGGIKLFGLWFYTCHGNLASLSENTELKWHAICTEV GVFFSILGTGLLWLEGGIKLFAVFTTLGNLAALASTCFFLMGPVK QLKKMPGATRLLSTUNLLCFFITIVALLFGIFTINCHLAALASTCFFLMGPVK QLKKMPGATRLATIVALLCFFITIVALLGFITINCHLAALASTCFFLMGPVK GLKKYMDSTPGSELPHHILISKLIFQLLAGSVSFCHSHRVLHFELD, FLOMTWYSLSYIPYARDAVIKCGSLLS  SYAMDMFQRVERIGEGTYGVVYKAKMRSTGOLVALKKIRLDLEM EGVPSTALREISLLKELKHPHIVRLLDVVHRKRLTHVEFFLNG DLKKYMDSTPGSELPHHILISKLIFQLLGGSFCHSHVHHRDLK PQNLLINELGAIKLADPGLARAFGVPLKTYTHEVVTLWYRAPEI LAATRFYTAVDINSICGIFABMYTAKTALHPFDSSPEPSPARQVVLQFF FRHLGTPSSDTWFGVTQLPDYKGSPFKMTRKGLEIVPFLEFEG RDLLMQLLQYPPSGYTTAKTALAPFPSSPEPSPARGVVLQFF RH  AGSVQLHWWIRGMEIQPG/KAAAITDLDPDFEPGSRRSCTWPL PREPIANDPSKPPEVEDLGEKVHTEGRSEPILLPSRLPBRGC PQPGILGAVTOPRKGSSRNANGNGSYSSENIERDLHHSKFIKV HNBATGKSSWMMINPEGGKSGRAPRRAASMOSSSKLLERGRKA PKKKPSGLAPPFEGATTSPVCHTRASSSFSNOSISRINLERSKA PKKPSGLAPPFGATTSPVCHTRASSLSFSNOSISRINLERSKA PKKPSGLAPPFGATTSPVCHTRASSLSFSNOSISRINLERSKA PKKPSGLAPPFGATTSPVCHTRASSLSFSNOSISRINLERSKA PKKPSGLAPPFGATTSPVCHTRASSLSFSNOSISRINLERSKA PKKPSGLAPPFGAGMLTATSPLEPPEPSFGARRRRRLPGG GVAALKROPGSAPGLAFRARAAGSGGGFGERGAAAAAAA ABMEELHALDPLAGGELBRAPTTGLGGFRERGAAAAAAAA	1			SLLSPEASPCRNDMNTRTPPEPSAKOPSMPCVPKACPSASPCCO
HKRWRRSSCSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSSSS	1			GWOGRRGRNSRSVSSGSNRTSFASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
PSPRRASDRRRYSSYRSHDHYQRGNUTGFUTYRYAEE AFAALESGHKLRQADEGPFDLCFGGRQFCKRSYSDLDSNREDF DPAPVKSKPDLDFDTLLKQAQKNED 5991 334 1379 RISSHFSQCSFSIYC\TKPEKGGNTTSFERKKTELYQELGLQAR DLRPQHYMSITVRNNRI INRMEYLKAVITYPECLLILDYRNINLK QWLPFSLPSQLSGGQLVTYPLFBFALFALLQCWMITTLGK GWLPFSLPSQLSGGGLVTYPLFBFALFALLQCWMITTLGK SILQPLILETLDALGDPKKSSWDRSKLHILLQNCKSLSELETDI KIFKESILETLDEEGLLEELCYBELYGEDYPEKSSAGIDHAEEM RISGLINRRLISFIGR/LARSSIASYGMKDWHGGIVEGI ELLLENYYRLADDLSNARELRVIIDDSGIIFINDSHRNYMM RIMIQLIMGTFSLSIFGGMGAFGMNLESSLEEDHRIFHLITGI MFMSGGLINRRLISFIGR/LARSSIASYGMKDWHGGIVEGI GGQDDEGQGITADGSOINI,SENSIASSLEEDHRIFHLITGI GGQDDEGQGITADGSOINI,SENSIASSLEEDHRIFHLITGI GGQDDEGGGITADGSOINI,SENSIASSLEEDHRIFHLITGI GGVFSILGTGLLMLPGGIKLPAVFYILGNLAALASTCFLMGPVK GLKKMFBATRLLATIVMLLCFIFFILCAALMWHKKGLAVLFCILQ GVFFSILGTGLLMLPGGIKLPAVFYILGNLAALASTCFLMGPVK GLKKMFBATRLLATIVMLLCFIFFILCAALMWHKKGLAVLFCILQ CLKKMPSATREISLLKELHPHIVRLLDVUINBEKCLYLVFEPLSQ GLKKWMDSTPGSELPHLIKSYLPOLLQGVSFCHHSHVHRDLK EGVPSTAIRRISLLKELHPHIVRLLDVUINBEKCLYLVFEPLSQ GLKKWDSTPGSELPHLIKSYLPOLLQGVSFCHHSHVHRDLK FQNLLINBLGAIKLADFGLRAFGVPLRTTHEVVILWYRAPEI LLATRFYTTAVDINSIGCIFAEMVTRKALFGOSLAKKRIEDLEM EGVPSTAIRRISLKELKPHPHIVRLLDVUINBEKCLYLVFEPLSQ GLKKTPSEDTHPGVTQLPDVKKARETGGULAHKRIELDLEM EGVPSTAIRRISLKELKPHPHIVRLLDVUINBEKCLYLVFEPLSQ GLKKTPSEDTHPGVTQLPDVKKARETGGULAHKRIELDLEM EGVPSTAIRRISLKELKPHPHIVRLLDVUINBERCLYVFEPLSQ GLKKTPSTATAVDINSIGCIFAEMVTRKALFFGDS\EIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  4 AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWPL PRELINDDSKPPEVEPDLGEKVHTEGRESPILLPSRLPEPAGG POPGTILGAVTGFRKGGSRRNAMGNGSYBELISQAIRSAPEKRLT LAQITEMMYNTYPYFKDKGDSNSSAGWKNSIRHNILSLHSKFIKV HIBATGKSSMWHLMPEGGKGSKRAMGSSFLGRFRAASMOSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRRRREADMWTT FFRRSSSNSSVSTRLSPIRPEGEVLAEEIPSSVSYAGGVPFT LNGGLELLDGINLTSSHSLLSRGEFSFLOHPGFPGSTLPTT, SMIAPPDWASADTPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGLDFNFEPDO GWALLRGGPGSAPCLERGSRAAAAAAA AMMEELHSLLDPLYRRQELLSHSSNOSI				HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSSS
IPGRMTRS9LKQRFSVYGEIEECTIHFRVQCDMYGFVTYRYAEB AFAANIESGHKIRQADEQFPICGGRQFCKGRYSDLDSNREDF DPAPVSKFPBLDPDTTLIKQAQKNIRR  FLSSFFSCSPSIYC\FKFBKQGNVTSFERKKTELYQELGLAR DLRFQHVMSITVRNNRIIMEMEVLKAVITBECLLILDYRNIALIK QWLFRELPSQLSGEGQLVTYPLFFEFFAIFALLQYWINTLQGKL SILQPLILETLDALGDPKRSSVDRSKLHILLQMGKSLSELETDI KIFKESILEILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNARAEVILDDSQSIFINDGKSLSELETDI KIFKESILEILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM RLNLQLTMGTFSLSLFGIMGVAFGMRLGSSLEEDHRIFWLMM RLNLQLTMGTFSLSLFGIMGVAFGMRLGSSLEEDHRIFWLITGI MFMGSGLIWRRLISFLGR/LARSSIASYGMKDWVINGIVEGI SGQDDEEQGITAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLHNEGGILKFAVFYTLGMLAALASTCFLMGPVK QLKKMFFSTRILATIVWLLCFIFTLCAALAWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVLKCSSLIS SQMDMEQKVEKIGSGTIGGKCKQATEWRLKGLAVLFCILQ FLSMTWYSLSYIPYARDAVLKCSSLIS SVAMDMFQKVEKIGSGTTGVVVYKAKWRSTGQLVALKKIRLDLEM EGVPSTAIRSISLLKELKHPNIVRLLDVVHNRSRLGLVLVFEISQ DLKKYMDSTFGSSLPHLIKSYLFQLLQGVSFCHSHRVHRRDLK PQNLLINEIGAILALDFGIRAGPVFKKLIFVETFLSQ DLKKYMDSTFGSSLPHLIKSYLFQLLQGVSFCHSHRVHRRDLK PQNLLINEIGAILALDFGIRAGPVFKLTYLTEVVTLWRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\LEIDQ\LFRI FRILGTSSEDTHFLWFGVTQLDFWSFPFWTRTKCLEIVPRLEPEG RDLMQLLQYDPSQRITAKTALAHPYFSSPEPSFAARQVVLQFF RH AGEVQLHVWIRGMRIQPG/KAAAITDLDPDFEPQSRPSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQGTIGAVTGPKGGSRRNANGSYABLISQAIESAPERRLT LAQIYEMWRTVPYFKDKGDSNSSAGWNSIRHNLSLHSKFIKV HNEATGKSSWMMLNPEGGKSKAPRRAASNDSSSKLRGRSKA PKKRPSGLPAPPEGATPTSPVCHFAKWSGSCSRNREEADMWTT FRPRSSSNASSVSTRISPIRFESEVLABEIPASVSSYAGGVPPT LAGGIELLLGLINITSSHGLIESRGLSGFSLOHPGVTGPLHTYYS SLPPREGFGLAAGAGCCFSSKQAREALTSDTPPPADRUMTQVD PILSQAPTLLLIGLGLPSSSKAAFVPPLFFBPDPSKGARRRRLPGR GVAALRRGGSSABVLCTRARGSSAAFVPPLFFPPSRGARRRRLPGR GVAALRRGGGSABVLCTRARGSAAFVPPLFFPPSRGARRRRLPGR GVAALRRGGGSABVLCTRARGSAAFVPPLFFPSPSGGARRRRRLPGR GVAALRRGGGSABVLCTRARGSAAFVPPLFFPPSRGARRRRRLPGR GVAALRRGGGSABVLCTRARGSAAFVPPLFFPSPSGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	i			PSPRRRSDRRRRYSSYRSHDHYORORVI OKERA TEERRIVIETOV
AFAAIESCHKLRQADEQPFDLCFCGRGYCKGSYSLDSNREDF DPAPVKSKPD3LPDTLLKQAQKNLRR  RLSSHFSQCSPSIYC/TKFDKQGNVTSFERKKTELYQELGLQAR DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNIANIK (MEPRILPSQLSGEGQLVTYPLFFEFFATEALLQYWINTLQGKL SILOPLILETLDALGDPKHSSVDRSKLHILLQMGKSLSELETDI KIFFKESILETLDEELLEELCVSKWSDPQVPFEKSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINDDSHRNVMM RLNLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWALTGGI MFMGSGLIWRRLDSFLGGMCAFTENFLRFWNGAMEKLRRVL SGQDDEEQGITAGDSQINL/SEVLDASSLSFNTRLKWFALTGGI GVFFSILGTGLLWLPGGIKLFAVPYTLGNLAALASTCPLMGPVK CKKMFEATRLATIVMLLGPITTETLCAALMWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLIS  5993 1650 594 AEGIGSWAVWAGIGWAGRHMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFQKVEKIGEGTYGVKARNRETGQLVAALKKTRLDLEM EGVPSTAIRSISLLKELKHPNIVRLLDUVHNERKLYLVEFLSQ DLKKYMDSTDSSLIPHLIKLYDLDLQCVSPCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGGIFAEMVTRKLFEDSELDQ\LFFIG RDLMQLLQYDPSQRTTAKTALAHPYFSSPEFSFAARQYVLQRF RH  AGSVQLHVWIRGRRIQPQ/KAAAIIDLDPDFEPGSRPSCTWPL PRPEIANQPSKPPEVPDLGEKVHTGRSEPILLPSRAGERSC PQFGILGAVTGPKKGGSRRNANGNGSYAELISQAIESAPERRLT LAQITEMWVRTVPYFKDKGDSNSSAGWKSIRHNISLHSKFIKV HNEATGKSSWMMINPEGGKSGARRARANGSSYKLERGSKA PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWTT FRFRSSSNASVSTRISPLRFESEVLABEIPABSSYKLGRSKA PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRRREEADMWTT FRFRSSSNASSVSTRISPLREESEVLABEIPAPPAGG SLAPPTWAASAJIFKALGTPPTYPPPARAVITYTYS SLEPPAEGGLAGGCCSSSQALEALITSDTPPPPARAVITYTYS SLEPPAEGGLAGGCCSSSQALEALITSDTPPPPARAVITYTY SMIAPPPWAASAJIFKALGTPPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGLDPNFFPDD  5995 2 2437 RPFGFGPASGAWLCTRARGSAAFVPPLFPFPSRGARRRRRLPGR GWAALRRGPGSAPGLPRGRARSRAAGDRSREERGAAAAAAA AEMMEELHSL\DPN RRCELLEARFYTGLGVSKGUNGSINSSINGI		į		IPGRMTRSELKORFSVFGEIEECTIHFRVOGDNYGFVTVRVARE
S991   334   1379   RISSHFSOCSPIYC\TKPKGCGNTSFERKTELYQELGLQAR	j			AFAAIESGHKLRQADEQPFDLCFGGRROFCKRSYSDLDSNREDE
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DLRFGHVMSITVRNINI IMRMEYLKAVITPECLLILDYRNINIK  QUEPRILPSQUSGEGQLUTYPPPFFRAFALQUWINTLQGKL SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI KIFKESILETLDEEELLEELCVSKKBDRQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDEHRIVMM RINIQLTMGTFSLSIFGLMGVAFGMNLESSLEEDHRIFWLITTGI MFMGSGLIWRLLSFLGFLARSIASSCMEMDWINGGIVEGL SGODDEEQGLTAQDSQINL/SEVLDASSLESNTFLKWERICFVC GVFFSILGTGLWIPGGIKLFAVFYTLGNLAALASTCHMGPVK GLKKMFEATRILATIVMLCPIFTLCAALWHKKGLAVLFCILQ FLEMTWYSLESYIPVARDAVIKCCSSLLS SVAMDMPQKVEKIGEGTYGVVYKARNRETGQLVALKKKTRLDLEM EGVFSTALRSIISLKELKHNIVKLDVHRERKIJVFFELSQ DLKKYMDSTPGSELPLHLIKSYLPOLLQGVSPCHSHRVHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIMSIGCIFAEMVTRKALFFGDS\EIDQ\LFFR FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPAARQVVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLEEKVHTEGRSEPILLPSLEPAGG PQGGILGAVTGPRKGGSRRNAMGNQSVAELISQAIESAPEKRLT LAQIYEMWVRTVPYYFKDKGDSNSAGWKNSIRNISLHKSTIKV HWRATGKSSWMMINPEGGKSGKAPRRAASMDSSSKLARGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKNSGSPCSRNREEADMWTT FFPRSSNNASVSTRISPHSESULAEEIPASVSSVAGGVPPT LMEGLELLDGLNLTSSHSLLSRSGLSGFSLQHFGVTGPLHTYSS SLFPAEGPLSAGEGGFSSQALEALITSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKAGGFRARASGGRGFREEERDAMAAAA AEMMEELMELDLIJDPLIBERDFPDP	5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYOELGLOAR
OWLFRIDPSQLSGEGQLUTYPLPFERRATEALLQWMINTLOGKL SILOPLILERIDDALGOPHRSVDRSKLHILLQNGKSLSELETDI KIFKESILPILDALGOPHRSVDRSKLHILLQNGKSLSELETDI KIFKESILPILDALGOPHRSVDRSKLHILLQNGKSLSELETDI KIFKESILPILDALGOPHRSVDRSKHHILLQNGKSLSELETDI ELLLENYYRLADDLSNAARELRVLIDDSQSIFINLDSHRNVYMM RINTLQLTMTSTSLSFEGMYAFGMNLESSLEEDERI FWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL SGQDDEEQGLTAQDSQINL/SEVLDASSILENTRILKWFAICFVC GVFFSILGTGLIMLPGGIKLFAVPYTLGNLAALASTCPLMGPVK QLKKMFEATRILATIVNLFIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS SVANDMFQKVEKIGEGTYVYAKNNETGQUVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEPLSQ DLKKYMDSTPGSELPHHLIKSYLFOLLQGVSFCHSHRVIHRDLK EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEPLSQ DLKKYMDSTPGSELPHHLIKSYLFOLLQGVSFCHSHRVIHRDLK FRMLGTPSGSTLPHHLIKSYLFOLLQGVSFCHSHRVIHRDLK FRMLGTPSGSTVAPLAVANGLGVAFKTSCEVPLLPFEG RDLMQLLQVDFSQRTTAKTALAHPYSSPEPSFAARQYVLQRF RH AGSVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPGSRPSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAMGNGYSTELISQAIESAPEKRLT LAQIYEMWMTVPYFKDKGSNSAGWKNSIRMISLINSKFIKV HNEATGKSSWMMLNPEGGKSGKAPRRAASMDSSKLLRGSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FFRPSSSNASSVSTRISPIRPSEVLABETPASVSSYAGGVPPT LANGIELLDGLNITSSHSLLSRSGLSGFSLQHBGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADULMTQVD PILSQAPTLLLLGGLPSSKLAITGVGLCFKPLEAPGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASQORMPQDLDLDMY MENLECDMDNI ISDLMDEGGLDFNFPPDP SAPAFGPSSNOSL SMAPPPVWASAPIFKALGTPVLTPPTEAASGORROPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORROPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVWASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVASAPIFKALGTPVLTPPTEAASGORGRGPSSLVPTL SMIAPPPVASAPIFKALGTPVLTPPTEAASGORGRGPSSLERGAAAAAAA AEMMELHSLLDPPRGABAGGGGGGGGGGEGEGEGAAAAAAAA AEMMELHSLDJDPN LIDDALGARFY/TGLGVKGCPLMSESSMOSIL	į.			DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNIK
SILOPLILETLDALGDPKRSSVDRSKLHTLLQNGKSLSELETDI KIFKESILEILDEELELCVSKWSDPQVFEKSAGIDHAEEM ELLLENYYRLADDLSNAARELEVLIDDSGSIIFINLDSHRIVMM RLNIQLTMGTFSLSLFGIMGVARFGMILESSLEEDHRIFWLTGI MFMGSGLIMRRLLSFIGR/LARFSIASYGMDMVHGGVEGL MFMGSGLIMRRLLSFIGR/LARFSIASYGMDMVHGGVEGL SGDDDEEQGLTAQDSQINL/SSVLDASSLSFNTELKWFAICFVC GVFFSILGTGLIMLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCNALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS SVAMDMFQKVEKIGEGTYGVVYKAKNRETCQLVALKKIRLDLEM EGVPSTAIREISLLKELKHNIVRLDDVVHIMBKKLYLVFEFLSQ DLKKYMDSTPGSELPHHIKSYLFQLLQGVSFCHSHRVHHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDINSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRNLGTFSEDTWPGVTQLPDYKGSFPKWTRKGLEETVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  1934 AGEVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPGRLPEPAGG PQPGILGAVTOPRKGGSRRNAWGNGSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHINLSLHSKFIKV HNBATGKSSWMLNPEGGKSGKAPRRAASMDSSKLLRGRSKA PKKKPSGLPAPPEGATFSVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAREIPASVSYAGGVPPT LMGGLELLDCLNLTSSHSLLSRSGLGGFSLOHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALERALITSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLITPTEAASQDRMPQDLDLDMY MENDLECDMONIISDLMDEGGGLDPNFFEPDP  5995 2 2437 RPFGFGPASGAWLCTRARGSAAFVPPLPFPSRGARRRRRRLPGR GVAALRRGPGSABGLPRGRAERSAAGSGRGFSRERRRAAAAAAA AEMMEELHSL\DP\RRQCLLEARF\TGLGVSKGFINRESSNOSI.	i i			QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQYWINTLOGKL
KIFKESILEILDEEELLEELCVSKUSDPQVEKSSAGIDHAEEM ELLLENYYRADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM RLNLQLTMGTFSLSIFGLMGVAFGMNLESSLEEDHRIFWLITGI MFMSSGLIWRRLLSFLGR/LARSIASYGMKDMYHGGIVEGL SGODDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLIMLFGGIKLFAALMWHKKGLAVLFCILQ CLKKMFEATRLIATIVMLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  5993 1650 594 AEGLGSWAVWAGLGWAGRHMARGGATGALGVGCKLPSAFCFFGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKHRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNBRKLYLVFEFLSQ DLKKYMDSTPGSELPHLIKSYLFQLLQGVSFCHSHRVIHRDLK FQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDINSIGGIFAEMVYTKALFPGDS\EIDQ\LFRI FRNLGTFSEDTWPGGYLDPYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPGSRFRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPKKGGSRRNAWGNSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSHSKFIKV HNEATGKSSWMMLMPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSNREEADMWTT FFPRSSSNASSVSTRLSPLRFSEVLAEEIPASVSSYAGGVPPT LAGGIELLDGLNLTSSHSLLSRSGLGGFSLOHPGVTGPLHTYSS SLFSPAEGFLSAGGGGFSSQALEALLTSDTPPPPADVLIMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAFGPSSLVPTL SMIAPPPVMASAPIPKALGTTVLTPTTEAASQORMPQDLDLDMY MENDLECDMONI ISDLMBEGGGLDFNFFEPD  5995 2 2437 RPFGFGPASGAWLCTRARGSAAFVPPLFRPSRGARRRRRLPGR GVAALRRGFGSAAFGLPRGRAERSAAGSGRGFSRERGAAAAAAA AEMMEELHSL\DP\RRQELLEARP\TSLGVSKGPRNSRSSNSIL	1			SILQPLILETLDALGDPKHSSVDRSKLHILLONGKSLSELETDI
ELLLENYYRLADDLSNAARELRVLIDDSGSIFFINDSHRNVMM RINNQJIVMSTFSLSEDIMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLISFLGR/LARSSIASVGMKDMVHGGIVEGL SGODDEGCGLTAQDSGINL/SEVLDASSLSPHTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVPYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFJFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLS  5993 1650 594 AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFCKVERIGEGTYGVVYKAKNRATGQLVALKKIRLDLEM EGVPSTATRE ISLLKKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVHHRDLK PQNLLINELGAIKADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKLLFFOSQ\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQVVLQRF RH  AGEVQLHVWIRGMRIQPG/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTOPRKGGSRRNAWGNGSVAELISQAIESAPEKRIT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNELATGKSSWMMLMPEGGKSGRRRRAASNDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWAGSPCSRRREADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLOGLNLTSSHSLLSRGLSGFSLQHPGWTGPHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPP PADVLMTQVD PILSQAPTLLLLCGLPSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNI ISDLMGEGGLDFNFEPDP  TSPSS 2 2437 RPFGPGPASGAWLCTRARGSAFVPPLFRPFSRGARRRRRLPGR GVAALRRGGSSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHELJ\DP\RQGELLEARF\TGLGGVSINSSSNOSI.				.KIFKESILEILDEEELLEELCVSKWSDPOVPEKSSAGIDHAEFM
RLNIQLTMGTFSLSLEGIMQAFGMNLESSLEEDHRIFWLITGI MFMGSGLWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL SGODEEGGLTAQDSQINL/SEVLDASSLSFNTRLKWFAIGFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLWGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSWTWYSLSYIPYARDAVIKCCSSLS SQADMEGGMAVWAGLGWAGRMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFCKVEKIGEGTYGVYYKAKNRTGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK FONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRALGTPSEDTWGGVTQLRDYKGSFPKMTRKGLEELVPRLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQVVLQRF RH AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRFRSCTWPL PPPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRIT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWMLNEGGIGSGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVCHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LANGLELLLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLARGVCGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMGGGGGLDFNFEPDP  TSPSS 2 2437 RPFGFGPASGAULCTRARGSAAFVPPLFRPFSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGFSREERGAAAAAAA AEMMEELHSL\DP\ROGELDERRF\GGLEGAFSCRGGFNSEERGAAAAAAAA			•	ELLLENYYRLADDLSNAARELRVLIDDSOSIIFINLDSHRNVMM
5992 2 609 AGPDFRLVCGVSGSGFPGGRQGATENRPLRFWNGAMEKLRRVL SGQDDEEQGLTAQDSQINL/SEVLDASSLSRNTRLKWFAICFVC GVFFSILGTGLLMLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS 5993 1650 594 AEGIGSWAVWAGIGWAGRHMEAGGATGALGWGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTATREISLKELKHPNIVRLLDVVINERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFOLLGGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPPVKGSFPKWTRKGLEEIVPNLEPEG RDLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  1934 AGBVQLHWWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNGSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNBATGKSSWMMLNPEGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRFESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHEGVTGPLHTYSS SLFSPAEGPLSAGGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDPNFPDPD MENLECDMDNIISDLMDEGGGGDPFFEPDF GVAALKRGPGSAPGLPGGRARSSAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\JROBLLEARFY\TGLGVSKGPLNSERSNOSI. AEMMELGELSL\DP\JROBLLEARFY\TGLGVSKGPLNSERSNOSI.				RLNLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGT
AGPUPLY PROGREGOLITADIS OINL/SEVLDAS SLSPNTELKER ALGEVC GVFFSILGTGLLWLPGGIKLFAVPYTLGNLAALASTCFLMGPVK QLKKMFEATRILATIVMLLCFIFTLCAALWHKKGLAVLPCILQ FLSNTWYSLSY IPYARDAVIKCSSLLS SVAMDMFQAVEKIGGTYGVYYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLLVFELSG DLKKYMDSTPGSELPLHHIKSYLFOLLQGVSFCHSHRVIHRDLK PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRHLGTBSEDTWEVTQLFPYKGSFPKMTRKGLEEIVVNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQYVLQRF RH  AGRVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNIRHNLSLHSKFIKV HNEATGKSSWMMINPEGGKSGRAPRRAASMDSSSKLLIRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRESSEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNITSSHSLLSRGLGFSCLOPPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGELDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGFSREERGAAAAAAA AEMMEELHSL\DP\RQCELEERF\TGLGVSKGPLNESSNOSI.	5992			MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGI.
SGODDEEQGITAQDSGINI/SEVIDASSISFNTELKMFAICFVC GVFFSILGTGLLWIPGGIKLFAVFYTLGNLAALASTCFIMGPVK QLKKMFEATRILATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  5993 1650 594 AEGLGSWAWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMD5TPGSELPLHLIKSYLFOLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKKLT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSKLLRGRSKA PKKKPSGLPAPPEGATTTSPVCHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPSESVLAEEIPASVSSYAGGVPPT LMEGLELLDGLNLTSSHSLLSRSGLSGFSLOHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGFSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRRAESRAAGSGRGFSEREGRAAAAAAA AEMMEELHSL\DP\RQELLEARF\TGLGVSKGPLNSESSNOSI	3992	. 4	609	AGPDFRLVCGVSGSGFPGGRQGQATENRPLRPWNGAMEKLRRVL
OLKKMFEATRILATIVMLCETITLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS 594 AEGIGSWAVWAGIGWAGRHMERGGATGALGVGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGYPSTAIREISLLKELKHENIVRLLDDVHNBRKLYLVFEFLSQ DLKKYMDSTPGSELPIHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQMLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTF9EDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLIMQLLQYDPSQRITAKTALAHPYFSSPEPSPARAQYVLQRF RH  AGRVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNGSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRUREEADMVTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRGLLSFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPP PPADVLMTQVD PILSQAPTLLLCGLPSSSKLATGVGLCPKPLEAFGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGFINSESSNOSI	1 1	j		SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC
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SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	į.		ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
1	1		DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
1			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
	ļ		RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
1	1		KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
	1	1	REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
1		1	TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
	İ		KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEO
			RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
1	ł	1	YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMO
i	1	ĺ	IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
1			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
1			VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVOFP
1		1	PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
1			STSSPAGAAIASTSGASNNSSSN
5996	1612	981	
1		1	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
1		1	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1		1	AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
		1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
5997	1	l	FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
i	ł	1	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
	1	1	AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
		1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
	i	l .	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1		1	AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1	1	ì	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
<u>L</u>	1	ł	FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
1	}		GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
1	1		ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
1			LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
		1	QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
1	1	1	ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
I	1	1	FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1 .			KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
Į.	1	1	QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
1	1	l	EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
1	l	i	LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
I	<b>\$</b>		VRHVTENRUDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
	I		LFRIVNVAKKIGNVMVTT\SRNVVOTGK\AVGOSVGGAFS\SAK
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6000	102	15.53	TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEBLIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLATASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEBLIQQEHADQASIRSLVTWGNYAWYYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKKGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEBLIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRBNGNYGKRKLLELIGHAVAHLKKADEANDNLFR
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEBLIQQEHADQASIRSLVTWGNYAWYYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKKGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEBLIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRBNGNYGKRKLLELIGHAVAHLKKADEANDNLFR
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWVYHMGRLSDVQIYVDK VKHVCEKFSSPYRI3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLHHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWYYHMGRLSDVQIYVDK VKHVCEKFSSPYRI 3SPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRBNGNYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
6000	101	1561	TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVYYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWVYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLATASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQWMNLRBNGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB
	-		TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWYYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLATASYRLDNWPPSQNATDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
	-		TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWYYYHMGRLSDVQIYVDK VKHVCEKFSSPYRISSPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB  AFAHSPSRGHRETHIHTPRHTPRCTMAESHLQSSLITASQFFEI WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
	-		TA\MSSWLSTFTTSTSQSLTEPPDEKP  TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL DDFEDKVPYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR KAEELIQQEHADQASIRSLVTWGNYAWYYYHMGRLSDVQIYVDK VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEFTSGLATASYRLDNWPPSQNATDPLRQAIRLNPD NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS SWNGB AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI

Deginning nucleotide location corresponding to first amino acid residue of amino acid sequence  6002  977  81  LAPAGSCHLYPETPREPERSPREPSHAAPHSSPCALSPUNTENLEVSCLAVERS EMPLSFTISRGFWILLSYVIGLLPFIPIPERSPEPSHASASAFK APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIFTUPPSIQIYSSRELEETLINKTREILSDDKHDMDQRANALKK SLLVAGAAQVDCFFQHLRLLCGALING LACIDA (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycine H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stocodon, /=possible nucleotide deletion, 1-possible nucleotide insertion)  LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFF FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKK MALSDGGKLYRTDLALILCAGDN  LAPPGGGLHYPPRTPLSRPPPSHHAPHPSPLPLPPADLHH SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSI EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPH EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKCKAPEMPLSFTISRGFWILLSYYLGLLPFIPIPEKFFFCFLPNIIN YPPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCI ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS  GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFK APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIFTUPPSIQIYSSRELEETLNKTREILSDDKHDWDQRANALKK SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACIT FLSTVLIGNKFDHCAEAIVPTLFNLVPNSAKWMATSGCAAIPE		l Amino acid	Predicted end	Predicted	SEQ
location corresponding to first amino acid residue of amino acid sequence s	ide	Amino acid segment containing signal pepti			
corresponding to first amino acid residue of amino acid sequence s	E⇒	Glutamic Acid. F=Phenylalaning C-clusion			NO:
to first amino acid residue of amino acid sequence  amino acid sequence	•	H=H1Stldine, I=Isoleucine K-Lucine	corresponding	i .	- 1
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stocolon, /=possible nucleotide deletion, \  Codon, /=possible nucleotide insertion)  LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFF FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKH MALSDGKLYRTDLALILCAGDN  LAPPGGGHTPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHE SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSI EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPM EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAA EMPLSFTISRGFWVLLSYYLGLLPFIP 1PEKFFFCFLPNIIN YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCI ESDFEAAFSVGATGVITOYPTALRHYLDNHGPAARTS  GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFK APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFI FTDVPSIQIYSSRELEETINKIREILSDDKHDWDQRANALKK SLLVAGAAQQYDCFFQHLRLDGALKLSAKDLRSQVVREACIT ELSTVLGNKFDHGABAIVPTLFNLVPNSAKVMATSGCAAIDE		L=Leucine, M=Methionine, N=Asparagine			1
residue of amino acid sequence    S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stocker		P=Proline, Q=Glutamine, R=Arginine			
amino acid sequence S		S=Serine, T=Threonine, V=Valine			j.
sequence   Sequence   Codon, /=possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide insertion    -possible nucleotide deletion,    -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion  -possible nucleotide disertion)  -possible nucleotide disertion)  -possible nucleotide disertion)  -poss	go	W=Tryptophan, Y=Tyrosine, X=Unknown *-Sto	1		
C-POSSIBLE HUCLEOTIGE INSERTION)  LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFN FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKH MALSDGGKLYRTDLALILCAGDN  LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHE SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSI EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPA EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAA EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIIN YPPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCI ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFI FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKK SLLVAGAAQVPCFFQHLRLLDGALKLSAKDLRSQVVREACIT ELSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIDE	•	Codon, /=possible nucleotide deletion	sequence		j
FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKH MALSDGKLYRTDLALILCAGDN  LAPPEGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHI SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSI EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPM EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAA EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPMIIN YPPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCI ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS APKTSGMPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFI FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKK SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACIT ELSTVLGNKFDHGABAIVPTLFNLVPNSAKVMATSGCAALDE		\=possible nucleotide insertion)	<del> </del>		
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VADALLI CHARLES VIGASGPOYGI SQSSRLSSSVSAMRVLNTGSDVE	EA	TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVER			1 1
YSSPINGE I PRIVADOTI ENVIRONDE CONTROL OF THE PRIVADOTI ENVIRONMENT OF THE	RS	VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSER YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGL		•	1 1
LIKNOPTI.SPUFI.PUF.CFTETDMEN DUKUNCASSNWSERKEGLIGI.	QN	LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDF			1 1
OVHKDDI ODWI FVI LTOLLY WAR AND LOCKYON WOLLD'S	FI	QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRE			1 1
FPNDLOFNILMR FTVIOTOTDEL WYWA II WY TENT AVONDO	ES	FPNDLQFNILMRFTVDQTQTPSLKVKVAILKY1ETLAKQMDPQ			1 . 1
FINSSETRLAVSRVITWITTEDKSSNVDKAAOSVI LCI DER NUM	GD	FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTE			1
FTMLLGALPKTFODGATKLLHNHLRNTGNGTOSSAGGSDI TO D	mp	FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPT			1
RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDTYSSLE	oc	RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDTYSSL		ľ	1 1
VIEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDDbt	ו מס	VIEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\ MSD PP			1 1
GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPVNYSDS1	Te l	GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNDVNYSDS1			]
PFNKSALKEAMFDDDADOFPDDLSLDHSDLVARLIKELSNING	ם מים	PFNKSALKEAMFDDDADOFPDDLSLDHSDLVARLIKELSNHNE		•	1 1
VEERKIALYELMKLTOEESFSVWDEHFKTILLLIPPIGDVE	on-	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLFTLCDKF3			]
I TRALALKVLREILRHOPARFKNYAELTVMKTI.EAHKODHKEVU	, no	IRALALKVLREILRHOPARFKNYAELTVMKTLEAHKOPHKENN	j	1	1
SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQ	QT	SAEKAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQ		İ	
KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVA	₹V	RVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVA		·	1 1
HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDV GOS	/S	RAY I GUELKPHLSQL'I GSKMKLLNLY I KRAQTGSGGADPTTDV	1		
6004 140 4098 GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKV			4098	110	6004
APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIK	/P	APKTSGNPANSARKPGSAGGDKUCACACKEGGAGAUDEDDET		İ	1 1
FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKI	A	FTDVPSIOIYSSRELEETI.NKTDETI CDDVUDNDODANAK WYZ	1		1 !
SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITV.	.R	SLLVAGAAOYDCFFOHLRIJDGALKI.SAVDI.DCOUDDBACITURE	1	ľ	l i
HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFI	7	ILSTVLGNKFDHGAEAIVPTI.FNI.VPNSAKVMATSGCAATBET	Į.		1
RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSL	. E	WITHVPRLIPLITSNCTSKSVPVRRRSFEFLDLILOENOTUSI.	Ī	Ì	
RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETL	v	CHAAVLVETIKKGIHDADAEARVEARKTYMGIRNHFPGEAFT		i	1
NSLEPSYQKSLQTYLKSSGSVASLPOSDRSSSSSGESLNPDES		SLEPSYQKSLQTYLKSSGSVASLPOSDRSSSSSOESI.NPDFCc		Ì	
KNSTANPSTVAGRVSAGSSKASSLPGSLORSRSDIDVNAAAGA	וא	(nstanpstvagrvsagsskasslpgslorsrsdidvnadagd)	į	}	
AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGD	vσĺ	HHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGDU	1	į	<b>!</b>
RAKLSAPLAGMGNAKADSRGRSRTKMVSOSOPGSRSGSPGDVIII	т I	AKLSAPLAGMGNAKADSRGRSRTKMVSOSOPGSRSGSPCDVT T	l.	İ	
TTALSTVSSGVQRVLIVNSASAQKRSKIPRSOGCSREASPSRI.ST	v	TALSTVSSGVQRVLVNSASAQKRSKIPRSOGCSREASPSRLSV	ŀ	ļ	
ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFOPLASRHHSB	e	RSSRIPRPSVSQGCSREASRESSRDTSPVRSFOPLASRHHSps	f	ĺ	
TGALYAPEVYGASGPGYGISOSSRLSSSVSAMRVINTGSDUERE	۱ ۵	GALYAPEVYGASGPGYGISOSSRLSSSVSAMRVINTGSDVERA	1	İ	
VADALLIGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS	ا ہ	ADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS		ļ	1
YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGILGION	NT I	SSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGIJ.GLON	1		1
LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDRT	τİ	LKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLUDRI			J
QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES	s	VARIDULAUWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES			1
FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD	>	THE CETTE AND DISTRIBUTED IN CONTROL OF THE CETTAK OND PGD	] :		
FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE	3	INSSETALAVSKVITWITEPKSSDVRKAAQSVLISLFELNTPE			

SEO	Predicted	Predicted end	Amino acid segment containing signal nontide
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1			H=Histidine, I=Isoleucine, K=Lysine,
1	ccrresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	L	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
L.	sequence	ļ	\=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
1			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
1	1	Ī	VTEAIONFSFRSOEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
1	Į.	į	GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
Į.		l	PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1			VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
1			IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
1	1	<b>[</b>	
1		İ	SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
1	1	ì	KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
ł			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
ł	ì	1	NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
1		]	KRQKKERMLLCRQLGDSSGEGPEFVEEEEEEVALRSDSEGSDYTP
1		]	GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
1		1	EDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
1		i	KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
1			TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
J	1		PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
[	<u> </u>	[	SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
1	1		CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
i	İ	İ	QWEAKEDNSEGEEILEEVGGDLEEEDDHHMEFCRVCKDGGELLC
1		l	CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
1	į		WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
1		ļ	YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
i			
1		[	S\RKKKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKKG
			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
1	1		EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
	į.	1	TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
	1	]	YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
	İ		DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
1		<b>{</b>	LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
[		<b>{</b>	LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
ł	1		QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
	ł	i	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
1			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
}			FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
i		}	AFSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLVV
İ	i		RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED
1			SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYVV
1	1		REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDLAR
1			NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
1			DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1			QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
			MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
ĺ	1		EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTOP
1	1		NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
1			QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
1	<b>i</b>		AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
I			<u>-</u>
1	j		DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT
1	į l		YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
1			NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
]			PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL
l			EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP
J	ļ		EPTPQQVAQQQ
6006	1	965	DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
1			GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
1	1		ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
ľ			CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF
	<u> </u>		LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	b=beucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
		<del> </del> -	QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
	ł		EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
1			SLAPRPCDVPTCPTL
6007	3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
ĺ	ł		GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
ĺ	1		EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
		İ	FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
			HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
İ		i	EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
		1	WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
	Į.	ĺ	QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
ł			LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
į.	}	İ	GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
	l		VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
1	1		SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
1			ILGFSHAFIFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
J	į		VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
1			LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
	}		HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
			GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRCPAPEHAGPAR
1			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
1			DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP
1			FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1			KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
1			SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYOVTAMIG
1 .			HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
1 1			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGCGYSV
1			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEORSO
1 1	,		APARYSLOSANASSLSSGQLKSPSLSOSOASRVLGOSSSKPAAA
			ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
	j		TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
1 1			LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
1 1	i		TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
1 1			GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
1 1	1		SPFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
1 1	İ		TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
1 1			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
1 1	į.		LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH
1 1	1		VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDODDVVENKTGASESEERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1 1	Į		EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
1			SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
1 1			QSQW:NASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA
6009	4272	1534	
]	-	*223	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
1		-	EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
] 1			RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
1		!	NGKRGGCEESGVI.EGETVIGKTOOT ENVIRON DENGGOODONES -
1	1	į	NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
1			VIOKEVOA SVPCPGEPSVDTA DA CRUZZIO DE LA CONTROL CONTRO
	1		VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
1 1	1		FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
1 1			AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
		j	DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
1	1	ł	RPLRVGLLQUGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
1	į	}	RDIJRGGDRGHUMITULCDI GELICGI CORDIT I ERRODA-
		·	RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDBLLWFGGR*LI11G

CEC	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
			L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLGG
l .	Ī	1	AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP
i	·	ŧ.	GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAAI
ì	1	1	CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
	1	l	R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
1	į		GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
ļ	1		TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAAF
1	1		LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
			IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
6010	1	3533	
1	i		AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
}	1	į.	PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
1			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
1	]	)	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
		1	IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
1	1		PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
1			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
l		1	IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
1	İ	1	TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1	}	ł	EAVDDIMVTINEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
ļ	1	1	TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPBELGGLASQMTSD
I	ŀ	1	YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
i		1	ALOVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
		ı	TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
l	Ì	1	KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
1	ì	1	
1	1		SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
	1	Ĭ	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
1	1	1	ELTVFQSKDVPEKTSSPBESIRMTKGITMATAKAVAAGNSCRQE
1	1	ŀ	DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
1		1	TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
	1	1	EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
ł	1	l .	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
	1	t	VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
1		1	SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1	1		KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1	1	ļ	LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011	446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
3011	140	2035	TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH
ł		į.	DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
1		}	FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
1			
1	1		GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED
ł	1	1	GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
		ļ	QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS
1			ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA
1	1		WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
1			TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF
1	1	1	GIFNLVYWATYLNREPQLKAPTPHQ
6012	351	5013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
1			EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD
1	1	1	CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
1		1	QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
1	l	1	REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR
1	1		EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
I .	1	1	PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
1		1	
i	1	1	QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
1	1		IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
1	I	1	QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
1	l	1	NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
1		1	ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD
1		1	CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
ł	j	1	NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW
1	1	1	NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL
		<del></del>	

SEO	Predicted	Predicted end	Amino agid gogment coult
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
· f	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence .	1 *	\=possible nucleotide insertion)
	<u> </u>		PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
İ			GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
1		1	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
	1		PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
ļ			KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
		į.	EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
İ	+		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
İ			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
	i		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1	1		GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
			KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
1	ļ.		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
ı	(		KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
	[ .		DDFSKVVDEEFCADIELIIDGNKNMVLEESCSQPCPGDCYLKDW
İ	]		SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
ŀ	1		ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
-			SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
ł	}		CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
ł			PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
1	]		SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
-		1	FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
			ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
	[		RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
			DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGOI
ŀ			LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
}			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
			DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
			EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
			TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
			RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
) .			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
			IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
1			ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
1			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
j. I			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1	1		QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ P
6015	13	2237	
		~~31	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
1	1		VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1	,		HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
ļ <b>i</b>	ļ		EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
1 1	į		GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLD
] ]	ļ		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
1 1	j		FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
1 1			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
j		i	SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
1 1		l	F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
<b>j</b>		Į.	KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
1 1			EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
j [		ļ	QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
'	ſ		\scgvgs\gncsnsssnfrgafileargslh\gl\ktglQlf
6016.	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

656	77 - 6 - 3	32 - 2 - 3	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Ì	\=possible nucleotide insertion)
			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
l	I	i	RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
ļ	į	Į.	GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
	İ	<b>{</b>	HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
}	ł	į	EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
	l.	ļ	GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
1	1		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
[	i	1	
l	ł	l	FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
	1	1	ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
i		1	SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
l	}		F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
Į	i	1	KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
}	1	1	EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
1	1		QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
1	1	1	SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
1		1	\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
6017	203	3469	SHOEIEONSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
1		]	NFALOTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
ļ			AEKKWQIYCSKKKDQEENKGATSWPEFYIDQLNSMAARKSLLAL
1			EKEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK
1		ł	TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
	i	ł	SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER
1	l .	Į	TRFOTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
İ		1	
			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDPFEMLRNE
1	ł	1	DELEFAKRFELVHIDTKSATQMPELTRKRLTHSEAYPHFMSILH
	}	ł	HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
i	1	1	FNIKNVVRMLVNENEVKQWKEQABKMRKEHNELQQKLEKKEREC
1	İ		DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
	1	Ì	LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPPPLPGGM
1	1		LPPPPPPLPPGGPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
1		Į.	PTNALKSFNWSKLPENKLEGTVWTEIDOTKVFKILDLEDLERTF
1		1	SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
ļ	1	1	QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
i	1	1	KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
1	1	j	KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN
1	1		KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP
1		1	SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
1	1	<b>\</b>	KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
1			KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
1		1	RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
1			FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
6018	13	2510	TISQSGGIRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
	1	1	ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
1			GEAVGADSGTSSAVSLKNRAARTTKORRSTNKSAFSINHVSRQV
f		1	TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
1		1	GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
1			GDLKGGNKAATQGNGDVGAGAATGHNGFFCSNCMHDSERRDVDT AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIW
l			
1			ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF
1			WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLI?LFLLLG
1			LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
1			PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
1			LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
i			HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
I	1		ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
I			QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
1		1	TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
1	]		MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
ł	l		VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
ı	1	1	SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
1		]	OALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	2	1066	TPNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA
		1 1066	

Seg Predicted and Incleation incleation and predicted and incleation control of the control of t	SEO	Predicted		
NO: nuclectide location corresponding to first amino acid residue of samo acid sequence corresponding to first amino acid residue of samo acid sequence corresponding to first amino acid residue of samo acid sequence corresponding to first corresponding			Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid residue of amino acid amino acid amino acid amino acid anino acid anino acid amino acid anino ttendine, N-Augharagine, P-Proline, A-Sparagine, A-Sparagine, P-Proline, A-Sparagine, A-S	i i			(A=Alanine, C=Cysteine, D=Aspartic Acid F-
corresponding to first amino acid sequence amino acid sequence sequence amino acid sequence s	""		l l	Glutamic Acid, F=Phenylalanine G=Glycine
to first a maino acid residue of service of section, Telleconine, Nachalisa, and amino acid sequence of section, Telleconine, Nachalisa, and acid sequence of section, Telleconine, Nachalisa, and the sequence of section, Telleconine, Nachalisa, and the sequence of section, Telleconine, Nachalisa, and the sequence of sequence of section, Telleconine, Nachalisa, and the sequence of sequence	ļ			H=Histidine, I=Isoleucine, K=Lysine,
amino acid sequence  seque	į.		L.	D-D-21 0 01
meino acid sequence  Metyposible nucleotide, isostidentella sequence  Sequence  Metyposible nucleotide in several sequence  FYPTSATESHESISSITYMOGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSLGUVGAVTPOLLLANGGOGYTOTEPHYMOGASSYARAPAP OSCALLANGGOGYTOTEPHYMOGASSYARAPAP OSC	1		a contract of the contract of	Secondary Q=Glutamine, R=Arginine,
amino acid sequence    Codon:   Abidic: NoteCotide deletion				S=Serine, T=Threonine, V=Valine,
Apossible nucleotide insertion	ı	1	1	Codon (
PUTESATERMOTISSOTLEMACQUIGTLEMANSANABAPA COLVONATULAS ELEPPTANKIN STETE ELEKSEVOP PRETED RAVITAS ELEPPTANKIN STETE PUSOLISKEMENT DER AVITAS ELEPPTANKIN STETE PUSOLISKEMENT DER AVITAS ELEPPTANKIN STETE PUSOLISKEMENT DER AVITAS ELEPPTANKIN STETE ERERNOEGOMINEPPOCES ELERERANISTERIALISKELING OUGADATATECPAY SOBAL OR ERER REPARKIN FRIBLISKINGTON OUGADATATECPAY SOBAL OR ERER REPARKIN FRIBLISKINGTON OUGADATATECPAY SOBAL OR ERER REPARKIN FRIBLISKINGTON OUGADATATECPAY SOBAL OR ERER REPARKIN FRIBLISKINGTON INDEPTOCESTET ARE LANDREW VOR PROMITE THE REPARKING FOR THE NAME OF THE PROMITE PROMITE THE REPORT OF THE PROMITE PROMITE PROMITE PROMITE AND PROMITE PRO	1		bequence	\
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TTVFGANTPIVSCNFPDTYHLRCYVYQARNLLALDKDSFSDP YAHLCEHRSKTTEI IHSTINPTWDQTIIFDEVEIYGEPGVVLQ NPPKVIMELPDNQQUSKDEFLGRSIFSPVVKLINSEMDITPKLLM HPWMGDKACGUVLVTAELLIRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAMGLRNKNROMASITSPSLVWENGEGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKELYMPPLVIKVIDHRQ FGRKPVVQGCTIERRLDFRFLOPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALSKASPATVHLTEKEERIV DWSKFYASSGEBEKCGQVIQKGYSKLKIYNCELENVABPPGUT DFSDTFKLVRGKSDRNEDPSVVGEPKGSFRIYPLPDDDSVPAPP RQPRELPDSVPQCCTVRIVINGLELQPQDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEXDLKISVYDVD TFTRDEKVGSTIIDLENPF\LSPGSIRTYGGRDYSUDDS KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEXDLKISVYDVD TFTREKVGSTIIDLENPF\LSPGSIRTYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTGGLYDEHVETRTLHSTPQD NIS\RYYLFWIINTKDVILDEKSITGEMSDIVVKGWIPGNBE NKQKTDVHYRSLDGESNFNWRFVPPPDVILPAEQLCIVAKKEHW SIDQTFFRIPPR\LIIQIWNDKPYLPAEQLCIVAKKEHW SIDQTFFRIPPR\LIIQIWNDKDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKANNPLKARTASLFECKSMKGWW PCYARKOGARVWAGKVEMTLEILMEKEADERPAGKGRDENMMP KLDLDNRPETSETMFTNCKTMKFIVWARFKWIIGLLFLLILL LEVAVLLYSLDRNISMKIVKDNV  6021 4953 549 EAIGEVSIGNSGNSFDTTGCRLASTTQYSRAVFDGNYYYLDW ATTREVVTLTSYWEDISHRLDAVNTLLAMAERLQTHIEALKSGI QGKIPANQLAELMIKLIDEVIETTRYTLPLTECKANVTULDTQI RKLASRSLSQIHEAAVRMSSATDVKSTLAEIEDMIDKLMOLTE EPQNSMPDIIIWMIRGEKGLAVARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPGENNOPKOTECHNVNIMGLSAVEKKENSPAE GTFTVFABMYENQALMFGKWGTSGLWGRHKFSDVTCKIKLKREF FLPPKGWBMEGEWIYDPERSLLTEADAGHTEFTDGVYKNESRPAE GTFTVFASMYENQALMFGKWGTSGLWGRHKFSDVTKKIKLKREF FLPPKGWBMEGEWIYDPERSLLTEADAGHTEFTDGVYKNESRPAE GTFTVFASMYENQALMFGKWGTSGLWGRHKFSDVTKKIKLKREF FLPPKGWBMEGEWIYDPERSLLTEADAGHTEFTDGVYKNESRPAE GTFTVFASMYENQALMFGKWGTSGLWGRHKFSDVTKKIKLKREF FLPPKGWBMEGEWIYDPERSLLTRADAGHTEFTDGPKYNEKKRD LTQTASSTAGAMBELQDGGGWEXSLIGHKFHKKGRSSTFFRR RWRKMAPSTHGAAAT FKLEGGLGADTTEDGDEKSLEKQKKSA TTVFGSAMYFIVGKFYDDAYJTHCVYVQARNLLALDKOSFSDP VAHLCFLHRSKTTEI HSTLNP"WOQTI IFDEVETYGEPQTVLQ NPPKVIMLEFDNDQVGKGBEIGRS IFSVVKLNSEMDITPKLLW HPWNGBKAGGBVLVTAELILLEKGKOSNLPILIPPQRANLLWIND QGIRPVVQLTABILLAGGGRNKNFFGMASITSPSLVVEGGGERV ESVVIKNLKKTPHPPSSVLLFMANSITSPSLVVEGGGERV	1		ļ	RWRRKMAPSETHGAAATEKLEGALCAPTTERCREVOLDIKA
YAHICELHRSKTTEIIHSTINDTWOOTIIFDEVEITGEPQTVLQ NPPKVIMELPDNOQVGKDERS   FSPWILLINSEMDITPKLLM HPWINGBKACGOVLIVTAELILIRGKDGSNLPILPPQRAPHLYMYP QGIRPVVQLTAIEILAMGLRINKINTQMASITSPSLVWECGGERV ESVVIKNIKKTPNFPSSVLPHKVFLPKEELIVPPLIKYS IDHRQ FGRKPVVQCTIERLDRFRCDEYAGKEDIVPQLKASLLSAPPCR ESVVIKNIKKTSNFPSSVLPHKVFLPKEELIVPPLKYS IDHRQ FGRKPVVQCTIERLDRFRCDEYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTIRPLIASKCLSANTALSKAMS PATVHLITRKEERIV DWSKFYASSGEHEKCQVIOKGYSKLKIYNCELENVABFEGLT DFSDTFKLVMSKSDERMEDBSVLSFKIYPPLDDDFSVPAPP ROFRELPDSVPQECTVRIYIVRGLELQPQDINGLCDEYIKITLG KKVIR NDRHYIPNTLINPFGRMYBLSCYLPQEKDLKISVYDYD TFFRDEKVOETIIDLENPPLSEGGSRICH   DEEYCVSGVNTW RDSLR   PTQ\LLQNVARFRGPPOPILESDGSRIRYGGRDYSLDR FEANKILHQHLGAPERLALHLRTQGJVPPHVETRTHSTPQP NIS\RYYLRVIINNTKDVILDEKSITGEEMSDIYVKGWIGNBE NKQKTDVHYRSLDGBGNFNWRFVPFPDYLAPQLCICVMAKEHFW SILQTFFRIPPRYLLIQUW NDDKFS\LDDVLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKANNPLLKATTASLFEQKSMKGNW PCYARFDGARVWAGKVEWTLEIKEKABDERPAGKGRDENNMP KLDLNRNPETSFLMFTNDCKTMKFIVMRFKWVIIGLLFLLILL LFVAVLLYSLDNYLSMKIVKNDV  6021 4953 549 EAIOFEVSIGNYGMKFDTTCKPLASTTQYSRAVFDGNYYYYLDW ANTKRVVVILTSYWEDISHRLDAWNTLLAMAERLOTNIEALKSGI QKIPANQLABIKIKLIDEVTGTYTYLPLTEGKANDVTLDTQI RKLRSRSLSQHHEAAVRRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKKLANYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKINNGPKUPVELRVNIWIGJSSGENASGKYC GKTQTIFLKYPQEKINNGPKUPVELRVNIWIGJSSAVEKKNSPAE GTFTVFABMYENQALMFGKMATSGLUGRHFKPSDVTGKKIKLRREF FLPPKGWBWEGGEWY VDPERSLIFADAGHTEFTDEVYQNESSYP GGDMKPABDTYTDANGGKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKKYSWADABKMYHTHRRRRLVKKKKKD LTQTASSTAGAMBELQDQEGWEYASLIGWKFFWKORSSTFFRR RWRKMAPSTHGAAAITKPLEVVQAANKHCRSSDTFRRR RWRKMAPSTHGAAAITKPLEVVQAANKHCRASDTFRRR RWRKMAPSTHGAAAITKPLEVVQAANKHLALALDKOSFSDP YAHLCFLHRSKTTEIIHSTLNP-WOOTIIFDEVEIYGEPQTVLQ NPPKYIMELFONDOVGKDEFLGRS IFEVVKLINSEMDITPKLLM HPWNGDKAGGDVLVTABLILLRGKDGSNLPILPPQRANLYMVP QGIRPVVQLTAIBLILBGKBCSNLPILPPQRANLYMVP QGIRPVVQLTAIBLILBGKBCSNLPILPPQRANLYMVP QGIRPVVQLTAIBLILBGKGGRNAFFESLVVENGGGERV	1	1		TTVFGANTPIVSCNFDDDVTVULDCVVVQADNVLALDVDGGG
NPRYLWELPDINGVOCKDEFLORS IF SPVVKLINSEMDITPKILW HPWMNGBKACGDULVTAELLIPPQRAPHLYMVP GGIRPVVOLTAIEILAWGLRIMKNFOMASITSPSLVPECGGERV ESVVI KNIKKTPNFPSSVLFMKVFLPKELYMPPLVIKVIDHRQ GFRKPVVGQCTIERLDRFACDFYACKEDIVPOLKASLLSAPPCR DIVIEMEDTRPLLASKCLSSMSTALSKASPATVHLTEKEERIV DWSKFYASSGEBEKCGQVIOKGYSKLKIYNCELENVABPECH DFSDTFKLVRGKSDENEDPSVVGEFKGSFRIYPLDDDSVPAPP RQFRELPDSVPQECTVRIVIVRGLELGODDNGLCDPYIKITLG KKVIE\DRDHYIPNINDVFGCHEONDFLLSEDGSRIYGGRDYSLDE FERNKILHOHLGAPEERLALHILRTQGLVPEHVETRTHASTFOP NIS\RYYLRVIINNTKDVILDEKSITGEMSDIYVKGWIFGNEE MKCKTUHVRSLEDGENINMFVPFFPOPILSEDGSRIYGGRDYSLDE FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTHASTFOP NIS\RYYLRVIINNTKDVILDEKSITGEMSDIYVKGWIFGNEE MKCKTUHVRSLEDGENINMFVPFFPOPILSEDGSRIYGGRDYSLDE FEANKILHOHLGAPEERLALHILRTQGLVPEHVETRTHASTFOP NIS\RYYLRVIINNTKDVILDEKSITGEMSDIYVKGWIFGNEE MKCKTUHVRSLEDGENINMFVPFFPOPILSEDGSRIYGGGENEMP KLDLENRFTSFLWFTINCKTMKFIVWRFVFWITGHEFIT HFLOKSPGGNC/RGLDMIPDKAMPLKAKTASLFEOKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKBADERPAGKGRDEENMMP KLDLENRFTSFLWFTINCKTMKFIVWRFKWVIIGLLFLLILL LEVAVLLYSLENVISMKIVRPNV  6021 4953 549 EAIQFEVSIGNYGNIFFITCKPLASTTQYSRAVFDGNYYYYLDW ANTEKPVYILTSYWEDISHLAWRISATDIVKSTLAEIEDWLDKLMOLTE EPQNSMPDIIIWINTGEKRIAVARIPAHQOLVSTGGENSGYCC GKTQTIFLKYPOEKNNGFKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLUGRKFKFSDVTGKKIKKEFF FLPPKGWEMEGEWIVDPERSLLTEADAGHTEFTDEVYQNESSYP GGDMKPAEDTYTDANGGKASPSELTCPPWEEMEDDAWSYDING AVDEKGWEYGTIPPDHKPRYAAEKMFTHRRRRLVRKKKD LTQTASSTACAMEELQDGCWEYASLIGMKFHKKORSSTFRRR RWRKMAPSTHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCFFORDYIYMAAEKMYHTHRRRLLAALDKNSFSDP YAHLCFLHRSKTEIIHSTLNFWDOTITPEEMDITPKLLW NPFKUIMELFONDOVGKDEPFLGRSIFSPLVVKRKKD HPVMNGKACGDVLVTASLILLRCKDOSDLPLIPPGRAPNILWVD GGIRPVVQLTAIEILLRGKDGSDLPLIPPGRAPNILWVD GGIRPVVQLTAIEILLRGKDGSDLPLIPPGRAPNILWVD GGIRPVVQLTAIEILLRGKDGSDLPLIPPGRAPNILWD GGIRPVVQLTAIEILLRGKDGSDLPLIPPGRAPNILWD GGIRPVVQLTAIEILLRGKDGSDLPLIPPGRAPNILWD GGIRPVVQLTAIEILLRGKDGSNLPLIPPGRAPNILWD GGIRPVVQLTAIEILLRGKDGSNLPFLLPFLUKGGERV ESVVIKNLKKTPWPSSVLEFMSPSSVLEFKEEL				YAHICFLERSKTTFITHSTINDTHDOTTIEDPRETYCHDOTTE
HPWMNGKACGDVLVTAELILRGKDGSNLFILPPQRAPNLYMVP QGTRPVVQLTAIELIAMSKMNFQMASITSPSLVVECGGERV ESVVI KNILKKTPNPPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYRGEDIYPQLKASILSAPPCR DIVIEMEDITRFILASKCISSMSTALSKMAS PATVHLTEKEEIV DWSKSYASSGEHEKCQYIQKGYSKLKITNCELENVAEFEGLT DFSDTFKLYRGKSDENEDVGFKGSFRIYPLPDDDSVPAPP RQFRELPDSVPQECTVRIYIVRCLELQPQDDMGLCDPYIKITLG KKVIE \DDWIN IPMTLMPVFGRMYELSCYLPQSKDLKISYYDVD TFTRDEKVGETIIDLENPF\LSRGSHLEGCYIPQKGYSKLKISYYDVD TFTRDEKVGETIIDLENPF\LSRGSHLGCYIPEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFQPIILSEDGSRIRYGGRDYSLDE FERMKILHQHGAPEERLAHHILRTGGLVPEHVETRTIAHSTPQP NIS\RYYLRVIINNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGECNFMRFVPPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DDKFS\LDDYLGFPRITCRHTI HEQKSPGGNC/RGLDMIPDLKNMFPVPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DDKFS\LDDYLGFPRITCRHTI HEQKSPGGNC/RGLDMIPDLKTMIPERAGKGTGEEMMBP KLDLPNRPETSFIJFTNPCKTMKFIVWRFFKWVIIGLLFILILL LEVAVILLYSIPMYLSMKIUPBWV  6021 4953 549 EAIQFEVSIGNYGNKFDTTCKFLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDANNTLAMAERLQYNIEALKSGI QKKIPANQLAELMLKI.IDEVIEDTHYTLPLTEKGANVTUDTQI RKLRSRSLSQHEAAVRMSEATDVKSTLAEIEDMLDKLMQLTE EPQNSMPDIIIMMIRGEKELAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFABMYENQALMFCKMCTSGLUGHKFSDVTGKIKLKREF FLPPFKGMBWEGGEWIYDPERSLLITEADAGHTEFTDBYVOMSRYP GGDMKPAEDTYTDANGDKAASFSELTCPPGEEMEDDAWSYDINR AVDEKGMEYGTIIPPDHKPKSWVAAEKMYHTHRRRLVRKKKD LTQTASSTAGAMEELQQGEGEYASLIGWKHMKGRSSDTFRRR RWRKMAPSETHGAAAIFKLGALGADTTEDGDEKSLEXQKHSA TTVVGSANTPIVSCMPLORYVYHLRCYVYQARNLLALDKOSFSDP YAHLCFHRSKTTBIIHSTLMPTWODTIIFDEVETYGEPQTVLQ NPPKVIMELFUNDQVGKDEFIGRS IFSPVVKINSEMDITPKILLW HPVMNGKACGDULVTAGLILRGKGOSNLDIIPPQCARPNLTMVP QGIRPVVQLTAIEILLRGKGOSNLDIIPPQCARPNLTMVP QGIRPVVQLTAIEILLRGKGOSNLDIIPPQCARPNLTMVP GIRPVVGLTHERUNGVFLIPPEGERVFUNDFLIFFUNDFUNDFUNDFUNDFUNDFUNDFUNDFUNDFUNDFUN	j	1		NPPKVIMELFDNDOVGKDEFI.GPSIFCDVIVI.NCEMDITEDVI.I.
GGTRPVVQLTAIEILAGELRMIKHPQASITSPSLVVECGGERV ESVVIKNIKKTPNPPSSVLPMKVETPREELYMPPLVIKVIDHRQ FGRKPVVGQCTIELDRFRCDFYAGKEDIVPQLKASLISAPPCR DIVIEMEDTKPLIASKCLSSMSTALKMASPATVHLTEKEEEIV DMSKSFYASSGEHEKCGGYTQKGYSKLKIVNCELENVABFEGLT DFSDTFKLYRGKSDENEDPSVVGEFKSFRIYPLDDDFSVPAPP ROPRELPDSVOPQECTVRIYIVGCLELQPQDNMGLCDPYIKITLG KKWIE\DRDHYIPNTLMPVFGRMYELSCYLPQEKDLKISYYDYD TFFTDEKVGETIIDLENPF\LSRFGSRGYSLDE FRANKIHQHLGAPEERLAHHILRTGGLVPEHVETRTLHSTPQP NISARYLFUYIUNTKOVILDEKSITGEEMSDIYVKGWIPGEE NKQKTDVHYRSLDGEGNFWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTFFRIPPR\LIIQIW\DRDKFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFS\LDDYLGFPRTLTCRHTI HELQKSPGGNC/RGLDMIDPLKAMFILARAFSLOTHIELLKSCI OCKIPANQLAELMLKLIDEVIDTTYTLPLTEGKANVYLDTQC RKLRSRSLSQHHEAAVRMKSEATDVKSTLAEIEDHLDKLMOLTE EPQNSMPDIIIMMIGGKRATARIPAHDVLYSTSGENASGKYC GKTOTIFLKYPOEKNAGPKVPUELRUNIMLGLSAVEKKFNSFAE GTFTVFABMYENQALMFGKWGTSGLVGRKKPDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFDEVYONGSRYP GGDMKPAEDTTTDANGDKAASFSELTCPGGEWEDDANSYDINR AVDEKGWEYGTIIPPDHKRVANAASHYHTRRRRLVRKCD LTOTASSTAGAMEELQDQGGWEYASLIGWKFHWKQRSSDTFRRR RWRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVVFSANTPIVSCNFDRDYIHLRCYVQARNLLALDKDSFSDP YAHLCFHRSKTTEI HSTLMFTWODTII FDEVELYGEPQTVLQ NPPKVIMELFONDOVGKUBEIGRS IFSPVVKLNSEMDITPKILW HPWNGDKACGDVLVTAELLIRGKGGSNLPILLPPORAPNILMVP QGIRPVVQLTAIEILLRGKGGSNLPILLPPORAPNILMVP QGIRPVVQLTAIEILLRGKGGSNLPILPPDPORAPNILMVP DGRIPPVVGLTABEILRGKGGSNLPILPPDPORAPNILMVP	1			HPVMNGDKACGDVLVTAELILRGKDGSNLDIL DDODADNI VATID
ESVVIKALKATPNFFSSVLFMKVFLPKELIYMPPLVIKVIDHRO FGRKPVVGCTIERIDFROPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSMSTALSKMASPATVHLTEKEEEIV DWMSKFYASSGEHEKCGQYIQKGYSKLKTYNCELENVABFEGLT DFSDTFKLYRGKSDENBEVVGEYKGSFRIYPLDDDFSVPAPP ROFRELPDSVPQECTVRIYIVRGLELQPQDNMGLCDPYIKITLG KKWIE\DRDHYIPNTLMPVFGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGSTIIDLEMPF\LSRG\SHC\G\TPECVSGVNTW RSSLR\PTQ\LLQMVARFKGPPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEEILAHLLRTQGZVPEHVETRTLHSTFQP NIS\RYYLRVIINNTKDVILDEKSITGEMSDIYVKGMIPGMEE NNGKTDVHYRSLDGEGMFNMFFVPFDTLPAEQLCIVAKKEHFW SIDQTEFFIEPP\LIIGUN\DNDKFS\LDDYLGFPFTLTCRHTI HFLOKSPGGNC\RGLDMIPDLKAMMPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILMEKEADERPAGKGRDEPMNNP KLDLPNRPETSFLWFTMPCKTMKFIVMRFFKWYLIGLLFLLILL LEVAVLLYSLPNYLSMKIVKPNV  6021 4953 549 EAIGFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLDW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLOTNIEALKSGI QGKIPANQLAELMKLIDEVIETTYTIPLTEGKANVTVLDTQI RKLRSSRLSGYHEAAVMRSBATDVKSTLABIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKYPVELRVMINGLSAVEKKFNSPAE GTFTVFAEMYENQALMFGKNGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEMGEGBUVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEMEDDAWSYDINR AVDEKGMEYGTITPDHKPKSWVAAEKMYMTHRRRILVRKKKD LTQTASSTAGAMEGLQDQEGWEYASLIGWKFHKODSTSDP YAHLCFLHRSKTTEIITSLNFTRNOTTIIFDEGEKSLKKKNSA TTVFGANTPIVSCNPDRDVIYHLRCVYQARNLLALDKDSFSDP YAHLCFLHRSKTTEIITSLNFTRNOTTIIFDEGEKSLEKKKHSA TTVFGANTPIVSCNPDRDVIYHLRCVYQARNLLALDKDSFSDP YAHLCFLHRSKTTEIITSLNFTRNOTTIIFDEFTYLGEPTVLQ NPPKVIMELFUNDQTGIGGSIFSPVVKLNSEMDITPKLLW HPWNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILLAMGLRNINKPCMASITSSSLVVECGGERV ESVVIKMLKKYPNFPSSULFMKNYFDFSSLLVECGGERV	1	1		QGIRPVVQLTAIEILAWGLRNMKNFOMASITSPSIAURCCCRDV
FGRKPVGQCTIERLDRFRCDFYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTRPLLASKCLSSMSTALSKMASPATVHLTEKEETIV DWWSKFYASSGEHEKCGQYIGKGYSKLKTYNCELENVABFEGIT DFBDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDFSVPAPP ROPRELPBSVPQECTVIYURGLELQPQDNMGLCDFYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDVD TFTRDEKVGGTIIDLENFF\LSFRG\SHCG\JPESVCVSGVNTW RDSSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGNYSLDB FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDCEGFNWFFVFFPDYLPADQLCIVAKKEHFW SIDQTTFFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKGGARVMAGKVEMTLEILNEKEADERPAGKGREPNNNP KLDLENRPETSFLWFTNPCKTMKETVWRFFKWVIIGLLFLLILL LEVAVLLYSLPNYLSMKIVKPNV  6021 4953 549 EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW ARTKPVYTLTSYWEDISHRLDAVMTLLAMAERLQTNIEALKSGI OGKIPANQLAELMIKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTE EPQNSMPDIIIWNIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPOEKNNGPWVVELRVNIWLIGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEMEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGGKASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKKDD LTQTASSTAGANEELQDQCGWEYASLIGWKPHWKQRSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHLCFHRSKTTEILTSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNSKTTEILTSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNSKTTEILTSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNSKTTEILTSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNSKTTEILTSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNSKTTEILHSTLNFTWDOTTIIPDEWIYGEPOTVLQ NPPKVIMELFEHNDOTGKRKFUNFCMSITSSELVVECGGERV HPWNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP GGIRVVQLTAIEILLAWGLRNNKNFCMSITSSELVVECGGERV ESVVIKMLKKYPNPSSVLIFMKVFJFKEELYMPPLLVKYLTNUTDHDO	ł	1 1		ESVVIKNLKKTPNFPSSVLFMKVFI,PKEELVMPPLVIKVIDHOO
DIVISMEDTRELLASKCLSSMSTALSKAASPATVHLTEKEERIV DWYSKFYASSGEHEKGGYIOKGYSKLKIYMCELENVARFEGLT DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDESVPAPP ROFRELPDSVPQECTVRIYIVRGLELQPQDDNGLCDPYIKITIG KKVIE\DRDHHY PNTILNPVFGRMYELSCYLPQEKDLKISYVPDV TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKFPQFILSEDSGRIKYGGRDYSLDE FFANKILHQHLGAPERLALHTLRTGGLVPEHVETRTHSTFQP NIS\RYYLRVIINNTKDVILDEKSITGEEMSDIYVKGHIPGNEE NKGKTDVHYRSLDGEGNFNWRFVFPPTVLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRTII HELQKSPGGNC/RGLDMIPDLKAMNPLKARTASLFEOKSMKGNW PCYAEKGARWMAGKVMTLEILINKEADERPAGKKGDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLEFLILL LFVAVLLYSLPNYLSMKIVKNV  6021 4953 549 EAIQFEVSIGNYGMKFPTTTCKPLASTTQYSRAVFDGNYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLALWLKLIDEVIEDTRYTLPLITEKKANVTVLDTQI RKLSRSSLSQIHEAAVRWRSSATDVKSTLASIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAENYENQALMFKKMSTSGLVGRKKFSDVTGKIKKKREF FLPPKGWEMEGEWIVPDERSLLTEADAGHTEFTDEVYQNESRYP GGDMKPAEDTYTDANGDKASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRLVRKKKD LTQTASSTAGAMEYSTTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRLVRKKKD LTQTASSTAGAMEYGETHGAALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHRCYVYQARNLLALDKDSFSDP YAHLCFLHRSKTTEIIHSTLNPTMOOTIIFDEVETYGEPTVLQ NPPKVIMELFDNDOVGEBELGRSIFSPSPVKLNSEMDITPKLLW HPWNGDKACGDVLVTAELILRGKDGSNLPILPPCRAPNLYMP QGIRPVVQLTAIEILANGLENNKNFQMASITSPSLVVECGGERV ESVVIKNLKKYNPNPSELYMEKYELMKKFENPLVIKVUMP	1			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPOLKASLISADDCD
DWWSKFYASSGEHEKCGQYIQKGYSKIKITWCELENVAPFEGLT DFSDTFKLYRGKSDENDEDSVVGEFKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPQDNMGLCDPYIKITIG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGFTITULENPP\LSREG\SHCG\IPPEYCVSGVNTW RDSLR\FTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FFANKILHQHLGAPEERLALHILRTGGLVPEHVETRTIHSTFQP NIS\RYYLRVIINNYULIDEKSITGEEMGILVKGGHDYSLDE FFANKILHQHLGAPEERLALHILRTGGLVPEHVETRTIHSTFQP NIS\RYYLRVIINNYULIDEKSITGEEMGILVKGGHPGNEE NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLICRHTI HFLQKSPGGRC\RGLDMIPDLKAMTASLFEQKSMKGNW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPMNP KLDLPNRPETSFLWFTNFCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV  BAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLANAERQOTNIEALKSGI QGKIPANQLAELMIKLIDEVIEDTRYLPLTEGKANTVYLDTQI RKLRSRSLSQIHEAAVRRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQULYSTSGENASGKYC GKTQTIFLKYPQEKINGPKVPVELRVINIGLGSAVEKKFNSFAE GTFTVVFAEMYENQALMFGKWGTSGLVGRKKFSDVTGKIKKKREF FLPPKGWEWEGEWIVDPERSLITEADACHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGPKAPSPSLITEADACHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGPKAPSPSLITEPPGWEENDAWSVDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR RWRKMAPSETHGAAAIFKLEGALGADTTEDGGEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFHRSKTTEIIHSTLNPTDQOTIIFDEVETYGEPQTVLQ NPPKVIMSLFONDOVGKDEFIGRSIFSPVKLUSEMDDITPKLLW HPWNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAMGLRIMKNFQNASITSPSLVVECGGGERV ESVVIKNLKKTPNFPSSVLFMKVFLYREELMMPLJIKVTDHPO	-	j i		DIVIEMEDTKPLLASKCLSSMSTALSKWASPATVHLTRUPPPTV
DESDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLDDDESVPAPP ROPRELPDSVPQECTVRIYIVRGLELQPQDNMGLCDPYIKITLG KKVIE\DRDHYIPNTLMPVFGRMYELSCTLPQEKDLKISVYDYD TFFRDEKVGETIIDLENPF\LSRFG\SHCG\1PEFYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLAHILRTQGLVPEHVETRTIHSTPQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDDEGSNFNWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTFFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGNW PCYAEKDGARVMAGKVEWTLEILNEKEADERPAGKGRDEPMMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRFKWVIIGLLFLLILL LFVAVILLYSLPNYLSMKIVKPNV  6021 4953 549 EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW ATHKPVVTLTSYWEDISHRLDAVMTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMKSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAENYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWMEGGEWYDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEMEDDAWSYDINR AVDEKGWEGGITIPPDHKPKSWVAAEKMYHTHRRRLVRKKKD LTQTASSTAGAMEELQDQDEGWEYASLIGWKFHWKQRSSDTFRRR RWRKKMAPSETHGAAAIFKLEGALGADTTEEDGDEKSLEKQKHSA TTVGGANTPIVSCNFDRDYIYHLRCXVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDCTIITDEVEITYGEPGTVLG NPPKVIMELFDNDQVGKDEFIGRSIFSPVVKLNSEMDITPKLLW HPVWNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILAMGGLRNKNSPGMASITSPSLLVWEGGGERV	1	1		DWWSKFYASSGEHEKCGOYIOKGYSKLKTYNCELENVAREEGIT
RGFRELDSVPQECTURITURGELGPQDNNGLCDPTIKITIG KKVIE   DRDHYI DRINIPYGRMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETI IDLENPF\LSRFG\SHGS\1FEEYCVSGVMTW RDSLR\PTQ\LLQNVARFKGFPQFILSEDGSRIRYGGRDYSLDE FFENKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIINNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEGNFNNRFVPFFDVLPAEQLCIVAKKEHFW SIQOTEFRIPPR\LIJOIW\DNDKFS\LDDYLGPFRTLTCHTI HFLQKSPGGNC/RGLDMIPDLKANNPLKAKTASLFEGKSMKGNW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPMNNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLLL LFVAVLLYSLPNYLSMKIVKPNV  6021 4953 549 EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEJTRYTLPLTEGKANVTVLDTQI RKLRSRSLSGIHEAAVRWRSEATDVKSTLAFIEDWLDKLMQLTE EPQNSMPDIIIMMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAENYENQALMFGKWGTSGLVGRKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTFFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGGEWEDDAWSVDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRLVRKKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKHWKGRSSDTFRRR RWRKKMAPSETHGAAAIFKLEGALGADTTEDGEKSLEKÇKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLMDTIIPDUETYTGDERKLEK WRRKKMAPSETHGAAAIFKLEGALGADTTEDGERSLEKÇKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLRKSKTEIIHSTLNFWDDTIIPDEVEITYGEPQTVLQ NPPKVIMELFDNDOVGKDEFIGRS IFSPVVKLNSEMDITPKLLW HPWNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILANGLENKMNFCMASITSPSLVVECGGERV	İ	1		DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPI.DDDDSVDADD
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TTTRDEKVGETIIDLENFF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FERNKILHQHLGAPEERLALHILRTGGLVPEHVETRILHSTPQP NIS\RYYLRVIINNTKOVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGECRFNWRFVFPFPDYLPAEQLCIVAKKEHFW SIDQTEFRIPPP\LIIQIW\DNDKFS\LDDVLGPPRTLTCRHTI HFLQKSPGGNC\RGLDMIPDLKAMNPLKAKTASLFEQKSMKGNW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFILILL LFVAVLLYSLBNYLSNKIVKPNV  6021 4953 549 EARQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRDAVNTLLAMAERLQTNIEALKSGI QKIPANQLAELMKLIDEVIEDTRYTLPITEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNINLGLSAVEKKFNSFAE GTFTVYFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEMEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKKKD LTQTASSTAGAMEGLQDQEGWEYASLIGWKFHWKORSSDTFRRR RWRRMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDVIYHLRCYVYQARNLLALDKDSFSDP YAHLCFLHRSKTTBIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDQVGKDEFLGRSIFSFVVKLNSEMDITPKLLW HPVWNGDKAGGDVLVTAEILLRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTPMFPSSVLFMKVFLPREELYMPPLVIKVIDHPO	1	1		KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPOEKDLKISVYDYD
RBSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVI INNTKDVILDEKSITGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEGNFNWRFVPFPDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMPDLKAKTASLFEQKSMKGNW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPMYLSMKIVKPNV  6021 4953 549 EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTTVFAEMYSEQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDMKPAEDTYTDANGGKASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRLVKKKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSDTFRRR RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTFIVSCNPDRDYITHLRCVVYQARNLLALDKDSFSDP YAHHLCFLHRSKTTBIIHSTLNPTWDOTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDOVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP QGIRPVVQLTAIEILANGERNMKNFQMASITSPSLVVEGGGERV ESVVIKNLKKTPNFPSSVLEMKVFLDKEELLMYDLUKUDHDO	1			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
FEANKILECHLGAPEERLALHILRTGGLVPEHVETRTLHSTPOP  NIS\RYYLRVIINNTKDVILDEKSITGEMSDIYVKGWIPGNEE  NKQKTDVHYRSLDGEGNFNNRFVFPFDYLPAEQLCIVAKKEHFW  SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI  HFLQKSPGGNC/RELDMIPDLKAMPLKAKTASLFEQKSMKGNW  PCYAEKDGARVMAGKVEMTLLEILNEKEADERPAGKGRDEPNMNP  KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL  LFVAVLLYSLPNYLSMKIVKPNV  6021  4953  549  EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW  AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI  QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANTVLDTQI  RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE  EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC  GKTQTIFLKYPOEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE  GTFTVFAEMYENQALMFGKWGTSGLVGRHKPSDVTGKIKLKREF  FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP  GGDWKPAEDTYTDANGDKAASPSELTCPFGWEWEDDAWSYDINR  AVDEKGWEYGGTIPPDHKPKSWVAAEKMYHTHRRRRLVRKKKD  LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFFRR  RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA  TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP  YAHLCFLHRSKTTEIHSTLNFTWDQTIIFDEVEIYGEPQTVLQ  NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW  HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP  QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERVV  ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLJIKVIDHPO	<b>!</b>	1		RDSLR\PTQ\LLQNVARFKGFPOPILSEDGSRIRYGGRDYSLDE
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QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLABIEDWLDKLMQLTE EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTITFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGHKKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRLVRKRKKD LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR RWRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPWMDDKACGDVLVTAELILRGKDGSNLPILPPCRAPNLYMVP QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLJIKVIDHPO			į	A-TTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
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SEQ Predicted beginning beginning nucleotide nucleotide location corresponding to first amino acid residue of amino acid sequence	id, E= cine,  *=Stop  *=Stop  *EKEEEIV AEFEGLT PSVPAPP YIKITLG ISVYDYD VSGVNTW RDYSLDE LHSTFQP WIPGNEE LHSTFQP WIPGNEE LKKEHFW LTCRHTI
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amino acid sequence Codon, /=possible nucleotide deletion    =possible nucleotide insertion	EKEEEIV AEFEGLT PSVPAPP YIKITLG ISVYDYD VSGVNTW RDYSLDE LHSTFQP WIPGNEE AKKEHFW LTCRHTI
sequence   \=possible nucleotide insertion}	EKEEEIV AEFECLT PSVPAPP YIKITLG ISVYDYD VSGVNTW RDYSLDE LHSTFQP WIPGNEE AKKEHFW LTCRHTI KSMKGWW
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EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGI	
GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEK	
GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEV	
GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDA	
AVDEKGWEYGITI PPDHKPKSWVAAEKMYHTHRRRRI	
LTOTASSTAGAMEELODOEGWEYASLIGWKFHWKQRS	
RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSI	
TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALI	
YAHICFLHRSKTTEIIESTLNPTWDQTIIFDEVEIYO	
NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMI	
HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRI	
QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVV	
ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLV:	
FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASI	
DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLY	
DWWSKPYASSGEHEKCGQYIQKGYSKLKIYNCELENT	
DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDI	
ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDI	
KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLI	
TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYC	
RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGG	
FEANKI LHQHLGAPEERLALHILRTQGLVPEHVETR	
NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKO	
NKOKTOVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIV	
SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPR: HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFE(	
PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGI	
PCIAERDGARVFAGRVEMILEILNEREADERPAGRG   KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIG	
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LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDI	
VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHI	
ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKI	「ロビクハストル
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6024 3 3260 FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLME	
LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVQI	
RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEG	JUCTSDTW
IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSE	
TROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTION	TFRSSDPA

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SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid F-
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Ī	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
1	1		PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
İ	•	1	HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
1	İ		EAGLLLYLKTGQMYPVPANHLDKRELLKLRNOMAFSI,FHRISKS
			ATROKTQLASLPQIIEEEKTCKYCSOIGNCALYSRAVEOOMDCS
ı		<b>{</b>	SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESOSKDNKKN
		ļ	HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGOYLHNFOCKH
1	1	[	GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
1	1 .		RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
- 1	1		DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
]	1 .		VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
ı	1		AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
ı	Į		KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
ł	į.		ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
ı			KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
- (	1		KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
1 .			YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
	,		KDGTVGELLKDWRRI NVAITRAKHKLILLGCVPSINCVDDI.FKI
6025			LNHLNSEKLIIDLPSREHESLCHILGDFORE
8025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
1 .	1		ARYGEAGEGPGWGGAHPRICLOPPPTSRTSFPPPRLPALEOGPG
ŀ	1		GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVOOWVSVADTELTD
ł	j		AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA
}	1		GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
	1		PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR
Ì			EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
1	1		AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
ł	1		TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
1	[ ]		KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
1	1		LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVOG
	1		YKEKVEFGVLVSFAYKVOGSDSDEEVVVATTRIETMI GDVAVAV
•	}		HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT
1	! [		PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR
i	1		KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
ŀ	l i		CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
	ł		KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
ł	1		KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
1	]	1	IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
] .		1	EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN
		j	RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSODGGUEGT VDD
1	1	ł	WIRSRLTEAVRLSNOGFOAYDFPAVTTAOYSFWLVELCDUVLEC
			LAPVING VDQ VAAECARQTLYTCLDVGLRLLSPFMPFVTERI.FO
	]	1	RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSTTPA
		1	VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGVVGCPC
		j	QAQVVVAVAEPWGLPAP\OGCAVALASDRCST\HLOLOG\TJ.DP
		· }	ARELG\KLQ\AKRVEAQ\ROAO\RLR\ERRA\ASGNPVKVDI.\E
6026	2674	514	VQEADEAKLQQTEAELRKVDEAIALFQKML
			GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
1 1		. 1	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
] [	1		TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
			YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
1 1		<b>1</b>	LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
[			VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
	1	. 1	ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML
	1	1	NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMKTN
	į		IRFMEPDSLFCVDPPEFOGONVROVHFRDMMEICI.PI.TAPESED
L			SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	ł company of the comp	to first	
	corresponding		L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	İ	\=possible nucleotide inscrtion)
			KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
ì	Ĭ	ł	SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
1		<b>[</b>	TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
1		ļ	KKCVNVTTKGLHPDOKEYEKNNTTTLMACLGGLLGIIGVICLIS
ł	l .	]	CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
ļ		}	·-
			TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
I	1	<b>;</b>	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSQRPRT
	[	İ	LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
1		ļ	TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
1	•	ŧ.	QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1		l	TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
1	1	1	FTNYNWREEHLERMLGOAGERRADVYVGVDVFARGNVVGGRFDT
I	1		DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
l	1		DPVALENRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
8028	120	3432	
i	1	1	LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDQDI NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSL\ODFIN
	1		1
İ	İ	1	WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII
	l.	1	ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR
Į.		1	SLDDARKRAKQFHEAWSKLMEWLEESEKSLDSELEIANDPDKIK
i	1	ł	TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
		l .	DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID
1	1	1	WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ
1.	1		ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR
l	}	ŀ	LEAALROAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT
	Į.	1	LIDOHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
1	į	1	IT_IRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ
i	Į.	1	WAETTLTDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK
1	1	1	VTKTYKRRAADPSSLOSHIPVLDKGRAGRKRFPASSLYPSGSQT
1	1	1	<u>-</u>
1		1	QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
	Į.	1	NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
1	]	1	GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
		1	YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
	i	1	FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
1	1		NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
1		İ	SÇAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
1		1	ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA
			ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
		I	IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
[	1	1	LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
1	_		AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
1	1	l	· ·
I			VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
1		I	IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
1			PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
I		Į.	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
1			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
ı			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1			EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
1		1	TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
l	1		YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
1	ł		ALOVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
I			TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
1		J	
1			KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
İ	ļ	1	SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
j			YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
ì	j .		ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
L	1	<u> </u>	DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Thereas are a series	····
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<u> </u>		TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
			EAMKCTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
	j		PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
		Ì	VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
	ļ	1	SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
		1	KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1	1	į	LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
		<b> </b>	APWNSLAWTYTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
ì			TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
1	}		SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
1			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
1	i		VERYREAI I KYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
ì			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
-		_	BTLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
1			RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
1			AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
	•		VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
1			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
1			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
1			DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
			IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
1			DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV
			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
1			FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
			YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
1			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
	1		IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELBEVAI
6032	39	2415	KFARLVNYNKMVFCPYYDAILSKILVRS
1		2313	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
1			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
	l		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1.			PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
	1		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1 1	1		SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
	j		ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
] [			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
]	.		IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
] .			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
]			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1	. <b>!</b>	i	W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
1 1	[		EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1			w\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
<u> </u>			RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
j l			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1 l	1		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
j			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
[	1		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
] ]	ł		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
[		į	ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
LL			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG

Deginning   Not corresponding   Contest   Co	CEC	Brodieted	Predicted end	Amino acid segment containing signal peptide
No. incleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence corresponding to first amino acid residue of amino acid sequence sequence sequence code,	SEQ	Predicted		
corresponding to first amino acid amino acid residue of amino acid amino acid sequence sequen				
Laleucine, Mamethionine, Nasparagine, esidue of residue of amino acid residue of amino acid sequence   Secrine, Tethreonine, Valine, Nasparagine, residue of amino acid sequence   Secrine, Tethreonine, Valine, Natyprophan, Yangyosine, Xalunkown, *-Stop Codon, /-possible nuclectide deletion, '-possible nuclectide deletion,' possible nuclectide insertion   Nasparagine, possible nuclectide insertion   Nasparagine, possible nuclectide deletion, '-possible nuclectide deletion,' possible nuclecti	NO:			
to first amino acid residue of amino acid sequence  sequence  sequence  description acid sequence  sequence  sequence  sequence  description acid sequence  sequence  description acid	1	l I		H=Histiding, I=isoledcine, K=Dysine,
### ### ### ### ### ### ### ### ### ##	i			
residue of amino acid sequence (COOn., *possible nucleotide deletion,	i		*********	
amino acid sequence   Codom, /-possible nuclectide deletion,   Lopossible nuclectide insertion    MRGELTSEGANAGLINISPOMSANAANAANATKESPVGF    PHHINRYPALP IPPNITOR IPPGERAYSPRIVADOM (PVPPPPDA)   IGPGIPRHARQINTLINIGEVVCANTISNTPRIVATISCKCYKNI   DISHPGWKSPVSQLDCLINRDNYISRCRLLEPDERTLIVGCRAST;   SIMDLAAPTERIKAELISSAPACYALAISPDERVCISCCSCOND     AVWOLHMQTIJVRQPGGTTOGASCIDISNDGTKLATGCLINTVR.     W\DLERGRQLOQHO/FFISPVSLICYCY/TEBNLAVGMENST\    W\DLERGRQLOQHO/FFISPVSLICYCY/TEBNLAVGMENST\    W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPYG\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPY\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPY\ASIN\  OSSUSSIVISCIDI \SVOTDKYIVTGS\CGNA     W\RTPY\ASIN\  OSSUSSIVISCIDI \SVOTDKYIT\  OSSUSSIVIT\  OSSUSSIVISCIDI \SVOTDKYIT\  OSSUSSIVIT\		amino acid	3	
Appossible mucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
MMCGELTSEGAAYAGLINISEQMGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		amino acid	seguence	Codon, /=possible nucleotide deletion,
MINISELTSEGANYAGLINISPOMSAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		sequence	_	\=possible nucleotide insertion)
PHHIMRYPAIPPNITGIEGKPAYSTHVSADGGGVPFFPPDA  IGPGIPPRAKGINTAMEGEVCANTISPTRHVYTGKGCVEVV  DISHGMKSPVSQLDCLARRONYTRSCRLLPDGRTLLVGGASTY  SIMPLAAPTPRIKABLTSSAPACYALA 18PDGKVCPSCCSDGN  AVWDLHNQTLVRQFQGFTDGASCIDISNDGTKLMTGGLNTTVR  W\DLREGRQLQCHD/FFTSVFSLGYCP\TEBRILAVGMENSN\/ EVLHVTK PDRYQLHHIBSCYLSLEFAHCKWF\VSTGKNILLN  W\RTPYG\ASIF\QSKSSS\VLSCDI\SVDGKYLTVTGS\GLK  ESGRRRRLKKRRSPCGTAGGPGETNNGFGACPRGPREEAAAA  FATVYEVIY  6034  2683  714  ESGRRRRLKKRRSPCFGTAGGPGETNNGFGACPRGPREEAAAA  VTFPSDEDIVSGAVEPKDPMEHAQNYTVDEVIGKAAK  VTFPSDEDIVSGAVEPKDPMEHAQNYTVDEVIGKAYAACVLKN  RQIPKLLBCQLGFTDIGIRLDCLDLKGKLDFKTCEALEEVYK  LQPKVVDLEOTNLDEGGASALFDHIEVYESATHLNISPKHHG  RGGQAAAMMRKTSIGLYA\DANNINGL  RGGYQAAAMMRKTSIGLYA\DANNINGL  BAQLGNILKRNGSLGITLDHITQSLETINLGHNPIGNEG  RHLKNGLISNSVIRLGLASTKLITCEGAVAVAEFIASPELLE  DERENE INTGGLAALLALKWNHLINGESYL\ADNINGL  DERENE INTGGLAALLALKWNHLINGESYLVADNINGL  DERENE INTGGLAALLALKWNHLINGEPKLARAVKSFI  TOKALLAEIONGCKRHLVLAREREKKOPPOLOSEPKRAVKSFI  TOKALLAEIONGCKRHLVLAREREKKOPPOLOSEPKRAVKSFI  TOKALLAEIONGCKRHLVLAREREKKOPPOLOSEPKRAVKSFI  OPPODEPLAAGVONGA-PPASPSDENDSDEDGGEEEEEGGRDE  PSGAIDTTDTGSSEPQPPPEPPRAGPPLINGLKFEFALLAPPS  PSGPEVKGGSGGLEHLESCSKREKELEBLLEASGESGOETL  LENASTIALPDISSGPP\SILHTAGVGCVVEILVGERFALLAPPS  FYFIMTFGAILTRINGSPFYBASPSISSBSTGEEEEEEGREBE  PSGAIDTTDTGSSEPQPPSEPPRAGPPENGRSPSHSRFFILMF  CHARALLAEIONGCKRHLVLAREREKKOPPOLOSEPKRAVKSFI  LENASTIALPDISSGPP\SILHTAGVGCVVEILVGERFALLAPPS  FYFIMTFGAILTRINGSPFYBASPSISSBSTEGHTAL  LENASTIALPDISSGPP\SILHTAGVGCVVEILVGERFALLAPPS  SSTSLDAI ISPLANYHMEVDIVONIQATSPCLHFPTDLQKVARMI  EEGYDSVPSVVRRRQFRWSEILKGVRRVTEPLINAPRAPRR  WOGALVERNSYPFAKLRILLEMSYLGGKMAYTEREABSVDIT  GOOGET ISTOVADALGI SLLKKSGTEVALERACSKQTLSSI  LDCCMEVSVSDKLAVUDEWRKERGLCKKEVAVLERRACSKQTLSSI  LDCCMEVSVSDKLAVUDEWRKERGLCKKEVAVLERRACSKQTLSSI  LDCCMEVSVSDKLAVUDEWRKERGLCKKEVAVLERRACSKQTLSSI  LDCCMEVSVSDKLAVUDEWRKERGLICKEVATLERRACSKGTLSSI  LDCCMEVSVSDKLAVUDEWRKERGLICKEVATLERRACSKGTLSSI  SSSSIBGSDSTLDNSGARAVYTENGRAPSPAAATATGI  BSPSGGGRLILPTONGOGGGGVSSSRYTY\SLCGPPERAGACK  DKCQFARHSVTILPSSKRFREDISPSPREGAGPSAAATAATGI			<del></del>	MNGELTSPGAAYAGLHNISPOMSAAAAAAAAAAAAYGRSPVVGFD
IGGI PRINARQINTLINHGEVYCAVTISNTPHRYTICGRCYKY   DISHPGNKSPYSOLOCIARDONT ISCRELIPOSPTLIVGGEAST    SIWDLAPPTRIKAELTSSAPACYALAISPDSKYCFSCCSDON    AWWDLHMOTIVROFGSHTOGASCIDISNIGHKLATGELDTYNIN   W\DLREGGLOGHD FFTSPYFSLGYCD\TEMBLAYGMENSN\\   W\LTPYF\SASTY\DKYGLHLHESCVLSLKFAHCCKWF\VSTGKNDLIN   W\RTPYG\SASTY\OKSTGLOGHT\DKYRT\USGASTY\DKYTUTGS\CDK\   W\RTPYG\SASTY\OKSTGLOGHT\DKYRT\USGASTY\DKYTUTGS\CDK\   RAFVYEVIY     G034   2683   714   ESGRRRIKRRSSPCFGTAGGPGETNIGPGACPRGPREEAAAA   VITPYSDEDIVSGAYEPKDHRHAQNYTUDKIGAYKACKLM\   W\RTPYSDEDIVSGAYEPKDHRHAQNYTUDKIGAYKACKLM\   RQIPKLIRQLOEFTDLGHRLDCLDLKGEKLDYKTCBALEEVFK\   LOPKVVDLEOTNILDEGASALFDMIFYYSSATHILIFISHKHIG   RGMQAAAMMKKTSCLQYL\DARNTPLLDHSAFFVARALGIRS\   LAVIHLENASLSGRPIMLLATALKMMNINGELYL\ADNIKINGL\   DSAQLGNLKKNCSLGILDLENNIVLUSGLAYICGGLKKQRKG\   RHLKNGLISNSVLRIGLASTKLTCEGAVADETIASSPYLLR\   DRENNITTGGLANLSLAKVNHSLLRILDLDGEPKRAVKSFI\   DRENNITTGGLANLSLAKVNHSLLRILDLDGEPKRAVKSFI\   TOKALLASILOMGCKRILVLARREREKEPPLGSARNETTATE\   OPDDEPAAGVONGAPSPASSDDSDSDSDSDSBEREEGERGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLGSARNETTATE\   OPDDEPAAGVONGAPSPASSDDSDSDSDSDSBEREEGEREGREND\   PROSALITATIONGCKRILVLARREREKEPPLGSARNETTATE\   OPDDEPAAGVONGAPSPASSDDSDSDSDSDSBEREEGEREGREND\   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEGERGRIC   PROSALITATIONGCKRILVLARREREKEPPLANPERSPREEG			ĺ	
DISHPENKSPYSOLDCLANDNYTRSCRLIPDGRTLIVGGEAST: SIMULADAPTPRIKAPISSAPACYLSPDSKUTSCCSDON: AVMDLHNQTLVRQFQGHTDGASCIDISMDGYKLMTGGLDNYTW: W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEMLAVGMENSN\\ W\RTPYG\ASIT\QSKSSS\VLSCDI\SVDDKYIVTGS\GDK W\RTPYG\ASIT\QSKSSS\VLSCDI\SVDDKYIVTGS\GDK RATVUSVIY  6034  2683  714  ESGERRRIKKRRSPCPGTAGGPGETNPGPGACPPGPREEAAA EIAPQGAPPVPGADGDIEEAPAEAGSPSPASPPADGRIKAAAK VTFPSDEDIVSGAVEPKDPRHIAQNYTUDEVIGAYKQACQKIM RQIPKLLIKRQLQFFTDLGHRLDCLDLKGEKLDYKTCEALEEVFK LOPKVUOLEQYINLDEDGASALPHNIEYYESATHINISPNKHIG RGMQAAAHMMRKTSCLQYL\DARNTPLLDHSAFFVARALRIKS LAVHHLENASLSGRPHLLATALKNIMIRESLYL\ADNIKINGL DSAQLGINLLKFNCSLQI\DARNTPLLDHSAFFVARALRIKS LAVHHLENASLSGRPHLLATALKNIMIRESLYL\ADNIKINGL DSAQLGINLLKFNCSLQI\DARNTPLLDHSAFFVARALRIKS VTT\V\UNNOLHTGMAFLGMTLPHTGSLETINIGHNPIGNE RHLKNGLISINSVURIGLASTKUTCEGAVAVAEPIAESPRLKR DLRENEIKYGGUMASLSLALKVNISTLEGAUAVAEPIAESPRLKR PSGALITRITGSSEP EPPPPPPBREGPEPEPAPPRAGEPEEEEEGERDE REHENGLISINGTKORGEPPPPPPPPBRAGEPPEPAPPRAGEPEEEEEGERDE PPGGEVKGGSCGLEHELSCSKNEKELEELLLEAGESGGETL LENASTLALPDSSCPPPPPPPPPFSTKQLLSFLGMW YFYIMTPGFALITRYGSEPPPPPPPPFSTKQLLSFLGMW YFYIMTPGFALITRYGLCCVIVENTGALGPLBYUR  6035  19  404  SYTIGITIHNTGSTEPPPSLTATERGRERERERERERERERERERERERERERERERERERE		ł		
SIMDLAPTPRIRABLITSSAPACYALAISPDSKUCFSCCSIOGN AVWOLHNQTLVRQFQG:TTDGASCIDISNDGYKLMTGGLDNTVR: W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEBALAVGHENSN\ BULHVTKPDKYQHILHESCULSLKFAHGGKWP\VSTGKNILM: W\RTPYG\ASIT\QSKSSS\ULSCIJ\SVDDKYITVGS\CDK RATVYEVIY  6034  2683  714  ESGRRRLKERRSPCFGTAGGPGETNPGPGACPPGPREEAAAA VTFPSDEDIVSGAVEPKDEWRHAQWYTUDEVIGAYKQACQKLN RQIPKLLRQLGEFTDLGHELDCLLKGEKLDYKTCGALEEVYK LQPKVVDLEQTNLDEDGASALPDMIEYYESATHINISPKHHG RGQAAAMHMKRTSCLQYL\DARNITPLLDHSAPFVARALIRS LAVIHLENASISGRPIMLLATALKNMMIRELYL\ADNILNGL DSAQLGINLKYNCSLQYL\DARNITPLLDHSAPFVARALIRS LAVIHLENASISGRPIMLLATALKNMMIRELYL\ADNILNGL DSAQLGINLKYNCSLQYL\DARNITPLLDHSAPFVARALIRS LAVIHLENASISGRPIMLLATALKNMMIRELYL\ADNILNGL DSAQLGINLKYNCSLQYL\DARNITPLLDHSAPFVARALIRS LAVIHLENASISGRPIMLLATALKNMMIRELYL\ADNILNGL DSAQLGINLKYNCSLQYL\DARNITPLLDHSAPFVARALIRS LAVIHLENASISGRPIMLLATALKNMMIRELYL\ADNILNGL DSAQLGINLKYNCSLQYL\DARNIJREREEKQPPQLGASMPETTATE OPHDEAACVQNGAPSPAPSPDSDSDSDGEEEEEEEGGRDE PSGAIDTRITGSSEPQPPPBPRSGPPLPNGIKRENKAVKSFI TOXALLAEIQNGCKRNLVLAREREEKQPPQLDASMPETTATE OPHDEAACVQNGAPSPAPSPDSDSDSDGEEEEEEEGGRDE PSGAIDTRITGSSEPQPPPBPRSGPPLPNGIKREFKALALPPS CONTROLLESSCRIPTERSLLLLRSAGNGERFIKEPELLDE PSGEVEGGSCCLEHELSSCRIPTERSLLLLRSAGNGERFIKEPELLDE SPSGEGGGGGGGGEVEPPHLESISCKNEEBLLLLBAGNGESGGRTL LENASTLALPDSSGPPSLETISCHLDSCHARESFHISSFHSSFHSLKY LENASTLALPDSSGPPSLETISCHCOCVETITGGLGPLPV VLRAALDSGAPGVEVSTPHLALILLARGSGRIPLENGLENGEV SGGGGGGEVEPPHLAALILLARGSGRIPCHAPHLOKAVEM BEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPSEVG ULRAALDSGAPGVEVSVSTCHAUSPCLAKEVATLGREYSDECL SGGGGGGEVEPPHLAALILLARGSFCHECHLENGLUKASEGNIPGERGERFERCHPELLOG GGGFPRHSVTLPSKKFFRKKELIKLLVCNIDGCLINGHIY GDOKETISTOVKDAIGTSLKKSGTSVATLSFRACSKQTLSSI LDCKMEVSVSDLLAVVDEWRKEMSLCKKEVATLGREYSDECL RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IRFFAEHIC\I GGGFPRHSVTLPSKFFRYSEKELKLLVCNIDGCLINGHIY GGGFPRHSVTLPSKFFRYSEKELKLBARALSSRCDRYSDEC SFSGGGGRELPPTQCOPGGGGOVTSTKTT\ELCRPFEENGACK DKCGFABGHERSLTRHPKKYETELCRTFHTTGCPPVSPRCH HNAEERRALAGARDLSAADRFLQHSFSPADSSSCRATI- SFSGGGGRELPPTQCDGGGGGSTTATTGCPPVSPCCH HNAEERRALAGARDLSAADRFLCHSFSPADSSSCRATI- SFSGGGFRILP		1	1	
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QPDDEPAAGVQNGAPSPAPSPDSDSDSDSGEEEEEEGERREE PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPE PPGPEVKGGCGLEHELSCSKNEKELEELLLEASQESGQETT. 6035 19 404 SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMV YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKT LENASTLALPPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV 6036 1745 356 LPDVEKLGRRGGKMDSVEKGAYTSVSNPRGGPSRGRPPKLQG SRGGQCGGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIG VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSK SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMI EEGYDSVFSVYRHQFFRWSEIQKGVREVTEPLNLNPAKRPRRC WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDII DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYV GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSI LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECI RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\I MEKGLINFMPKNRNLAVNIGEKK  6037 2936 1919 WTSWMMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTT GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRI SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRFFERGACK) DKCQFAHGIHELBSLTRHPRYKTELCRTFHTIGFCPYGPRCHH HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGI DSPTSITPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLS PSMGLPGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGY: SSSSSHGGSDSTTLDNSRRLPIFSRLSISDD  6038 1450 426 SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAI YKGTKHAKKKALEAMKNKQKSVTAKDSAKTTTSITTNTIN		ļ	İ	TOKALLAEIONGCKRNLVLAREREEKEQPPQLSASMPETTATEP
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TERDETTAMULENVILHEWERISEICVAKISEPEADVESVIGVS NLIGVLQKPKGSLKSSKKKNCKVRPADEILESNKENEKCVSSEG EKKIECWELTTEPSLTHNSSGLISPIRKKPLEDLVCKLADISINY VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKGSIVQAKPLE IAKLVQKNPAVQFLYQKLIGWINSDQRKDFGFLVDLLYSALRCC DINDMERKKVLDDLTKVLKWISLIKIIEKACPSSDKHALVTFHL KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWILLSLVLSQ HVKNDYLIGDVYVERIIVRHEITLFKTRKLSEASSDSSVSFIC DVAYNYFSSAKGCLLWPSBEDLLLTLFQCLCAQSKEKTHLDPFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKRQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMRNDGSWEK MRQSLPMQWIHRPLLEGRESLNYLCFKTDFKCDDIKTHPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP IFLIGFCEILQKNNITYDDLRVLGNMSGLLQLLFFRSREHSTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIGSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFMSCLQ TKSIDDSELHGILKIITSKKEHVLLGSTNGGFGHLAIFMSCLQ VSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLFVNLISEWK EFFSQGHSLLLPHLVTVTGENKDVSETSFQNMMLKWCSTLTY ISREQLLSHKLPARLVADQKTNLPEVLGVILTMKLI ISREQLLSHKLPARLVADQKTNLPEVLGVILTMKLI LTFFKAASSQLRALYSMYLRKKYKSLNKLLYHLFRLMPEMPTYAR TAVEVPNKDPKTFFFEEQLSIRETTMLPHIPALCSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQETSSVOT STQLFNGMTVKARATTREVMATYTITDLVIBLIIQLPSNYPLGS ILVESGKRVGVAVQQWRMMMLQLSTYLTHQMSINEGLALWKNN VURFFSGVEDCMICFSVHHGPNYSLPKKACRTCKKKFHSA\CLY KWTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSKGY GAQAFGGLSTYPAASPTPHAAFLADDVSNNAMANGSSLAAQGKE LVDKNIDRFIPITKLKYYFANDTMYVGKKLGLLFFFYLHOMEV QYQDTPVAPRFPDVNAPDLVILPSMALTISTULNTENLETHINDEN	ļ			DATIWIKSCRPIIRPNSGFWEOLTHVEEOLEGYMTUUMVCOD:
NLLGVLGKPRGSLKSSKKKNGKVRPADEILESNKENEKCVSEGE EKIECWELTTEPSITHNSGLISPIRKFLEDUVCKLADIS INY VWERKSEGHIRFLSTILDSFSSSRVFRMLLGDEKGSIVQARFLE IAKLVQKNPAVQFLYQKLIGWLHEDQRKDFGFLVDILYSALRCC DNDMERKKVLDDLTKVDLKNISLLKIIEKACPSSDKHALVTPHL KGBILGEKLVNLADCLCHDLESRVSSESHSERENTLLSVLISQ HYKNDYLIGDVYVERIIVRHETLFKYKKLSEAESSDSSVSFIC CKLKNTWLSGVNLLVIQTDSSYKESTELHSALWLKNQVQASSL DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSWRNDGSWEK MRQSLPMQMIHPPLLESRLINVECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQMCEELDNPP IFLIGFCEILQNGNNITYDDLRVLGMMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEWHYKKRESFFPLTEGNLHTIGSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ KKSIDGBLHGILKIIISWKEHEDIFLFSCNLSEASPSVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCOLACDLSAFFDSTTLDTIGNLFVNLISEWK EFFSQGIHSLLDFILVTYGENKUSETSFQNAMLKPMCETLTY ISRQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRAPP VQIAVYHMLYKLMPELPQVTQDNILKSYGDEEEPALSPPAALMS LLSIGEDLLENVLGCIPVGGVTLTKPLESEDFCYVLGYLTWKLI LTFFKAASSOLRALYSMYLRKTKSLIKLLYHLFRLMPENPTYAB TAVEVPNKDBYTFFPEELOLSIRETTMLPYHIPHLACSVHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTITDIVIBLIIQDFSNYPLGS STQLFNGMTVKARATTREVMATYTITDIVIBLIIQDFSNYPLGS STQLFNGMTVKARATTREVMATYTITDIVIBLIIQDFSNYPLGS STQLFNGMTVKARATTREVMATYTITDIVIBLIIQDFSNYPLGS GSAPSHSLFILOPRSGGSLCPSRAW/PDPHQLSTNGMNVRQVSLTYP GSSAPSHSLFILOPRSGGSLCPSRAW/PDPHQLFDDTSSAQSKGY GAQAFGGLSYPAASPTPHAAFLADPVSNNAMAGSSLAAQGKE LVDKNIDRFIPITKLKYYFANDTMYVGKRGLLFFFPVHOMEV QYQODTPVAPRFEDVNAPDLVIBALLISLULTUNTENDLETHINDEN	6041	2	3996	GHIPDITEREVRIMIPL
EKECWELTTEPSITHNSGLISPIRKKYREDUVCKLADISINY VIERKSEQHIRFISTLIDSFSSSRVFRMLLGDEKQSIVQAKPLE IAKLVQKNPAVQFLYQKLIGWLINDQKROFGFIVDILYSALKCC DIMERKKVLDDLTKVDLKWINSLIKIIEKACPSSDKHALVTPML KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLISLVLSQ HVKDYDLIGDYVERIIVKHETLFKTKKKSEAESSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTIFQLCAQSKEKTHLDPPLI CKLKNTWLSGVMLLVHQTDSSYKESTFLHLSALMLKNQVQASSL DINSLQVLLSAVDDLLNTLESBDSYLMCVYIGSVMPNDSEWEK MRQSLPMOWLHRPLLEGRUSLNYECFKTDFKEQDIKTLPSHLCT SALLSKWVLIALRKETVLENNELEKIIAELLYSLQWCCEELDNPP IPLIGFCEILQKMNITYDDIRVLGNMSGLOLLFMSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FISKEEKKEFSAQCIPALLGWKNITYDDIRVLGNMSGLOLLFMSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FISKEEKKEFSAQCIPALLGWKNITYDDIRVLGNMSGLOLLFMSSPEUGV NIEIIRFISLFIKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCOLLACISAFFDSTTLDTIGNLFVNLITSEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCSTLTT ISKEQLLSHKLPARLVADQKTNLPSVITLIANTLAPLLLFRARP VQIAVYHMVJKIMPELPQVQDNLKSYGDEEEPALSPPAALMS LLSIGEDLLENVLGCIPVGOIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRAHYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTFFTEELOSIRFTTMLPVHTPHTAREAVYHMTL KDLPAMVRLWNNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT TAVEVPNKDPKTFFTEELOSIRFTTMLPVNGSINEGLALWKON VURFFSOVEDCMICFSVTHGFNYSLPKKACRTCKKKFHSA\CLY KWTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQARGGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVCKKLGLLFFFYLHOMEV QYQDTPVAPRFPDVNAPDLYIPSMAPTITYVLVAGLALSTQDRFS PDLLEGLAGSALAWLTLEVLALILSLNILLSTANDRILTETHINGE	1	1	3000	TERDERTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
VWERKSEQHLRILSTILDSPSSRVPRMLIGDEKQSIVQAKPLE IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPHL KGDILGEKLWNLADCLEDLESRVSSESHFSERWTLLSLVLSQ HVKNDYLIGDVYVERIIVRLHETLFKTKKLSPAESSDSSVSFIC CKLKNTWLSGVNLLVHQTDSSYKESTFJLHSALMLKNQVQASSI CKLKNTWLSGVNLLVHQTDSSYKESTFJLHSALMLKNQVQASSI DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK MRQSLDMQWLHRPLLEGRISLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELERIIJELLTLYGUMCEELDNPP IFLIGFCEILQKNNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLIIARLILGSSISSDEVKPHYKRESFFPIEGRNHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGFHLAIFMSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSBASPEVLGV NIEIIRFLSLFLKYGSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLFVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFONAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQVTQDDVLKSYGDEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGGIVTIKPLSEDFCYVLGYLLTWKLI LTFKAASSQURALVSMYLKKTKSLNKLLYHLFRLMPENPTYAB TAVEVPNKDPKTFFTEELQLSIRETTMLPVHIPHLACSVYHMTL KOLPAMVRLWNNSSEKRVENIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREWMATYTIEDIVIELIIQLPSNYPLGS STQLFNGMTVKARATTREWMATYTIEDIVIELIIQLPSNYPLGS STQLFNGMTVKARATTREWMATYTIEDIVIELIIQLPSNYPLGS STQLFNGMTVKARATTREWMATYTIEDIVIELIQLPSNYPLGS STQLFNGMTVKARATTREWMATYTIEDIVIELIQLPSNYPLGS STQLFNGMTVKARATTREWMATYTIEDIVIELIQLPSNYPLGS STARFGSCGSLCPSRAW/PDHQLFDDTSSAQSRGY KWFTSSNKSTCSLCEETFF MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP GSBAPSHSLPLQPRSGGSLCPSRAW/PDHQLFDDTSSAQSRGY GAQRAFGGISYPAASPTHAAFLADPVSNMAMAYGSSLAAQGKE LUDKNIDRFIPITKLKYYFAVDTMYMGRALGLLFFPYLHQDWEV QCQDTPVARRFDVMAPDLYIPAMAPITYVLVAGLALGTLORFS PDLLGLQASSALAWLILEVALIJUNGTLATENLY NE PPLLGLQASSALAWLILEVALITENLY NE PPLLGLQASSALAWLILEVALITENLY NE PPLLGLQASSALAWLILEVALITENLY NE REPORTER TO AND AND AND AND AND AND AND AND AND AND	j	İ		NELL VLOKPKGSLKSSKKKNGKVRFADETLESNKENEVCUSES
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HVKNDYLIGDVYVERIIVRHETLFKYKKLSEAESSDSSYSIC  BVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI  CKLKNYWLGSVAUDLLNTLLESEDSYLMCYVIGSVMPNDSEWEK  MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLFSHLCT  SALLSKMVLIALRKETVLENNELBKIIAELLYSLQWCEELDNPP  IPLIGFCEILQWNITYDNIRVLGMMSGLIQLLFNRSREHGTLW  SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTTQSLCP  FLSKEKKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ  TKSIDDGELLHGILKIIIISWKKEHEDIFIFSCNLSEASPEVLGV  NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL  YSIPLVQLFACVSCDLACOLSAFFDSTTLDTIGNLPVALISEWK  EFFSGGIHSLLIPILVTVTGENKOVSETSFQNAMLKPMCETLTY  ISKEQLLSHKLPARLVADQKTNLPEYLQTLLANTLAPLLIFRAPP  VQIAVYHMYKLMFELPQVTQDNLKSYGDEEEEPALSPPAALMS  LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI  LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFPRLMPENPTYAR  TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL  KOLPAMVRLWWINSSEKRVFNIVORFTSKYVSSVLSFQEISSVQT  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQDFSNYPLGS  GSPAPSHSLPLQPRSGGSLCSRAW/PDPHQLFDDTSSAGSRGY  GAQRAPGGLSYPAASPPTPHAPLADPVSNMAMAYGSSLAAQGKE  LUDKNIDRFIITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV  QYQQDTPVAPRFDVNAPDLYIPAMAFITTYVIVAGLALGTQDRFS  PDLLGLQASSALWAULTLEVLAUUTSLUTHUNDELTHINDE	i			DNDMERKKVLDDLTKVDLKWNSLLKITEKACDSSDRUAT UMDUT
DVAYNYFSAKGCLLMPSSEDLLLTLFOLCAQKEKTHLPDFLI CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALMLKNQVQASSL DINSLQVLLSAVDDLLATILESEDSYLMCVYIGSVMPNDSEWEK MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCCBLDNPP IPLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFÇNNAMKRMCETLTTY ISKEQLLSHKLPARIVADQKTNIPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB TAVEVPNKDPKTPFTEELQLSIRETTMLEYHIPHLACSVYHMTL KDLPAMVELWMNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS IIVESGKRVGVAVQQWRNMMLQLSTYLTHQNGSIMEGLALMKNN VDKRFEGVEDCMICFSVIHGFNYSLPKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYHQDWEV QYQQDTPVAPRFDVNARPITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLVLYWDTDLTTATALNER	J	j		REDITION OF THE PROPERTY OF TH
CKIKNTHISGVNILLVHQTDSSYKESTPIHLSALWLKNQVQASSL DINSLQVLLSAVDDLLNTILLSEDSYLMGVYIGSVMPNDSEWEK MRQSLPMQWLHRPLLEGRISLNYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP IPLIGFCEILQKNNITYDNLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLEHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLINTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLIKLLYHLFRLMPENPTYAB TAVEV?NKDPKTFFTEELOLSIRETTMLPHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRPTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQDPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALMKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF  6042 1306 253 MAELAPASPEDIKASVSNGDTTLLCSRRGSCGMMEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAGSRGY GSQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLYWDTDLTTATALNER	ı			I AVAILIBLE OVIVERIIVELHETIFKTKKI.SFARSSDSCHORTS
CALANIASGVILLSAVDDLINTILESEDSYLMCVYIGSVMPNDSEWER  DINSLQVILSAVDDLINTILESEDSYLMCVYIGSVMPNDSEWER  MRQSLPMQWLHRPLLEGRESLNYECFKTDFREQDIKTLPSHLCT  SALLSKWVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP  IPLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFRRSREHGTLW  SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGGLHTIQSLCP  FLSKEEKKEFSAQCIPALLGWTKKDLCSTMGGFGHLAIFNSCLQ  TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSERSPEVLGV  NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL  YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLFVNLISEWK  EFFSGGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY  ISKEQLLSHKLPARLVADQKTNLPEYLQTILINTLAPLLLFRRRPP  VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS  LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI  LTFFKAASSQLRALYSMYLRKTKSINKLLYHLFRLMPENPTYAB  TAVEVPNKDPKFFFTEELQLSIRETTMLPYHIPHLACSVYHMTL  KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT  STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS  IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN  VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY  KWFTSSNKSTCSLCRETFF  6042  1306  253  MAELAPASPDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP  GSSPASHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY  GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE  LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV  QYQQDTPVAPRFRDVAAPDLYIPAMAFITYVLVAGLALGTQDRFS		1		DVAINIFSSAKGCLLMPSSEDLLLTLFOLCAOSKERTUL DDELT
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SALLSKMULHRPLLEGRLSLAYECFKTDFKEQDIKTLPSHLCT SALLSKMULHARKETVLENNELEKIIAELLYSLQWCEELDDRPP IPLIGFCEILQKMNITYDDLRVLGNMSGLLQLLFNRSREHGTLW SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGRLHTIQSLCP FLSKEEKKEFSQCIPALLGTIKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLABSEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGRLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLDPALVADQKTNLPEVIGTLLNTLAPLLLFRARP VQIAYYMLYKLMPELPQYDQDNLKSYGDEEEEBASPPAALMS LLSIQEDLLENVLGCIPVGGIVTIKPLSEDFCVVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPERPTYAB TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWMSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVLHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITTVIVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSTLYLUTURDITTELTULN AS	ı	1 : 1		DINGLOVEDSAVDDLLNTLLESEDSVIMCIVICSIMPNDGERED
IPLIGFCEILQKMNITYDNLRVLGMMSGLLQLLFNRSREHGTLW SLI IAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCI PALLGWTKKDLCSTNGGFGHLAI FNSCLQ TKS IDDGELHHGILKI I ISWKKEHEDIFLFSCNLSEAS PEVLGV NIEI IRFLSLFLKYCSS PLAESEWDFIMCSMLAWLETTSENQAL YS IPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETTLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQ1AVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCI PVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQBISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELI IQLPSNYPLGS IIVESGKRVGVAVQQWRNMMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GSARAPGGLSYPAASPTPHAAFLADPVSNMAMAGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILISLAUTUNDTULTILLW RE	Į.			FALLSCHIMETERSTEINFECFKTDFKEQDIKTLPSHLCT
SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLPILVTVTGENKDVSETSFQNAMLKPMCETTLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLIKLLYHLFRLMPENPTYAB TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KMFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVUNGLALGTQDRFS PDLLGLQASSALWUTLEVLAILLSLYLVTNTDLATTDLUK PK	ĺ			SALUSAMVUIALRKETVLENNELEKTIAFILVSIONCEFIDNIDD
TRSIDDELLHGILKIIISWKEHEDIFLFSCNISEASPEVLGV NIEIIRFLSLFIKYCSSPLAESEWDFIMCSMLAWLETTSENGAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNIKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB TAVEV9NKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KOLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFLTYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLETLIN BY	1	İ		CLIENCE LOKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
NIEIRESLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIRFLSLFIKYCSSPLAESEWDFINCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLPRLMPENPTYAB TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS IIVESGKRVGVAVQQMRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFLTYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTGLTLTUN DE	i	1		STITAKTILSKSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
YSIPLVQLFACVSCOLACDLSAFFDSTILDTIGNLEVINLISEWK EFFSQGIHSLLIPILVTVTGENKDVSETSFQNAMLKPMCETLTY ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEPALSPPAALMS LLSIQEDLLENVLGCIPVGOIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVENIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFLTYUVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVMTULTTLIN	1	1		TESTEDORISMOST PALLGWTKKDLCSTNGGFGHLAIFNSCLQ
EFFSQGIHSLLLPILVTUTGENKDVSETSFQNAMLKPMCETLTY  ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP  VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEPALSPPAALMS  LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI  LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR  TAVEVYNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL  KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT  STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS  IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN  VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY  KNFTSSNKSTCSLCRETFF  GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY  GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE  LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV  QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS  PDLLGLQASSALAWLTLEVLAILLSLYLVTVMTDLTTLIN BY	ŀ	1 1		NIBILDELGIER GIERRENGE GERNEN G
ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPILLFRARP VQIAVYIMUYKLMPELPQYDQDNLKSYGDEEEPALSPPAALMS LLSIQEDLLENVLGCIPYGOIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVYNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFILYUVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTILN BY	1	1		WEIGHT HOLES CHARGE PLAESEWDFIMCSMLAWLETTSENQAL
ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPILLFRARP VQIAVYIMUYKLMPELPQYDQDNLKSYGDEEEPALSPPAALMS LLSIQEDLLENVLGCIPYGOIVTIKPLSEDFCYVLGYLLTWKLI LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAR TAVEVYNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT STQLFNGMTVKARATTREVMATYTIEDIVIBLIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFILYUVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTILN BY		1 1		FERROGENERAL
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SIQLFNGMTVKARATTREVMATYTIEDIVIBLIIQLPSNYPLGS IIVESGKRVGVAVQQWRNWMLQLSTYLTHQMGSIMEGLALWKNN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF  6042 1306 253 MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVMTDLTTLIN	1	1		RULPAMVRLWWNSSEKRVFNIVDRFTSKVVSSVI.SEOPI SEVOR
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GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVATDLTTLIN			· · · · · · · · · · · · · · · · · · ·	MAKLAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
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QYQQDTPVAPRFDVNAPDLYIPAMAFITYUVAGLAGTQDRFS PDLLGLQASSALAWLTLEVLAILLSLYLVTVATDLTTTDL			1	GAURAPGGLS I PAASPTPHAAFI.ADPUSNMAMAVGGGI.AAGGER
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	1		i ·	PDERGEOGRAPH AND THE VERTILIST VILVE AND THE TRANSPORT OF THE PROPERTY OF THE
GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK			<del></del> - <u>-</u> - <u>l</u>	GIALVONIGGELFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	)	sequence	\=possible nucleotide insertion)
	sequence		ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
		1	
6043	403	599	LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
1			PLPPLQNKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
i	1	1	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
ł	ŀ		AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
6045	155	2299	
1	1		AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
ı	1	Į.	SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
]	}	]	DWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
I	1		RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
I	Į.		VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
1	1	1	EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
1	1	1	KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
l	1	1	MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
1	1	[	VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
1	1	1	
<b>{</b>	i	1	GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
1	l	1	QRQGPPLQQRPPPQGQQHLSGLGPPACSPLPQRLPSPTSAPQQP
l	1	1	ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
1	· I	· I	ATRQTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
1	į	1	AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
1	1	l	AAGGPPHPOLNKSOSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
1		1	LRKSFASLFSD
		1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
6046	212	10/5	SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
1		1	
1			QAPLSPGLPAMGGPGPGPCEDPAGAGGAGGGSEPLVTVTVQCA
	ł	]	FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
1		1	WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
ſ	1	l l	SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
Į	İ		VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
		l	KGGRVVIFOREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
İ		[	IEEKINKIKWLPOONAAHSLLSTNDKTIKLWKITERDKRPEGYN
	1.	1	LKDEEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
1	•	ſ	INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
1	ı		NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
1			
1		]	HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
	1		TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1 .	1	1	WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
l			LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
1		ļ	TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
	_	1	KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1		1	ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1		I	EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1	1	1	
ı	1 .	1	SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1		i	PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1	1		DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
1	i		SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
1	}	1	NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKKDKKKKESSKE
1	1	1	LESPLTPGKYCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
1	l	i	LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
1			TONGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
1			EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
1			
ı	1	1	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
1			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1			YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
1			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ
Į.	<u> </u>		APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
Ī			EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK
	_ 1		

SEQ Predicted beginning incleotide beginning nucleotide location corresponding to first amino acid segment containing signal pepting for first amino acid residue of amino acid sequence sequenc
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ
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corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequ
amino acid residue of amino acid residue of amino acid sequence se
residue of amino acid sequence  S=Serine, T=Threonine, V=Valine, m=Trytopine, x=unknown, *=Sto Codon, /=possible nucleotide deletion, \
amino acid sequence s
Sequence   Codon, /=possible nucleotide deletion,   =possible nucleotide insertion)     EDGKESTSDCKLPTSEESRLGSKEPPPSVHVPVSSPLTOHO   IPYMHGYSYSQSYDPNHPSYRSMPAVMMONYPGSYLPSSYSF   YGSKVSGGEDADKARASPSVTCKSSESKALDILQQHASHYK   SPTISDKTSQERDRGGGVVGGGGSCSSVGGASGERSVDRP;   SPSQRLMSTHHHHHLGYSLLPAQYNLPYAAGLSTAIVASQ   STPSLVPPPRR   AMTGVFDRRVPSIRSGDFQAPFQTSAAMHPSQESPTLPESS, DSDYXSPTGGAPHGYCSPTSASYG\KALNPYQYGHOVNGSAV   SPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTE PEVRI   NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAAM   GLTQTQVKIWFQDKRSKIKKIMKNGEMPPEHSPSSDPMACN   QSPAWWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY   AASSINSHLPPPGSLQHPLALASGTLY   KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWWASSINSHLSTYSLVDSVGNTKTFDVEHSHVFLGNLVLNI   DCGGQDTFMENYFTSQRDNIFRANVEVLIYVPDVESRELEKOMM   YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI   RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF   FARIIEADEVLLFERATFLVISHVQCKEQRDAHRFEKISNIIK   FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYWVWMSDPS   PSAATLINIRNARKHFEKLERVDGPKQCLLMR   KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWWASSIVYQLIPNVQCHANLFKKISNIIK   FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYWVWMSDPS   PSAATLINIRNARKHFEKLERVDGPKQCLLMR   KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWWASSIVYQLIPNVQCHANLFKKISNIIK   FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYWVWMSDPS   PSAATLINIRNARKHFEKLERVDGPKQCLLMR   KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWWASSIVSHKSIIFANYIARDTPRIGATIU   PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMKSIIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMKSIIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PNTAMKKVLLLMGKSGSGKTSMRSIIFANYIARDTPRIGATIU   PN
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SPITSDKTSQERDRGGGGCGVGGGGSCSSVGGASGGERSVDRP. SPSQRLMSTHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQ SPSQRLMSTHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQ STPSLYPPPRR  AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESS. DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAG YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRI NGKPKKVRRPRTIYSSFQLAALQRRFQKTQYLALPERAELAAS GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNS QSPAVWEPQGSSRSLSHPHAHPPTSNQSPASSYLENSASWY. AASSINSHLPPPGSLQHPLALASGTLY KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNI DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKOMM YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  6051 566 1718 KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATIU
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AMTGVFDRRUPSIRSGDFQAPFQTSAAMHHPSQESPTLPESS. DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQTHGVNGSAG YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTE PEVRI NGKPKKVRKPRTIYSSFQLAALQREFQKTQYLALPERAELAAS GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNS QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY. AASSINSHLPPPGSLQHPLALASGTLY  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSSLSTYSLVDSVGUTKTFDVEHSHVRFLGNLVLNI DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKOMF RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIR FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAG YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTE PEVRI NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAAI GLTQTQVKIWFQNKRSKI KKIMKNGEMPPEHSPSSDPMACNS QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY AASSINSHLPPPGSLQHPLALASGTLY  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSPDAKIFCLVHKMDLVQEDQRDLIFKEREDDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
PAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTE PEVRI NGKPKKVRKPRTIYSS FQLAALQREFQKTQYLALPERAELAAN GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSDPMACKY QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY AASSINSHLPPPGSLQHPLALASGTLY  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNI DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMI YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIR FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
NGKPKKVRRPTIYSSFQLAALQRRFQKTQYLALPERAELAAS GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNS QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY AASSINSHLPPPGSLQHPLALAGGTLY  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWSPNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNI DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKOMM YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTPRLGATII
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GSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWY: AASSINSHLPPPGSLQHPLALAGGTLY  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWI PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGAVII RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNI DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDME YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR  KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATTI
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PNTAMKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATII RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFIGNLVLIM DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMI YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMI YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
YQSCLEATLQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDI RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR GOS1 566 1718 KGLERTCCAMEESDSEKTTEKENLG?RMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
RISRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLF FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6051 566 1718 KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6051 566 1718 KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWV PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRPLGATII
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PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRIGATTI
RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNL
DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEXDMH
YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDL
RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLR
FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIK FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS
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PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATIL
RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFI.GNLAU.NI.
DCGGQDTFMENYFTSQRDNIFRNVEVLIYVPDVESRELEKDMU
YQSCLEAILQNSPDAKIFCLVHKMDLVOEDORDIJFKERFERDIJ
RLSRPLECSCFRTSIWDETLYKAWSSIVYOLIPNVOOLEMNI.D
FAETTEADEVLLFERATFLVISHYOCKEORDAHRFEKTSNTTV
FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPS
PSAATLINIRNARKHFEKLERVDGPKQCLLMR  1704 KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPI
HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPC
HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSN
LKKSQLGFLNVTNYCHLAHELRLSCMERKKVOTRSMDDSAT.AST
RFNLILADTNSDRLFTVNDVTVGGSKYGI INLOSLKTPTI.KVFN
HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLARTDGCDTLL
PASLFVNSHPAGIDRPG\MLCSFRTPGANSCAWSINTONNICES
TGLSRRVLLTNVVTGHRQSFGTNSDVLAOOFALMAPILENGCDS
GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILODEOVIMAST
MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG
QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS
1 1054 FPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
DMTTEEIDALVHREIISHNAYPSPLGYGGPPKSVCTSVNNVLCH
GI?DSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHONGFOVCPHF
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Deginning   No:   uncleotide   location   corresponding   location   corresponding   to first   smin acid   smin	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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corxesponding to first mino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence control of the control of amino acid sequence se		•		Glutamic Acid, F=Phenylalanine, G=Glycine,
amino acid residue of amino acid residue of amino acid amino acid amino acid acquence  2364  2364  2364  2364  2364  2364  2364  2366  236	1	1		H=Histidine, I=Isoleucine, K=Lysine,
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sequence    Codon, /=possible nucleotide deletion,	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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6056  43  3358  SGGGPVNVRSDQLSPSQLSQSISQISQISQRFRISSLPPPSBRA LAPPRAPDTALTIMEVAPVSPSDNPSQLSPSREPRSEPREFNEN YLAYMESKGAHRAGLAKVIPPKEMKPRQCYDDIDMLIPAPIQO MVTQGGLFTQYNIQKKAMTVKFFRQLANSGKYCTBYTLDVEDL ERKYWKALTYAPIYGADINGSIYDERGDEWNIARIATVLDVVE EECCISIEGVNTPYLYRGMKKTFAMHTEDDDLYSINVLHFGEBP KSMYAIPPBEGRELERIAQGFPFSSGQCDAFLRHAMTLISPSV LKKYGIPFDKITQRAGSFMITFPYGYHAGNHGHGNCABSTMFAT VRHIDYGKVAKLCTCRAWNYKISMIPHYRRFODRYGUKGGKD IYTIDHTKFTPASTPEVKANLQRRKVVKASRSFQCARSTSKRP KADEEESVSDVDGAGVVPNDSVTDLHYFKRFODRYGUKGGKD IYTIDHTKFTPASTPEVKANLQRRKVVKASRSFQCARSTSKRP KADEEESVSDVDGAGVVPNDSVTDLHSVEKSEGAAVKLRNTEA SSEESSASRMOVSONLSDHIKLSGRSCLSTSVTEDIKTEDIKX YAYKSVPSISSEADDSIPLSTGYKEPKSSDPSELSWYKSPBSCS SVAESMGVLTGGESDVEHGMGLBPGEIBAVPSGERRSFKVPS IABGEMKTSKSWRIPLSRPPARSDFSLESWKSSPBSCS COLGGHLGARCKRNAMTAGCCLANTAVARMERICAT CTILMPYHKPDSSMEEMDARWETKLJGEVVTSGKKTKPLIPEMCF IYSEENIESTSPNAFLEBEDTSLLISCKCVVVHASCKTFPLIPEMCF IYSEENIESTSPNAFLEBEDTSLLISCKCVVVHASCKTFPLIPEMCF IYSEENIESTSPNAFLEBEDTSLLISCKCVVVHASCKTFPLIPEMCF IYSEENIESTSPNAFLEBEDTSLLISCKCVVVHASCKTFPLIPEMCF IYSEENIESTSPNAFLEBEDTSLLISCKCVVVHASCKTFPLIPEMCF IYSEENIESTSPNAFLEBOTSLLISCKCTVVHAVATGTFSW AVPEVRSKACEKVISVGTUTTKHRATTYSCCVMAVTSGTFVEV MFDOGSFSRDTFPSDIVSGNQGCTVILTFRHATTYSCCVMAVTSGTFVEV MFDOGSFSRDTFPSDIVSDQAGCTTLTGRGALKGTKKMKMAHMACA AKYFGSNIAMMYQUEFEDSQLAMKGEDIVTLDEHKVVAGA CCIQCSYGCPASFHYTCAHAAGVI,MEDDWPYVWNITCPBHKV NAKKGEKLISTVQUEFEDSQLAMKGEDIVTLDEHKRVKNGGA CIQCSYGCPASFHYTCAHAAGVI,MEDDWPYVWNITCPBHKV NAKGCHLGTCVVMSLSSPHVSQAGCTTYLGFWISKRSQCNIF LSGTY  FVARLKEGEGGGLGPFKEKGRARGERRKMMLTRCCFVPLVQ GSLYLVICGODDGPGSEDPERDDHEGGPRPRVPRKRGHTSPKS FVARLKEGEGGGLGPFKEKGRARGERRKMMLTRCCFVPLVQ GSLYLVICGODDGPGSEDPERDDHEGGPRPRVPRKRGHTSPKS FVARLKEGGEGGLGPFKEKGRARGERRRKMMLTRCCFVPLVQ GSLYLVICGODDGPGSEDPERDDHEGGPRPRVPRKRGHTSPKS FVARLKEGGEGGLGPFVCGCTFTLASAKAFT TSLFTHDPAKICSBDHAGSSATTSCSQPFKVVCVYIAFYSTDTR LVQKVCPDYNYHSDTPYYPSG  HPLPSASLGLPSVSLGVSLCVKSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFGVGATTLUCHAAGPEGSGELLTFCAASVKAL PSPVTLSQLGGLHFGGEHSSKVQELLEGGVCESVERVRRSR RLFTDTFGTGVGVKTARMYRRGLKTHCVRGAPSPKGLECTGARSS SREAGFWASLNCTLDPSAS	1	<b>!</b>		
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FVARLKEQEGEGGLGPRKEKGRARGRERRKKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKGHISPKS RPMANSTLIGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDPYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLITHHNTGLSEALBILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP  4 3650 QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	1			
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RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFMC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLITHNTGLSEALBILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP  4 0059 QODFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEJAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHWQAHKKWK	1	· ·	-55	
WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFMC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQCKAGBP SREAGPWASLNCTLDPSASTP  2 3650 QQDFSSLADLTDHRAHRCPGDGDDDPQLSWVASSFSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	j i	1		
ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVVSSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERMAAAPPGCTPPALLD ISMLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	] 1			
TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1  986  HPLPSASLGLPSVSLGVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERMAAAPPGCTPPALLD ISMLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	i	!		
LVQKVCPDYNYHSDTPYYPSG  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTTFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISMLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	<b>,</b> .	1		
LVQKVCPDYNYHSDTPYYPSG  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTTFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISMLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	]			TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR
6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSMQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLITHNTGLSEALBILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEJAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	L l			
SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISMLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGPEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP QUIGDGCDLGTDHRAHRCPGDGDDDPQLSWVASSFSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	6058	1	986	
VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGPEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QDFESLADLTDHRAHRCPGDGDDDPQLSWVASSFSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	, 1			
ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	i l			
PTPLTHHNTGLSEALEILAEAAGPEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE / RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK				
PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE / RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLORTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK				
RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGBP SREAGPWASLNCTLDPSASTP  QDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLPKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	i i			
SREAGPWASLNCTLDPSASTP  6059 2 3650 QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK		l		
SREAGPWASLNCTLDPSASTP  6059 2 3650 QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	1	j		RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP
QDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK				
QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	6059	2	3650	
SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK	1	j		
RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK		•		
	. I	1		
EHLAKSEKEAKKDDFMCDYCEDTFSOTEELEKHVLTRHPOLSEK	İ			
	I			EHLAKSEKEAKKODFMCDYCEDTFSQTEELEKHVLTRHPQLSEK

SEO	Predicted	1 50. 32 1 3 3	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	i i	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	}		ADLQCIHCPEVFVDENTLLAHIHQAHANQKHXCPMCPE\QFSSV
1	j		\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
· {	1		ERGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
1			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
ŀ			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
	ŀ		SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
1			VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
}	Į.		KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
ŀ			ECMPPEROTUL VILLE I I DVO I GROGVER PROPERTY OF THE
1	<b>i</b> .		FSNFESFQTHLXLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
Ĭ	l i		YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
1			VHVKHSHLGNPAKAHKCIFCGETFSTEVELQCHITTHSKKYNCK
1	Į į		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
1	į l		PADLOGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
	i !		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
1	į į	•	NGLREHLOTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
			TGTCRICKMPLQSEEEFIEHCCMHPDLRNSLTGFRCVVCMQTVT
}	i l		STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
i	<b>!</b>		SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
	lj		PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM
	!		FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
<u> </u>			VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
ı			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
ł			DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
Í			LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
ŀ	l I		HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV
· ·	•		ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
!			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
ļ	1 1		SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
İ	i i		EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
			EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
	l į		QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
			GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
1	i	-	LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
1	i i		LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
1	į		VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
			ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
	1		VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
	İ		SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
]			HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
			RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
1			PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
] [			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
, ,			LALHRRRHMLV
6062	71	1079	
		10/3	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
] [	<b>!</b>		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1	Ì		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1	I		EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
j	ŀ		LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE
1 1	ļ.		EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
[ ]	· 1		INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
6053			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
j J	}		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1 1	1		TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
]	1	j	EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
<u> </u>			LBICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE

SEO	Predicted	Predicted end	I Draino and a second s
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
ł	ļ	1	INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6064	913	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
		İ	TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
ı		ļ	AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV
1	i	}	LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
			SSG\KRKEGIIHTLIVDNREIPEIAS
6065	1153	641	MSVRVARVANVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
1	1	}	AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
ł	l		ELYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
6066		3753	EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
0006	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
	1		EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
i			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
1	i	Į.	QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA
1			ISWPŁLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR FSWSHQFDLSDNFISOTLNIVTWSPCGOYLAAGSINGLIIVWNV
ľ	1		
l .			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
1	1	İ	
	Į	į	SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
1			GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKPFQS GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT
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ŀ	1	ĺ	EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF
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1		1	TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
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1			PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL
I			GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV
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6074  168  1110  PGARCMATELQCPDSMPCHRQQVNSASTPSPEQLRPGDLILDHA GGNRASRAKVILLTGYAHSSLPAELDGSGACGSSLINSEGNGGSG DSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTI IR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVS IMRSGEAMEQGIRDCCRSIRIGKILIQSDET QRAKVYTAKFPPDIVRRKVILMYPILQTG\NTVIEAVKVILEHG VQBSVIILLSIFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD  1091  PPTQQPGEVEHH\YGYVPILGNKTLFSRCHQCVIVSSSSHLLGT KLGGEIERAECTIRNNDAPTTGYSADVGNKTTYRVVAHSSVRVV LRRPQEFVNRTFFTVFIFMGPPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRMCFDDLFRGETGKDREKSHSMLSTGWFTMVIA VELCDHVHVYGMVPDNYCSORPRLQRMPHHYSEVKGPDECVTYI QNEHSRKGNHHRFITEKRUPSSWAQLYGITFSHPSWT  107  HPSPTERPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTELSMHWVQAPGKGLEMMGAFDPED GFTIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDIWGQGTMVTVSAPTKAPDVFPIISCRHEKDNSPVV LACLITGYHFTSV\TVTMYMGTOSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV PTAQPGAEGSLAKATTAPATTRNTGRGEEKKKEKEEGGEERE TKTPECPSHTQPILGVYLLTPAVQDLMLRDKATTCPVVGSDLKD AHLTWEVAGKVPTGGVEEGLIERHSNGSQSQHSRLTLFRSLMNA GTSVTCTLMHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWILCEVSGFSPPNILLMILEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL BVSYVTDHGPMK  6077  3687  1268  LIPPMNIQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIO AGPNCGWCTNSTFILQEMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVILRRSGEP OTFTLKFKRAEDVPIDLYYM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PPSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA	l i		500	I-VEATKKVKDHRGTTPNVGWLPOLLALDPDTPOCTPA
GGRRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG DSSYDAPAGNSFLEDCESRQIGAQLKLLPMNDQIRELGTIIR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVSIMRSGEAMEGGLADCCRSIRIGKILIQSDEET QRAKVYJAKFPPDIYRKVLLMYPILQTG\NTVIEAVKVLIEHG VQPSVIILLSSFSTPHGAKSIIQEPPETTILTTEVHPVAPPHFG QKYFGTD PPTCOPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP NMERYAVSPGRNNGPDLFRGETEGKDREKSHSWLSTGWFTMVIA VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVPSSWAQLYGITFSHPSWT  107 HPSPTEAPRVQHLTWCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTELSHHWVRQAPGKGLEWMGAPDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYVCATD HGDYAFPIWGGGTMVTVSSAPTKAPDVPPIISGCRHPKUNSPVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQNRQGEYKCVVQHTASKSKKEIFRWPSSPKAQASSV PFTAQPQAGSGLAKATTAPATTRNTGRGEEKKKEKEKEGEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEKLERHSNOSSQSHSRLTLRRSLWNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNILLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK  6077 3687 1268 LLPDMNLQPIFWIGGISSVCCVPAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGWPTSARCDDLEALKKKGCPPDDIENER GSKDIKKNIVTNRSKGTAEKUKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKODLENVKSLGTDLMN EMRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGGVFNELVCKQRISGNLDSPEGGFDAIMQVA	6074	168	1110	
DSSSYDAPAGNSFLEDCELSRQIGAQLKILIPMNDQIRELQTIIR DKTARRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKPEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET QRARVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAWKVLIEHG VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD  1091 PPTCOPQEVEHH\YGVVPILGNKTLPSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP NMERAYAVSPGRNRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA VELCDHVHVYGMVPNYCSQPRRLQRMPYHYYEPKGPBCVTYI QNEHSRKGNHHRFITEKRVVSSWAQLYGITFSHPSWT  107 HPSPTEAPRVORLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV KKPGASVKVSCKVSGYTLTELSHHWVRQAPGKGLEMMGAPDPED GETIYAQKFQGRVINTTEDTSTDTAYMELSSLRSEDTAVYVATD HGDYAFDIWGQSTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHFTSV\TVTWWGTOSQA\QRTFPEIQRRGSYYMTS SQLSTFLQQNRQGEYKCVVQHTASKSKKEIFRWPSSPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEREQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD ANLINEVAGKVPTGGGVEGLLEHRINSGSQGHSRTLPLRSLMNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDRPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFKA\MSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK  6077 3687 1268 LLPDMMLQPIFWIGGISSVCCVVFAQTDENRCLKANAKSGGECIQ AGGNCGWCTNSTFIQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKTNTNSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGGVFNELVGKQRISGNLDSPEGGFDAIMQVA				GGNRASRAKVIILITGYAHSSI.DAFI.DSGACGGSSI.MSFGNSGGG
DKYASRGDPMFSADRLIRLVVEEGLNQLPYRECMYTTPTGYKYE GVKPEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET QRAKVYYAKFPPDIJRRKVLLMYPILQTG\NTVIEAVKVLIEHG VQBSVIILLSLFSTPHGAKSIIQEPPEITILITEVHPVAPTHFG QKYFGTD QKYFGTD  DPTCOPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTFETVFIFWGPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRNRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI QNEHSRKGNHRRFITERKVPSSWADLYGITFSHPSWT  6076  1721  107  HPSPTEAPRVQHLTMCTWRILFLVAAATGTHAQVQLVQSGAEV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEMMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDLWGGTMVTVSAPTKAPDVFPIISGCRHPKDNSFVV LACLITGYHPTSV\TVTWYMGTOSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQNRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEKKKEKKEKEEQEERE TKTPECPSHTQBLYVLLTPAVQDLWLRDKATFTCPVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSGSQHSRLTLERSLWMA GTSVTCTILMPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFMA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASSGL EVSYVTDHGPMK  1268  LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECTQ AGPNCGWCTNSTFLQEMPTSARCDDLEALKKKGCPPDDIENDR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSFEGGEDAIMQVA				DSSSYDAPAGNSFI.EDCELSROTGAOLKI.PMNDOTPFI.OTTTP
GVKFEKGNCGVSIMRSGEAMEGGLRDCCRSIRIGKILIQSDEET QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG VQPSVIILLSLESTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD  1091 PPTCQPQEVEHH\YGYVPILGNKTLFSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRNRQFDDLFRGETGKNEKSHSWLSTGWFTMVIA VELCDHHVYGNVPPNVCSQRPRLQRMYPHYYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT  107 HPSPTEAPRVQBLIMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTITELSMHWVRQAPGKGLEMMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFPIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQNRGGYKCVVQHTASKSKKEIFRWESSFKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEKKKEKKEKEEQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD ARILTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKK\ RSTTFMA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLINASRSL EVSYVTDHGPMK  1268 LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECTQ GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP GTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS	<b>!</b> i	•		DKTASRGDFMFSADRLIRLVVEEGLNOLPYKECMVTTPTCVKVE
ORAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKULIEHG VQPSVIILLSLFSTPHGAKSIIQEFPEITILITEVHPVAPTHFG QKYFGTD  1091 PPTCQPQEVEHH\YGYVPILGNKTLFSRCHQCVIVSSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGMKTTVRVVAHSSVFRV LRRPQEFVNRTPTVFIFMGPPSKMQKPQGSLVRVIQRAGLVFP MMEAYAVSPGRMRQFDDLFRGETGKDREKSHSKLSTGMFTMVIA VELCDHHWYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVPSSWAQLYGITFSHPSWT HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDIWGQGTWTVVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWMGTQSQA\QRTFFEIQRRDSYYMTS SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWESPRAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGEEKKKEKEKEGQEERE TRTPECCSHTQPLGVYLLTPAVQDLWLRDKATTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLDRSLWNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSINLLASSDPPE A\ASSWLLCEVSGSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK  6077 3687 1268 LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIEMPR GSKDIKKNKNTVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTINKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA	1			GVKFEKGNCGVSIMRSGEAMEOGLRDCCRSIRIGKILIOSDEET
VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD  PPTCOPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLGT KLGPEIERAECTIRNNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIFWGPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRMRQFDLFRGETGKDREKSHSWLSTGWFTMVIA VELCCHVHVYGMVPPNYCSQRPRLQRMYHYYYEPKGPDECVTYI QNEHSRKGNHHRFITEKRVPSSWAQLYGITFSHPSWT  6076  1721  107  HPSPTEAPRVOHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEMMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQWRQGEYKCVVQHTASKSKEIFRWPESPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGEEKKKEKEKEQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCPVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSQSGHSRLTLPRSLMNA GTSVTCTILNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK  LUPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYIM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLINKGEVFRELVGKQRISGMLDSPEGGFDAIMQVA	<b>!</b>			QRAKVYYAKFPPDIYRRKVLLMYPILOTG\NTVIEAVKVLIEHG
OKYFGTD  OKYFGTD  OKYFGTD  OKYFGTD  OKYFGTD  OKTOPOGEVEHH\YGYVPILGNKTLFSRCHQCVIVSSSHLLGT  KLGPEIERAECTIRNMDAPTTGYSADVGNKTTYRVVAHSSVFRV  LRRPQEFVNRTFETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP  NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA  VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI  QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT  OMEHSRKCHHRFITEKRVFSSWAQLYGITFSHPSWT  OKETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD  HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV  KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEMMGAFDPED  GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD  HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHFKDNSFVV  LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS  SQLSTPLQQNRQGEYKCVVQHTASKSKKEIFRWPESFKAQASSV  PTAQPQAEGSLAKATTAPATTRNTGRGEEKKKEKKEEGEERE  TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD  ARLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLMNA  GTSVTCTILNHPSLPPQRLMALREPAAQAPVKLSLNILLASSDPPE  A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\  RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL  EVSYVTTHGPMK  OKSTITEMA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL  EVSYVTTHGPMK  LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ  AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR  GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP  QTFTLKFKRAEDYPIDLYYIM\DLSYSMKDDLENVKSLGTDLMN  EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS  PFSYKNVLSLINKGEVFRELVGKQRISGMLDSPEGGFDAIMQVA	1			
KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA VELCHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI QNEHSRKGMHRRFITERRVFSSWAQLYGITFSHPSWT  6076 1721 107 HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPRD GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEFKKKEKEKEGQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLINLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK  6077 3687 1268 LLPDMMLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA	·			
KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNTFFETVFIFWCPPSKMOKPQGSLVRVIQRAGLVFP NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI ONEHSRKGNHRFITEKRVPSSWAQLYGITFSHPSWT  107 HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGABV KKPGASVKVSCKVSGYTLTBLSMWWRQAPGKGLEWMGAFDPED GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD HGBYAFDIWGGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV LACLITGYHPTSV\TVTWYMGTQSQAQRTFPEIQRRDSYVMTS SQLSTPLQQDWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEGEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA GTSVTCTLTHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTFFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGBVFNELVGKQRISGNLDSPEGGFDAIMQVA	6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHOCVIVSSSSHLLGT
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AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA				EVSYVTDHGPMK
AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR GSKDIKKNKNVTNRSKGTAEKLRPEDITQIQPQQLVI.RLRSGEP QTFLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVCKQRISGNLDSPEGGFDAIMQVA	6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIO
GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA				
QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA	1			GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA				
PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA	· I	•		
		1		
	<u> </u>			

WO 01/53312 PCT/US00/34263

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	•	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	4	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
•	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
		Ī	LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
	Ī	ļ	GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
1	1		
ł		<b>†</b>	CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
1		ļ	EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
<b>.</b>		İ	FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
1	ļ	1	NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
ł	1		NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
1		ŀ	FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
1		l	VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
į.	ļ	l	IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
1	l	ľ	KSAVTTVVNPKYEGK
6078	1426	180	_l
1	1	1	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
	1		GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
1	1		NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
1			GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
1			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
	i		LAVMQAYDPEINKLNTILQEQRMAFNIAEAFKDVSEPIVFLQQM
	1		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1		Ī	LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
ļ.	f	į	FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
1	l		RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1	1	111	
1			GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
1	İ		LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
1	Į.	i	NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
1	(		HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFL
İ	1		LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
	İ		YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
i	İ		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
1	1	i	MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1	ĺ		VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
İ	1		ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWKRQK
			HSS
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
1	_	11.33	
l			TLRQQCLDSGVLFKDPEFPACPSALGYXDLGPGSPQTQGIIWKR
I			PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
I			YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
I			LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
[	1		EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
j			SAAEAEAITSQKLVKSHAYSVTGVEEVNFQGHPEKLIRLRNPWG
1			EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
1.			QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
1			PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
1			SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
j	Ì		TQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
1			
ì	İ		KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
ļ .			PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
1	İ	,	GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
			ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
1			PESVGOPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
			LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
			LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
[			
			EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
1			KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
]			KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
<b>L</b>			FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
			<u> </u>

SEQ	Predicted	15.71	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	\A-Aidmine, C=CVSCelne D-Aenartic Acid n
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		<pre>( \=possible nucleotide insertion)</pre>
	<u> </u>		DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEVISKOAVA
	1		SEVMGPVEAAPEYRVIVDANNLTVEIENELNITHKETPDKVCVP
I	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLOOTI.TNATIM
1	ĺ	1	VVSVIASTTQGQQLSEEELERLEEACDMALEI.NASKHDTVEVVE
1			SKMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMILG
			AQRKTLSGFSSTSVLPHTGYIYHSDIVOSLPPTPPDFSVAD\DI
- 1			RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
	•		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
ĺ			ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
L	ł		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
6084	1865	309	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPATE
1	1		DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
			FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
- [			VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
	'		SRMSFIAPNLSIIIGASTAAKINGVAGGLTNISKMPACNIMIIG
1			AQRKTLSGFSSTSVLPHTGYIYHSDIVOSLPPTPPPFSVAP\n;
	1		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDETERKEDVW
1			QEPPPVKQVKPLPAPLDGORKKRGGRRYRKMKERICI.TETD\VO
	1		ANKMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVROTOVNEATVA
1	1		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTDLOGLET
6085	2	1456	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
1		÷150	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
1	1		GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1	i _1		DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDEEDEEER
ļ			KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALR
			RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
	l		VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW
.	}		SPTENTVFASCSADASIRIWDIRAAPSKACMITTATAHDGDVARU
1 1			I SWSRREPFLLSGGDDGALKIWDLROFKSGSPVATEKOHVA DVm
			SVEWHPQDSGVFAASGADHOITOWDLG/TVERDPFAGDURADDC
1 .	1	j	LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFPT
6086	2419	1357	ISV
1 1		1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1 1	1		YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
1 1	1	•	NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV
1 1	1		FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
] ]		İ	HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
1 1			LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG TUHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
] ]		ļ	CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
<b></b>			DDKL DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
1 1		į	LVAVIYLVSIVVAVPLCVWELOKLEVGIHTKAWFTAGTFLTTT
] [	1	ł	PISLWVILQHLVHYTOPELOKPITRILWMVPTVGIDGWIAIWWD
	į		GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYDNIVLTLEDVD
1	ļ	1	QQKHFPPLCCCPPWAMGEVLLFRCKLGVLOYTVVRPFTTTVATT
1	į.	1	CELLGIYDEGNFSFSNAWTYLVIINNMSOLFAMYCIJI.FVVIIV
	į į	i i	EELSPIQPVGKFLCVKLVVFVSFWOAVVIALLVKVCVTSEKUTW
j l		. [	EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFGVKDVIOGADD
1 . 1	ŀ		GSCFDSFLAMWDVSDIRDDISEOVRHVGRTVRGHPRKKT.FDFDA
1 1		1.	DQNEHTSLLSSSSQDAISIASSMPPSPMGHYOGFGHTVTPOTTP
6088	1684		TTAKISDEILSDTIGEKKEPSDKSVDS
· `	2001	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
]	1	1.	LERQRLLRCPPPPVRRSEKPNWDYHAETOAFCHPLOPNESI DI I
ĺ	İ	. [ ]	KTAFVNSCYIKSEEAKROOLGIEKEAVIINIKSNOFISEOGTER
[ [	1.	{ :	SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNI.AUR
<u> </u>		1 ?	QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
		<u></u>	IQMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A

SEQ	Predicted	Predicted end	I Amires and discount and the second
ID	beginning	nuclectide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isolcucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
	f	<del></del>	PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
1	1		TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
1			PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
1	i		LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
1	1		PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
	1		QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
1			LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
1		1	VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLOKDD
1			KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
1	l .	1	DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
1	1		LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
	ł		LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
}		1	DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
1	[	l	AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
Į			REYEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES
			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
1	Į	1	EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
1		İ	TFNTTVDIKLKOWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
1	)	ł	EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI
		<u>}</u>	SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
	į	]	KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
		1	SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
			FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
1			KEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
6090	194	1560	ALHQEK
		1360	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
		Ì	FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
		}	LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
			P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
		ĺ	CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
İ			SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL
i l			PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
		1	
		l .	LVKESKNVYKAVGHVNVATPSDVSHEDEHERESVDI.DTI.NTI.I.
]			LVKESKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHOTISLALILFSNYYAFFKLLRDRL
			LVKESKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDHRFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTFWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDHRFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVOLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKIGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDERFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDURFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSGGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDHRFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAEEASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDHRFS SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTFWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRTPSTSKPGSAFSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDIRFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSGGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDRRFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYXVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAEASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPJSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGGEPPRGQ LQPSRPTARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD/RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRFATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPNKGLVQVTTHRLCRLPSSRAHLPTKEA KVSANKLSKTSQQPSDAGSRPLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDIRFS  SSTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWKKYSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAFSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHYYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDPPADHAVRPLHGARGGQPPVPQQHVLERQVQLSGGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYXVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
6091	3279	412	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDRRFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGQQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYXVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPPLGAKCKKKHTLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARRSVSASHG PRKPSASQRPTRQTPSSAALITAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS
			LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDERFS  SSRTREMEEKEILRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLIGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVCHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTENKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQPSDAGSRPLLRTGRLDPAGSCSRLASRAVQ RSLAIIRQARQRREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHYSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTOKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSSSPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6091	3279	412 3190	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VIGKAYSYSASPQRDLDRRFS  SSTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG PSDFPADHAVRPLHGARGQQPPVPQQHVLERQVQLSQGQNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRWVKSVGSVGDSPRE PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYXVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSQQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKREYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPPLGAKCKKKHTLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARRSVSASHG PRKPSASQRPTRQTPSSAALITAAAVAAPPHCPGGSASPSSSKAS SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S≈Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
ļ	Sequence		VIOLIKTNKKHIHSRSTLECAYRTHLVAGIGFYOHLLLYIOSHY
1			QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
1			LGDLSRYONELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
1			, , , , , , , , , , , , , , , , , , , ,
1	'		AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
	·		LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
1			TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
1		)	LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
1		į	RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
			PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
1			SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
		ĺ	EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
		ł	MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
	1	1	PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
1		}	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
1	,		LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
		i	DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
1		1	VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
}		1	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
1			VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
}		<b>]</b> .	VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
1			MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
			KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
1			PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
		1	PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
1			VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
1			ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
1 1			YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
, ,			ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
6094			IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
}		1	VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
1 1			FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
			RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
[ ]			QAHVDFEAMLRQHRLSEBERRRQQQEEDEQETAALLEEARKRRL
{			LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
1			GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
F005		1500	GQPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
			GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
} i			YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
1 1		,	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
L		<u> </u>	EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

			<u>'</u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMOONPAGEL
	1		EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR
		1	VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
	1	Į	FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
	ł		CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
		ì	MGFYIHSCPKMKYKGOYRPSDLLCPETYVWVPIEQCLPSLENSK
			YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS
	Į.	Ī	EEAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLI
. *****		) 3/3	QEKAIPLALEGKOLLARARTGSGKTAAYAIPMLQLLLHRKATGP
			1 "
	j		VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA
			EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV
			DEADLLFSFGFEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
		1	LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
			LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSR
	l	1	CHIISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP
	j	1	EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
	Í		LTFVLPTEQFHLGKIEELLSGENRGPILLPYQFRMEEIEGFRYR
	ŀ	1	CRDAMRSVTKQAIREARLKEIKEELLHSEKLKTYFEDNPR\DLQ
	1	1	LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL
		<u>l                                      </u>	PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
6097	1,673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPP
	1	1	PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
	ļ	1	YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL
	Į.		ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ
	1	1	LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL
	1	1	RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS
	1	1	RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
-	1	i	DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
	ł	İ	RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
	1	}	PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
	1	1	VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET
	1	1	QPPPSLPGTPO0
6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
	1	1	EGKIFKNWGTQTEKEDTSNINPROTETSVNASRSPEKCAQORQK
		}	RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLORTNPRKOL
	i		\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
		}	TAWEKNKSVSYEQCKPVSVTPQGNDFKYTAKIRTLAETERFF\D
	i	l .	ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6099	168	1074	
0033	100	10/4	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
	1		EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
	1	1	RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
	I		NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	1	1	\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
	1	1	TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
		<u> </u>	ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
		}	QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
	1		RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
			VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN
	ļ		VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP
	1	1	SASQRNSRDIGSNSGCC
6101	1	1399	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
	1		GKNVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
	1		AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF
	-l	<del></del>	The state of the s

C 020	I Dona 27 at a 5		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
Ŧ	amino acid	scquence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	bequeinee	<u> </u>	\=possible nucleotide insertion)
1			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
l			KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
	<b>f</b> .		LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1		1	QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
	ł		AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
1	1		MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1	i	ł	G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
6102	70	2415	FIGANESVSLKLTEPKDLLIFRACCLL
1	1	,412	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
1	•		LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
1			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
1	1		KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
	,		HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
1	1		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
1	1		PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
ł	1		HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
i	i i		KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
1			GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
1			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
1	1		LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
Í			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
	1	•	AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
1	<b>i</b>		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
	<u>[</u>		KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
	1		ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
	į		ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
1 .	į į		PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
1		•	MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
i :	i		RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
<b>}</b>			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATOGPGMVVG
1 1			DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKOTFORVFT
			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNOHNAPIPOGG\RG
			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTOIONIAASFD
į l	1		QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCOKFGEYHK
j 1	1		DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
j 1	1		DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
! !	j		ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
1 6104 1			GAPILTDDVSLQVFMDHLKKLAVSSAA
	124	72.7	
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
6104	124	732	KLPQSRPGFPSPPWGPALAVQ\AQPCLOSOOMIPVEVKRI/RSI.
6104	124	732	KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPOKLIKVKNNIDVCPECGH
2104	124	732	KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	124	732 989	KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEG9PFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEMPWQVSIORNGSHF
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEG9FFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGAROLVOPGPHAM
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGFFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYGGTASSADVALVELEAPVPFTNYILPVCLPD PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
	·		KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL YTGETPSEQDQGKRIIERDRKRPSWFTQN PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Sequence	\=possible nucleotide insertion)
	sequence		
			LQVQPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
		Í	AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPQG
1		1	WSRARHQPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV
<u>[</u>	ţ	1	LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
ļ	}	1	IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
<b>,</b>	i .	į.	GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
ł	1 -	l .	STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
	}	1	HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
		1	GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV
		1	
L		<b>.</b>	LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
6107	623	168	SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE
I			DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
1	A .		KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
1	ì	1	RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
	_		CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
l	1	1	YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
1	1		LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
1	1	1	WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
ì	1	1	
1		l .	FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
Į.	1	1	ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
	1	1	AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL
	1	1	GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE
1	1	1	PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
	1	1	PVTQPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
1 5255	_		LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFF
1	1	1	MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVO
1	1	1 -	RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN
1		1	HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
İ			SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
1		1	
1			GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
l		1	SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
Į.			QQSSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT
1			YDPNBPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
1			GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGGGAFSQ
1	1		ARSSSTGSSSSTGGGGGGESQPSPLALI.AATCSRIESPNENSNNS
1	1		QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG
1			SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
1	1.		NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
1	1		IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
ŀ	1		VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS
I		1	
1			GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
}	1		SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE
1	1	1	Q\NQQTQAAPKSI.SRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA
I	1	j.	ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
1	ı	ì	VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
1		1	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
· I	1	1	GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTRREACT
i	1	1	CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
Ì	I		HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
1	1	1	RFMRSDHLSKHIKTHONKKGGPGVALSVGTLPLDSGAGSEGSGT
1	1	1	ATPSALITINMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
1		1	
L	_l	<u> </u>	SANGF

SEO	Predicted		
ID	beginning	Predicted end	were sequent containing signal passida
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid E
	location	location	Grutamic Acid, F=Phenylalanine, G=Glycine
i	corresponding	corresponding	H=H1stidine, I=Isoleucine, K=Lvsine
ĺ	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid		P=Proline, Q=Glutamine, R=Arginine
i	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown, +-cross
	sequence	sequence	Codon, /=possible nucleotide deletion
6111	1637		\=possible nucleotide insertion)
	103/	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
l l			SVEAVARLKRSRLKVRFCTNESOKSRAELVGOLORLGFDISEOF
	]		VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDOIDTS/STDNC
į	1		VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYVKETSG
1	1	1	LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALOAIGVERHO
1	1		AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG
6112	<del> </del>		YVDNLAEAVDLLLQHADK
6113	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
0113	1779	567	WEGRSWAACGVN_QGAWGERSGVRASEAESPGKRADVSWWSPOT.
1			ETMVDHLANTEINSQRIAAVESCFGASGOPLALPGRVLLGEGVL
			TKECKKAKPRIFFLFNDILVYGSIVLNKKYRSOHIIPLEEUT
			LELLPETLQAKNRWMIKTAKKSPVVSAASATEROEWISHIEECV
1			RRQLRATGRPA\STEHAAPWIPDKATDICMRCTOTRFSALTERH
1			HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAOORK
	ĺ	•	EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATG
			PAAWSSTPRGWPGLPSTADPRPAEHLSPSOLHCPGPOFGSSRSC
			PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
6114	818		KPQNTHRSW
"""	97.0	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
			RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\ PAROVOC
1 1			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPAPTDDAGP
1 1			HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSOVT
6115	324		GRPQWFLRGLVLFSL
	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
6116	595	1430	SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
	3,3	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKBEEDESYTPVQ
1			AARPQTLNRPGQELFRQLFRQLRYHESSGPLETLSRLRELCRWW
1	. 1		LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
1 1	1		WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
1 1	1		ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE
1 1	ļ		GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
6117	1433	222	LYRDVMLENYRNMASLGK
1		244	VGVPSPAPPCSWBVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
1			GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA
1			SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV
]	į.		NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
1	1		VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN
1 . 1	Ī		TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
] 1	]		\EQLKQI\PTHDYQKGDQYDVCAICLDBYEDGDKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDB
] [	1	}	GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
L		1	SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
1	1		KEKEKETOKEXICE KODERGINDANI MONITORIA MERGKVKK
1 1	1	1	KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
1. 1	ļ	İ	NKQ1LVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
			DSQMEFLBIGGSKPFRSYWEMYLSN/NDSLARSFSVGFKQDSQP
1 1		[	TTWKAKKYI HOL TAANDU DI HUMAYYODI WAANAY TOO TOO TOO TOO TOO TOO TOO TOO TOO TO
	ļ		ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA
6119	1217	462	
			DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNTSSREGDPUNTSAPPHORDERUGDUNDTLDVGT
( )			LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR
1			QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR
	1	1	DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
		1	GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	1 -	\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAVR
8120	,05	1	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
	<b>[</b>	İ	SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
1	ļ.		ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG
i		4	G\VLPNIQAVLLPKKTESQKDEGANDP
		100	FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
6121	1612	107	FVRAQARGSRQPVRRPLIGAGSRDRCKSCGRHEFBRVERTHIAM
1	1	ł	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
ł	1	į.	KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
1	ł	Į.	VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
1		<b>1</b>	QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
l l	1		MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
1			ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
	l .		TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
		i	PDINIYOLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
1	Ī	1	SHPVRGVOVMKVGKLOLHQGMFPQAMKNLRLAFDIMRVTHGREH
	ł		SLIEDLILLLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT
į	1	1	LCFVSCVNLSYWKFCSVFV
6133	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG
6122	1 2	2324	NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
- [	1	1	QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA
ì	ı	1	GGQITGLTLTPAQQQLLLQQAQAQAQALLAAAVQQHSASQQHSAA
l	ì	1	GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
1	ŧ.	1	GATISASAATPWIQIPESQPIQIAQDIQQDQQDQQQAMADQQI
1	1		LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
1	Į.		LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS
			LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
		1	FSPTTIFRFEALNLSPKNMCKLKPLLEKWLNDAENLSSDSSLSS
}	1	1	PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
1	ſ	i	EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
1		1	IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
ł	1	ì	VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
1	ļ	1	SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
1	1	i	AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
- [	ı	ŀ	GALSPALMSNSTLATIOALASGGSLPITSLDATGNLVFANAGGA
[	i		PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA
1	1	j .	TSTSAESIONSLFTVASASGAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL
0123	1		HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
1	1		ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT
1	1	1	KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
1	1	1	SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
1	1	1	PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
1	l .		EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
			ELMYLKÖKÖNYSSSZÖÖNNG-MDA 19 LUGUKAR UDI 19-2
ì		1 .	DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
			HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
			SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
1			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
1			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
1			PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
			QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
1		1	SDINVRSWCIOESTREVCKADAEIASSLPAAQREAEGYYQKPEK
1			KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAOHFLPAGDSVSONDFPSEAPISLNLSHNICNPMTGNSLPQY
}	1	1	AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
ı			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP
- 1		1	EENMYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
	ŀ	ł	QFPSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
ı	1		ALEGRAVE YRIVOTE KUCHTERONI OF T AND ASSESSMENT

Deginning   nucleotide   location   corresponding to first   nucleotide   location   corresponding to first   nucleotide   corresponding to first   nucleotide   formation   corresponding to first   nucleotide   feet	SEQ	Predicted	Predicted end					
No:   nuclectide				Amino acid segment containing signal peptide				
corresponding to first amino acid amino acid residue of residue of residue of amino acid sequence sequ	NO:			Glutamic Acid P. Phase 2				
to first amino acid sed of amino acid sequence provided and acid sequence states of amino acid sequences of amino acid sequences of amino acid sequences of amino acid sequences of amino acid sequences of		location	corresponding	H=Histidine T-Isolovaine, V. Tarri				
amino acid residue of amino acid sequence control and  sequence control acid seq	1			L=Leucine M=Methionine N=Acrons				
residue of amino acid sequence  Sequence  Sequence  Arryptophan, Y-Tyrosine, X-Daknown, *=Stop Codon, /-possible nucleotide deletion, /-possible nucleotide insertion)  PTTERISO/THMENOA/WVCKEYFFGF/NUPPRAYMNLDIWITTTA  ANNAMPPLANDSYCON  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU ANNAMPPLANDSYCON  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU ANNAMPPLANDSYCON  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU ANNAMPPLANDSYCON  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU ANNAMPPLANDSYCON  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVOLFEITSERGRVYSPGEPLAGTYRVRU  SEEALRLAGERGMERVALFEITSERGRVYSPGERGERLEGERVSPGESLADGE  REGALSSEGTERGE DER APPORTVILLPPISSER SEELLIPPLISTER  HEARD SEEALRLAGERGMERVOLFEITSERGRUPPLISTER SEELLIPPLISTER SEELLIPPLISTER SEELLIPPLISTER SEELLIPPLISTER SEELLIPPLISTERGE SEELLIPPLISTER S	Ì		amino acid	P=Proline, O=Glutamine P-Arginine				
amino acid sequence SEQUENCE SEQU			residue of	S=Serine, T=Threonine, V=Valine				
Sequence    Codon, / - possible nuclectide deletion,   - possible nuclectide insertion   PTTEHSD/THMENGA/WCKEYPGF   NEFRAYMILDIWTTY   A			amino acid	W=Tryptophan, Y=Tyrosine, X=Imknown *-Stor				
PITTERSOT PHIRMENGA_VUCCESTYGGT_WEREANMILDIWTTT_\Lambda_NEROSTYCGNU	ļ	1	sequence	Codon, /=possible nucleotide deletion				
6124 1573 236 SPEARLAGEROMGRUGIFETSLEHGRUVYSPGEFLAGTURVEL GALPFRATEVICLISCOSYNKADITAWUEGYFENSLSLAGK GSLPAGEHSFPFOFLLPATAPTSEEGFFKKTVHQURAALITERF SKOHKESLEVYSLISHINGRYVYSGALQLHADVENOSGGTSPVASLLLOKY SYKARKHINDRYTLGSFGCANGKARMPAGNUFETSTSLSLAGK SVULTASTDLRGYVYGGALQLHADVENOSGGTSPVASLLLOKY SYKARKHINDRYTLGSFGCANGKARMPAGNUFEDILVPALPOSPEDA REGARASKOPTYSLUSTIANS IPDIEGPWASACKIFSYKLVKTOR SVULTASTDLRGYVYGGALQLHADVENOSGGTSPVASLLLOKY SYKARKHINDRYTLGSFGCANGKARMPAGNUFEDILVPALPOSPEDA REGARASKOPTYSCH STENEY PEGASASKOPTYGGA PEDALPOSTANGKARVINDRYPEDPID A REGARASKOPTYGGA PEDALPOSGGANE PEDALPOSPEDA REGARASKOPTYSCH STENEY PYFAGESGGOVEPTTSTLILPPYSSWOYPYEAPPSTROSGGOVE PSLITBES  1 904 KTEPKLITGAPTYSVPBSCCEVCRGDELSSHEDGDI FROPANR RAHSYNRSHYDPP SRONGGLASFFGARSHRGALMDSOGASGT LVOLVINNHKHRGOVCHOSKOTYTYSHGSSMIPPHLRAFGI VECVLC TCNYTKBCKKLHICPRYPCKYYPOKIDGKCKCVCGG KRAKEEL PEGGAPINKRYFGSETHPYYPYSSYMPBCCHTRKLALETERPPOV EVHWYTIRKG LLOMPHITES KRAMEELDIPPHURATITLSOWK PTEGGAPLOMOSSERVARTELEDLINVULTILESEKGHC PEGGAPINKRYFGGEFTHPYYRSYNGALGAVAVFTGIF DEVSAVOVOYEHYRAFAVAGLPARLAMPINSLINMAYTLLIGISML HRGGAMGLOWFORDESPROSGRIPHINGTORRAAVLOO HUTTPITAPPHPARCHALLORGKRYNVHINGTORRAAVLOO HUTTPITAPPHPARCHALLORGKRYNVHINGTORRAAVLOO HUTTPITAPPHPARCHALLORGKRYNVHINGTORRAAVLOO HUTTPITAPPHPARCHALLORGKRYNVHINGTORRAAVLOO GRINMELAGONFISGEBEFILLITERSEKGHCHALLORGKRYNTHARAVAGLPARLAMPINSLINMAYTLLIGISML HRGGAMGLAWARDROOKTIVHRHOYS SARTESPATILALGVIS CLGFVVILKCONGLAMBLEGGANTULTURTORRAAVLOO GRINMELAGONFISGEBEFILLITERSEKPLOSPATILALGVIS CLGFVVILKCONGLAMBLEGGANTULTURTORRAAVLOO GRINMELAGONFISGEBEFILLITERSEKPLOSPATILALGVIS GRINMELAGONFISGEBEFILLITERSEKPLOSPATILALGVIS GRINMELAGONFISGEBEFILLITERSEKPLOSPATILALGVIS GRINMELAGONFISGEBEFILLITERSEKPLOSPATILAGVIS GRINMELAGONFISGEBEFILLITERSEKGHCHARSTETTOMKFFOR NGCGRIDLARGINGTORRAAVAGLORGKRUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVAGLORGKNUKAPROTAMPERDEGTR GGARPEKTARAPVA	<u> </u>	sequence		\=possible nucleotide insertion)				
6124  1573  236  SDEALRIAGERGMGRVQUETSISHGRVVYSPGEPLAGTVRVRL GAPLIPFRAIRVTCISSGVSMKANDTAWVVEEQTYNSSILADK GAPLIPFRAIRVTCISSGVSMKANDTAWVVEEQTYNSSILADK GAPLIPFRAIRVTCISSGVSMKANDTAWVVEEQTYNSSILADK SKDHKCSLVFYILBJIALIST FDIEQPRWASARKKFSVKLIVTG SVVLTASTDLKGVYVGALQLIADVRONGSGKVIVGVRAAHTTRF SKDHKCSLVFYILBJIALIST FDIEQPRWASARKKFSVKLIVTG SVVLTASTDLKGVYVGALQLIADVRONGSGVVASILGKV SYKAKRWIHDVRTIAEVEGAGVKAWRAGHEGILVPALPGSAL PGCSLIHIDYTQUSLKAPEATVTLFVFIGHIADVRONGSFVVASILGKV SYKAKRWIHDVRTIAEVEGAGVKAWRAGHEGILVPALPGSAL PGCSLHIDYTQUSLKAPEATVTLFVFIGHIADVRONGSFVASILGK HEGGESLHIDYTQUSLKAPEATVTLFVFIGHIADVRONGSFVASILGK HEGGESLHIDYTQUSLKAPEATVTLFVFIGHIADVROPEATFA PFEGASGGPVFTTSTLLPPPSSGRVPCAPEAPSYEGSCGVF PSILTPES  6125  1 964  KTCFKLTCAFTVSVPDSCCRVCRGDGELSWEISDGDI FRQANR EARHSYNRSHTVPPPSRSGGRSGRFFGARSHSDGDI FRQANR FRAMSYNRSHTVPPPSRSGGRFFGARSWIPPLGTSTGATV PYFAGSGGRFFTAVYSSVPMEDGETTRKTALETERPOV EVHVWTTRKS LIGHFILESTERMFEEDLIKVTTTLSQWKI PGGSFDNKGYFGGEFTHVYTSSVPMEDGETTRKTALETERPOV EVHVWTTRKS LIGHFILESTERMFEEDLIKVTTTLSGWKI PEGGASILGPKLGVFTANDARAMATVLLIGGREN PTEGGANIGOPYLADVRONGARATVLLIGGRENFALLIGLEST LIGHGAMSLGPPKLEDVFANTVLHBURG/SAFTYLLGLLSWL HEGGAMSLGPPKLEDVFANTVLHBURG/SAFTYLLGLLSWL HEGGAMSLGPPKLEDVFANTVHBURG/SAFTYLLGLLSWL LIGHGAMSLGPPKLEDVFANTVHBURG/SAFTYLLGLBAR BOSGVVGTEPHYLDYFARMALLYGFVOURINFRAAVLDO MITTLFTAMPVAMCLVLORGERP\LIFTSUSCEVSTAGYCLALLIF PGGFEVALGARHVDAVGGALATVHBURG/SAFTYLLGLBARS LIGHGAMSLGPPKLADFFAHMMLGTDTOTMKALHINKYSCHAPTLAGARS LIGHGAMSLGPPKTAAPVAGLARSKEVENTVATSSRAPPSECTTRWKTFOR NKOCRILDIADLARILALGENFLLOFENDAGSTERRKGDFERFIP PYVDVSKTCALEGDV-VEOTFYMMELVOPSISSFFTTHWKTFOR MKOCRILDIADLARILALGENFLLOFENDAGSTERRKGDFERFIP PYVDSKTCALEGDV-VEOTFYMMELVOPSISSFFTTHWKTFOR MKOCRILDIADLARILALGENFLLOFENDAGSTERRKGDFERFICH RHCDVMKOCKLOKSBLALCLGLKINBP  SGSGVGGERAPEKTAAPVRALDVSHALVVUDEGGRKVLSMFGCC GGARPEKTABAPVRALDVSHALVVUDEGGRKVLSMFGCC GGARPEKTABAPVRALDVSHALVVUDEGGRKVLSMFGCC GGARPEKTABAPVRALDVSHALVVUDEGGRKVLSMFGCC GGARPEKTABAPVRALDVSHALVVEGERCLSTHAGA GYHYGVASCGACCRAFTKRTALKALALALALALALALALALALALALALALALALALAL		Į		PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A				
SDEARRLAGERGRRVQUFFEISTSIGRVWSPEGFTEGTVRWL GAPLEFRAIRVTCIGSCUSWANDTAMVEBYFNSSISLADK GSLPAGEHSFFFOFLIPATAFTSFBOFGKIUHQVAALHTERF SKOHKGSLVFYILSPIANISTIDHEGYWASATKKFSYKLVKTG SVULTASTDLRGVVWGQALQLHADVENGSKUTSFVVASLIGKV SVYAARWIHDVRTIABVEGGAGVAMRRAGOHEQILVPALPQSAL PGCSLIHIDYYLQVSLKAPBATVTLPVFIGNIAV/NPCPSEPPA RRGARSWGPPTGG\SPAGPGERGAGVAMRAGOHEQILVPALPQSAL PGCSLIHIDYYLQVSLKAPBATVTLPVFIGNIAV/NPCPSEPPA RRGARSWGPPTGG\SPAGPGERGAGVAMRAGOHEQILVPALPQSAL PGCSLIHIDYYLQVSLKAPBATVTLPVFIGNIAV/NPCPSEPPA RRGARSWGPPTGG\SPAGPGERGAGVAMRAGOHEQILVPALPQSAL PGCSSLIHIDYYLQVSLKAPBATVTLPVFIGNIAV/NPCPSEPPA RRGARSWGPPTGG\SPAGPGERGAGVAMRAGOHEQILVPALPQSAL PGCSSLIHIDYYLQVSLKAPBATVTLPVFIGNIAV/NPCPSEPPA RRGARSWGPPTGG\SPAGPGERGAGVAMPATPASSCGGVV PSTAMBEGGPPTTSILIPPESSWGYPTEAPPSYEGSCGGVV PSTAMBEGGPPTTSILIPPESSWGYPTEAPPSYEGSCGGVV PSTAMBEGGPPTTSILIPPESSWGYPTEAPPSYEGSCGGVV PSTAMBEGGPPTTSILIPPESSWGYPTEAPPSYEGSCGGVV PSTAMBEGGPPTTSILIPPESSWGYPTEAPPSYEGSCGGVV TONVTKGECKKHLCPNRYPCKYPGKIPGKCCCVCPG/RACKEL PGGSFDMKGYFCGETPPYPCSVCHYGESGLASHENGALPPSQCGGGV PTECKCHYCLSCHYCLCCVCCAPCACCACC PCVLKKGYTCGETPPYCKYPCCHYCLCCVCCAPCACCACCACCACCACCACCACCACCACCACCACCAC	6124	1573		NKNANFPLSRDSSYCGNV				
GSLPFERIRYTCIGSCOVSNKANDTAWVERGYTPGKILDY GSLPFERISPFFOFLINTAPTFFESFFFFERIVHQVRAALHTERF SKDHKCSLVFYILSPIANISIPDIEOPNVASATKKFSYKLVKTU SVVLTASTDLRGYVVGQALQLHADVENGKTSFVVASLLCKV SYKARRWIHDVRTIAEVEGAGVKARRRACHHEDILVPALPQCSAL PGCSLIHIDYTLQVSLKAPRATVTLTVPUTALVONCPSEPPA RPGAASMGPTPGG\PSAPPOERARAAAGGHHIDVPLSTYKS HSGORDILAATLSSVPGABEPECPOGGSFASHPHPPLCISTGATV PYFABGSGGPVFTSTLILPPEYSMGYPYEAPPSYEGOCGGVE PSLTPES  1 904 KTCFKLTCAFTSVPDSSCCVCKGGGELSMEHSDGD\FROPANR EARHSYNTRSTVPDPSSCAGGGLSRFPGARSHRCALMDSQASGT LVQIVINNNKHGGCVCVSNGKTYSHGSSMFPRLRAFG\VECVLC TCRYVKGGFCKKHCNNYPCKYPGKIDGKCKXCPC\RAKEEL PGGSFDNKGYFCGETINFYLSTYRSKGYBPTRAFG\VECVLC TCRYVKGGFCKKHCNNYPCKYPGKIDGKCKXCPC\RAKEEL PGGSFDNKGYFCGETINFYLSTYRSKGYBPTRAFG\VECVLC TCRYVKGGFCKKHCNNYPCKYPGKIDGKCKXCPC\RAKEEL PTGGGA\GNGSKTVCTTLEDDLVKULVLERSEKGHC SVAVQGYGFKKHCNNYPAMALLYGEVGLLEHFKLUTKTLSGWKL PTGGGA\GNGSKSVCTTLEDDLVKULVLERSEKGHC  6126 1224 389 RLSEBRECHFSRRKFQNNFBWGGAFYHVANGGGLCAVPTG1F PGGSPDNKGYFCGETINFYLSGWKTABAGGAAVFTG1F RGGAMCLGPRYLKUVPAMALLYGEVGLLEHFKAUATTLSGWKL HRGGAMCLGPRYLKUVPAMALLYGEVGLLEHFKAUATTLSGWKL HRGGAMCLGPRYLKUVPAMALLYGEVGLHEHVGNRRAAVLDG WITHPIFAMPVAMCVLYLDGRWPPWGLFLUVGLAFYGLALLH PGGFVALGAHVVANGGGLCAVPTGATY THRYTHPRYHPSGCKTR  1335 463 VLPRECLUVYVANDSSRSPTLGRLDAAGFWVWGFPDADEKGY LERELDAFFLHMLMKLGTDDTVKKNLHKVKQFMTTODASKO GRIMMELLGOPFLLGPFRUNGCTSKRKGDFFRIPA YYDVSKTGALBGPFUNGTHLJFFRENDLGSTFKNLGFRYNA DSSGYFISAABLRNN-RIGDLFHKKATSERKLEFYTTOMKT FOR NKCKRILDINDLARILLAJGDNFLLJOFFRUNGCTSKKRKGDFFRIPA YYDVSKTGALBGPFUNGTHLJFFRENDLGSTFKNLGTHSKTG GGAARPEKTAREGFPAAPGSLRHAGGLGFTALPFRQTTTAMK FOR NKCKRILDINDLARILLAJGNFLLJFFRENDLGSTFKNLGTHSKTG GGAARPEKTAREGFPAAPGSLRHAGGLGFTALPFRQTTTAMK GGAARPEKTAREGFPAAPGSLRHAGGLGFTALPFRQTTTAMK GGAARPEKTAREGFPAAPGSLRHAGGLGFTALAGG\APA TCLNGHKEBEDGGGAGGEGGGGCAUALSSLRATAGG\APA TCLNGHKEBEDGGGAGGGGGGARRAGGRTTAGCHARAG\APA TTCLHGHKEBEDGGGGAGGGGGGGARRAGGRTTAGCHARAG\APA TTCLHGHKEBEDGGGGAGGGGGGGARRAGGRTTAGCHARAGA GARPFKCLRVGMLKGCVFRUNGKTGRKKAGENDFRGWGA GGAARPEKTARAGYSTTLGARGFTGGAGGGGGABRRAGGRLLLTLPLLLRQTAG AALLGLVRRLCAGGRGGGGGGABRRAGGRLLTTLPLLLRQTAG COULABTTOVC	0121	13/3	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL				
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TCNVTKQECKXHCPNRYPCXYPOKIDGKCCKVCPG/KRAKEEL PGQSFDNKGYFGGEETMPYTSVEMDEGETTRKIALETERPPQV EVHVWTIRGILQHFHIEKISKRMFEELPHFKLVTRTTLSQMKI PTEGEA0130MCSSRVCRTELEDLVKVLVTERSEKGHC  RLLGEAPCPRSRRRPQMMPEMGOAFVHVVANGGLCAVAVSTGIP DSVSVQVGYEHYAEAPVAGLPAFLAMWPNSLVMNAVTLLGLSML HRGGAMGLGPRYLKDVFAMALGYDVQMLKHTQNRRAAVLDO WLTLPIFAWPVAWCLYLDRGWRPYWLISLECVSLASYGLALLH PGGFEVALGAHVVPAVGOALRT/HRHYG/SATPSATYLALGVIS CLGFVVLKLCDHQLARWRLFQCLTGHEWSKVCDVLQFHFAFIEL THFNTHPRFHPEGGKTR  1335  463  VLPRRCLVFVVNTMDSSEPTLGRLDAAGFWQVWGRPDADEKGY IEEKELDAFFLHMLMKLGTDDTVMKAALHKVKQOFMTTQDASKD GRIRMKELAGHFLSEDBRFLLDFRENDLDSSVEFMQIWRKVDA DSSGFISABELRNFLRDLFHHKKAISEAKLESYTGTMMKIPR NKDGRLDAFFLHMLMKLGTDDTVMKAALHKVKQOFMTTQDASKD GRIRMKELAGHFLSEDBRFLLDFRENDLDSSVEFMQIWRKVDA DSSGFISABELRNFLRDLFHHKKAISEAKLESYTGTMMKIPR NKDGRLDARGHLSEDBRFLLDFRENDLDSSVEFMGIWRKVDA DSSGFISABELRNFLRDLFHKKAISEAKLESYTGTMMKIPR NKDGRLDARGHLSEDBRFLLDFRENDLDSSVEFMGIWKNDA DSSGFISABELRNFLRDLFHKKAISEAKLESYTGTMMKIPR NKDGRLDARGHLSEDBRFLLSFRENDLFSKUDLERFERLIL RHCDVNKIGKLQKSELALCLGLIKIND SPGSLDGRAMEDAQKPQSAWCGGRKTRVVATSSRRAPPSEGTRR GGAARPEKTAEEGPPAAFGSLRHSGFLGFHACPTALPEPQVTSA MSSGVVGIEPLY KAEPASDDSKGSSETETEPPVALARG/PAP TRCLPGHKEEEDGEGAGPGEQGGKLVLSSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRT1GSIEVSCPASMCEGITKRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVPDLPFPGP FPAGPLAVAGGPRKTAAPVNAIVSHALSVUEPSKLYAMDDPAGLOG VMMEVLVLGVAGRSLTLQDELAFREYVLLKALALANDSVWIEDEPPRAG GHLPAVATLCDLFDRETVLLKALALALANDSVWIEDEPPRAG GHLPAVATLCDLFDRETVLLKALALALANDSVWIEDEPPRAG SCEKLLHEALLEYEAGRAGPGGGABRRRAGRLLITLPLLRQTAG KVLAHFYGVALGRAGARREREREGOLRASRSTIDLAK HPCNASMECDKCQRRCKNRAFCYFCNSVOKLPICAQCGKTKCMM KSSDCVIKAGRYSTGLANVGLOPPCAWVCHGRKCLSTHACA CPLITDAEC VECERGWONDGGRIFSCSPCDARSGYDA VMKNLSSDKYGDTSYHDEEDBYRAEDDEEEDGGRKDDFTESS DLFTINLNGGTYAGGYTSCHANGGEGEGGGASGYDA VMKNLSSDKYGDTSYHDEEDBYRAEDDEEEDGGRKDSDTESS DLFTINLNGGTYAGGYGTSCHAGEBECEBGGRKDSDTESS DLFTINLNGGTYAGGYGTSCHAGEBECEBGGRKDSDTESS DLFTINLNGGTYAGGYTSCHANGE	ł	1		I VQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC				
FÖGSFÜNKGYFGEETMPVYESVEMEDGETTRKIALETERPPOU EVHVWTIRKG LOHHILKSI SKRMEELDHRKUJTRTILSQMKI FTEGEADISQMCSSRVCTTELEDLVKVLYLERSEKGHC  1224 389 RLISEAFCPRSRRFGWNFEWGAFVHAVAGGLCAVAVFTGIF DSVSVQVGYEHYAEAPVAGLPAFLAMPYNSLVMAVTILLSIML HRGGAMGLGPRYLKDVFAAMALLVGPVQWLRUMTOMRAAVLDO WINTLPIFAMPVAWCLYLDRGRPYWLKDVGARMAVLDGISCAVAVFTGIF POGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVIS CLGFVVLKLCDHQLARWELPGCLTGHFWSKVCDVLOFHFAFLFL THFNTHPRFHPSGGKTR  6127 1335 463 VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY IEEKELDAFFIHMLMKLGTDDTVMKANLHKVKQGFMTTQDASKD GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKVDA DSSGFISABLRNPLRDLFLHHKKALSBAKLEFYTGTMMKIFDR NKDGRLDINDLARILAQUENFLQFKMDACSTKKRGDPEKIFA YYDVSKTGALEGP\EVPGFVLDMMELVQPSISGVDLDKFREILL HCDVNKDKGIKJOKSELALCIGLKINP  6128 2511 843 TCRMSRRQLERWVWSSQQVQARGRNVRAPRIGKIAMGLEMSSKD SPGSLDGRAWEDAQKPGSANCGGRKTRVATSSRRAPPSEGTRR GGAARPEKTABEGPPAAPGSLRHSGPLGPTALDFEPQUYSA MSSQVVGIEPLYIKABPASPDSPKGSSETETEPPVALAPG\PAP TCLDGHKEBEDGEGAGPGEQGGKLVKSDERKLCUGDVSA GYHYGVASCEACKAFFKRTIQGSIEVSCPASNEGEITKRRRAC QACRFTKCLRVGMLKEGVELDRVRGGRKYKRRPEVDFLPFFGP FPAGPLAVAGGPSRKTAAPVNALVSHLLVVEPBEKLYAMPDPAGPD GHLPAVATLCDLPDREIVVTISMAKSIPGFSSLSLSDMSVLQS VMMEVLVLGVAQRSLTLODELAFREYVLLKALALANDSVHI EDEPELWS SCEKLLHEALLEYEAGRAGPGGGABRRARGRILTTLPLLRQTAG KVLAHFYGVKLGKVPMHKLFLEMLEAMMD ARPARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK KVLAHFYGVKLGKVPMHKLFLEMLEAMMD KSSDCVIKAGVYSTGLANVGTOPFCRAWCHGRKLISTHACA CPILTDAEC VECERGWONGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCNRLGGGHFGCGEGGGAGRFCCGCKTKCMM KSSDCVIKAGVYSTGLANVGIFFCCACCGKTKCMM KSSDCVIKAGVYSTGLANVGIFFCCACCGKTKCMM KSSDCVIKAGVYSTGLANVGIFFCCACCGKTCCMTHACA CPILTDAEC VECERGFWONGGRIFSCSFCDDFTLCEDDQFEHQAS CQVLEAETFKCVSCNRLGGOHSCLRCKACFCDDHTRSKVFKQBKG KQPPCPKCGHETQETKNLSMSTRSLKFGCQTGGEGGGASTYDA VMKNLSSDKYGDTSYHDEEDEFFKEDEEEEGEGRKDSDTESS DLFTHINLIGGTTASGYAHFYEGE	Į	1		TCNVTKQECKKIHCPNRYPCKYPOKIDGKCCKVCPG/KKAKERI.				
6126  1224  389  RLISBAPCPRSRRFQMNPEWGQAFVHVAVAGGLCAVAVFTĞIF DSVSVQVGYEHYAEAPVAGLIPAFLAMPYMSLIVIMAYTLIGLSMI HRGGAMGLGPRYLKDVFAMALIYGPVQMIRLWTOMRAVLLIG WITLPIFAMPVAMCLYLDRGWRP\MLFLSLECVSLASYGLALLH PQGFEVALGAHVVPAVGLIRT\HRHYG/SATPSATYLALGVIS CLGFVVLKLCDHQLARWRLFQCLTCHFWSKVCDVLQFHFAFLFI THFATHPPRHPBGGKTR  6127  1335  463  VLPRRCLVYVVATMDSSREPTLGRLDAAGFWQWQRFDADEKGY IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTQDASKD GRIRMKELAGMFLSEDENFLLLFRENPLDSSVEFMQUWRKDA DSSGFISAABLRNFIRDIFLHHKKAISEAKLEEYTGTMKIFDR NKOGRLDLNDLARILAQENFLLQFKMDACSTERKEGDFEKIFA YVDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFRELL HCDVNKDGKLQKSELALCGLKINP  6128  2511  843  TCRNSRRQLEEWVWSSQQVQARGRNVRAPRIGKIAMGLEMSSKD SPGSLDGRAWEDAGKQCGGRKTRVYATSSRRAPPSEGTTR GGAARPEKTASEGPPAAPGSLRHSGPLGPHACPTALEFEQVTSA MSSQVVGIEPLYIRAEPASPDSPKGSSETETEPDVALAPG\PAP TRCLPGHKEEEDGEGAGGEGGGGGCKLVLSSIPKRLCLVGDVAS GYHYGVASCEACKAFFKRTIGGSIEYSCPASNEGEITKRRKAC QACRFTKCLRYGMLKEGVRLDRVKGRGQKYKRREPVDPLFFPGP FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDAGPD GHLPAVATLCDLFPRETVVTISWAKSIFGFSSLLSDDMSVLQS VMWEVLVLIGVAQRSILTLDLEFAEYVLDEEGARPAGLGELG\ AALLQLVRRLQARSILTLDLEFAEYVLDEEGARPAGLGELG\ AALLQLVRRLQARSILTLDLEFAEYVLLDEEGARPAGCEGLG VMEVLVLIGVAGRSILTLDLEFAEYVLLDEEGARPAGLGELG\ AALLQLVRRLQARSILTLDLEFAEYVLLDEEGARPAGLGELG\ AALLQLVRRLQARSILTLDLEFAEYVLLDEGARPAGLIGHLG\ VVNEVLVLIGVAGRSILTLDLEFAEYVLLDEGARPAGLGELG\ AALLQLVRRLGCKVPMHKIFLEBLIEAMMD  6129  1764  771  ARPARSSHEGKMPKKKGARRKKAENRREREKQLRASRSTIDLAK HPCNASMECDKCQRRQKNRAFCFYGNSVGKLPICAQCGKTKCMM KSSDCVIRHAGVYSTGLAMVGAICDFCEAWCHGKRCLSTHACA CPLITABCVVSCRICRGCRCCRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKOLDSMTSLKFRGQTGGEEGDGASGYDA YMKNLSSDKYGDTSYHDEEEDBEVEABGDBEEEDEGRKDSDTESS DLFITNINLGRTYASGKAHYEEOEN	ŀ	Ĭ.		PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKTALFTERPROV				
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DSSSQVGYEHYABAPVAGLPAFLAMPKNSLVIMAYTLIGLSKI. HRGGAMGLGPRYLKDVPAMALLYGPVQMLRLWTQMRRAAVLDQ WLTLPIFAMPVAMCLYLDRGWRP\WLELSECVSLASYGLALLH PQGFEVALGAHVVPAVQALRT\RRHYG/SATPSATYLALGULS CLGFVUKLCDHQLARRRLFGCLTGHFWSKVCDVLQFHFAFLFL THFNTPBPRPHPSGGKTL THFNTPBPRPHPSGGKTL GRINKMELLGAMFILLBREPPLLSSVEFMQUWGRFDADEKGY IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQGFMTTQDASKD GRIMMELLGAMFILSHFILLFREREPPLDSSVEFMQUWKYDA DSSGFISAAELRNFLRDLPHHKKAISEAKLEEYTGTMMKIFDR NKDGRLDLNDLARILALQENFLLLFREREPPLDSSVEFMQUWKYDA DSSGFISAAELRNFLRDLFPLHHKKAISEAKLEEYTGTMMKIFDR NKDGRLDLNDLARILALQENFLLLFREREPUGPSISKFENIFA YYDVSKTSALEGP\EVOFVKDMMELVQPSISGVDLDKFREILL RHCDVNKDGKLQKSELALCLGLKINP TCMSRRQLERWVWSSQQVQARGRNVRAPRIGKIAMGLEMSSKD SPGSLDGRAWEDAQKRSQSWCGGRKTRVATSSRAPPSEGTRR GGAARPEKTAEEGPPAAFGSLRINGFLGPHACPTALPEPQVTSA MSSQVVGIEPLYIKAEPSPDSPKGSSETSTEPVALAPG\PAP TRCLPGHKEEEDGEGAGPGQGGGKLVLSSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSIEYSCPASNEGEITKRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRKYKRREDVDPLPFPGP FPAGPLAVAGGGRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD GHLPAVATLCDLFDREITVTISMKSIPGFSSLSLSDQMSVLQS VMWEVLVLGVAQRSSLTLODELAFAEYLVLDEEGARPAGLGELG\ AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS SCEKLLHEALLEYEAGRAGPGGGABRRRAGRLLITT.PLLRQTAG KVLAHFYGVKLEGKVPMIKLFLEMLEAMMD  6129 1764 771 ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK HPCNASMECDKORROKNRAFCYFCNSVQKLPICACCGKYKCMM KSSDCVIKAGVYSTGLAMVGAICDFCEAMVCHGRKCLSTHACA CPLITDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFFHQAS COVLEAETFRKCVSCNRLOGNSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEGGGAGSGYDA YWKNLSSDKYGDTSYHDEEDEFYREEDDEEEEDEGRKDSDTESS DLFFTULNLGERTYASGYAHYEEOD	6126	1224	700	FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC				
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### PQGFEVALGAHVUPAVCQALRT\HRIYG/SATPSATYLALGVIS PQGFEVALGAHVUPAVCQALRT\HRIYG/SATPSATYLALGVIS CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL THFNTHPRFHPSGKTR  VLPRRCLVFVVTNTNDSSREPTLGRLDAAGFWQVWQRFDADEKGY IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD GRIRMKELAGMFLSEDENFLLIFRRENPLDSSVEFMQIWRKYDA DSSGFISAAELRWFLRDLFLLHFRENPLDSSVEFMQIWRKYDA NKDGRLDLNDLARILALQENPLLQFKMDACSTEKRKGDFEKLFA YYDVSKTGALEGF\EVDEFYVKDMMELVQPSISGVDLDKFREILL RHCDVNKOKIQKSELALCLGLKINP  6128 2511 843 TCRMSRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD SPGSLDGRAWEDAQKPQSAWGGRKTRVVATSSRRAPPSECTRR GGAARPERTYAEEGPPAAPGSLRHSOPLGPHACPTALPEPQVTSA MSSQVGIEPLYIKAEPASPDSPKGSSETETEPPVALAGC\PAP TRCLPGHKEEBCGGGGCKLVLSSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSIEYSCPASMECEITKRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPSVDPLFFPGP FPAGPLAVAGGPRKTAAPVMALVSHLLVVEDEKLYAMPDPAGPD GHLPAVATLCDLFDRETVVTISWAKSIFGFSSLSLSDQMSVLQS VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEGGARPAGLGELG\ AALLQLVRRQARLEREREYVLKALALANDSVHIEDEPRLWS SCEKLLHEALLEYEAGRAGFGGGGBRRRAGRLLTLPLLRQTAG KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD  6129 1764 771 ARFARSAHEGKMPKKKTGARKKAENRRERERQLRASSSTIDLAK HPCNASMECDKCQRRGKNRAFCYFCDSVQKLPICAQCGKTKCMM KSSDCVIKHAGUYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDMGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCKNRAFCYFCDSVQKLPICAQCGKTKCMM KSSDCVIKHAGUYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDMGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCKNRAFCYFCDSVQKLPICAQCGKTKCMM KSSDCVIKHAGUYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDMGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCKNRAFCYFGNSQCFGGGGGGGGGGGGGASGYDA YWKNLSSDKYGOTSYHDEEEDBYEAEDDEEEEDBGRKDSDTESS DLFTNLNLGRTYASGYGHYEGEBT		l . i		HEGGAMGI CERVI KENDER DARK I KORNON DE CONTROL CERVI KENDER DARK I KORNON DE CONTROL CERVI KENDER DARK I KORNON DE CONTROL CERVI DE CONTROL CE				
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ARFARSÄHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETPKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	( 1		. }	VIII AUEVOUNT POUNTAGE TO THE TOTAL				
HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	6129	1764	771	ADEAD CAUDCAMDARAMENT TO A				
RSSDCVIKHAGYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA CPLTDAEC VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	1 1			HPCNASMECDICOPPONIDA POUR DE LA CONTRACTION DEL CONTRACTION DE LA EAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	j			KSSDCVIKHAGUYSTGLAMUGA TORRORANISA
CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLLSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	ļ i			CPLTDAEC\VECERGVWDHGGDTEGGGEGUDET CORD				
KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN		. 1	1	COVLEAETPKCVSCNRLGOHSCLDCVACECDDUMBCVID				
YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEOEN	[	j		KQPPCPKCGHETQETKDLSMSTRSLKFGDOTGGFFGDGA GGVGA				
DLFTNLNLGRTYASGYAHYEEOEN	, !	j	1	YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS				
577 GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE	6130		_	DLFTNLNLGRTYASGYAHYEEOEN				
	0130		577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE				

	1	S - 34 - 3 - 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
!	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence	_	\=possible nucleotide insertion)
			DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
}	1		ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
		1	LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ
ĺ		1	MNYAAQPDKDDPCCSACNIQ
6131	3	1811	SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
0131	,	1011	PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLLVLGGCLGVF
l	1		
ĺ		(	GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
	l	i	SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
l	1	1	QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
i		}	SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
i .	i	Ī	DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
I	1	1	KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
	1		DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQLY
Į	1	1	EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
1			TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
1			PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
ł	]	J	EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
		1	PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
6132	96	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
0132	1 30	1241	AMEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
l	l .		PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
1			
Į.	1	1	FORLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
1	1	j	SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
1	1		ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
ł		i	VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
1		ļ	LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
		1	TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
i	1	i	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1		ł	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
		f	PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
		l	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
ļ	]	1	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1	1	1	TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSLASFVT
	ĺ	1	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
		1	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
ı	ļ	•	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
1			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
J		}	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1		ļ	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
1		1	KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1		i	CNKCRVOFLFAKDKIEHKLOHHKTFRKPKOLEGLKPGTKVTIRA
i		1	
		1	SRGQPRTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYPPVQRS
1		1	IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST
1	i	1	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
I		1	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1		1	STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
Į.			LASGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1	1	1	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
1	1	1	VNEETLFOKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
1	1	1	VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
ŀ	1		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
i		1	RGOMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1	1	1	RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
I .	I .	1	WIGHT ALIDCHATHER ATHURAS THE A A EVOCOSKI KED

SEO	Predicted	I Decad about	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- [	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
l l	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
j	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
į.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	2040000	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	†		DVCIVOTUNDE HAVEVECARDED STREET
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1	1		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6134	2	4256	
		1	PVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
ı	1	l	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
	1	ł	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
[	1	1	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1	ĺ		STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
İ			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
l	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
	1		/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1	]		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
1		•	KICEWAPESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
ł	1 :		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
	ļ		IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
ļ	i j		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
	f		SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTRDRVHDR
1	i I		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
i	1 1		STATPPPTPTHPQALALPPLATEGAECLNVDDODEGSPVTOFDE
			LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEOAAEHPRNPO
	1		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTORROOLD
1	i		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
[			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
Ì	,		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
ŀ	i i		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
i			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
1	! <b>!</b>		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
	ŀ		LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
6135	2	4256	FYGFEEADLDLMEI
1	-		FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1	i	[	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
	1	Ì	IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1 1	1	,	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1 !	i	, ]	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1	1	ļ	VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1 1	1	l	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
	}	i	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
j !		!	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
<u> </u>	ļ	ľ	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
į j			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
, ,			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
	1		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
[ ]			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
]			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
[		İ	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
	}	ľ	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
			The rest of the re

		,	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	
		residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible rucleotide insertion)
	1	l.	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
	ļ	Į.	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
		İ	STATPPPTTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
	1	Ì	LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
ļ	1	1	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
1	1	1	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
1	1	1	VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
1	1		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
1			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
		Ì	RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
ļ			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
l .	į.		LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
Į.		1	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
L			FYGFEEADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
ł	ì		SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
1		1	DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
1			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
1	ļ		SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
1			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
	1		SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
I .	I .		
L			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCFKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHPSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRFGPGAWLRVV LEKPFGHDHFSAQQLATELGFFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MMNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRFGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSHGAALTAPKQGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRIFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKQGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFFFSSGRIFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRFGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLITLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWMMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWMFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLAISGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFFQSPTGLDGEQLVVLTTSPSQPHRRNSLSLPLINRAKKV
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALGGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDFESNFQGLQAHLLQHVRI PYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVIQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNPWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRIFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG
6137	4587	934	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASMNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFFW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFFQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLLGEAGRGHSFSFHGAALTAPKGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFFW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQULATAHYGFPW AHTHLWLVDERCVPLSDFESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKETHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MMNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRFGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWILVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKRQSEDPLPELHEDLHNEK
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLPPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSSLQVIKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFFFSSGFLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEGLVVTTTSPSQPHRRMSLSLPLINRAKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLITTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTONLKELQTMKADLTRHVLVEDVWVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LIGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSFHGAALTAPKQGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWFWTPILLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTONLKELGTMKADLTRHVLVEDUMVLKEQIE HLHRQWEDLCLRVAIRKQEEDBLNTWVVFNENKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVPHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLHELKNKEIHFQRRRTTCAL TLEAGEKLLLITTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEGSLASWTONLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKIQLKQMGDQL IKASNKSRAAEIDDKLNKNINDRWQHLFDVIGSRVKKLKETFAFI
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRFGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWILVDERCVPLSDPESNFQGLQAHLLQHVIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNENNKELCAWLVQM ENKVLQTADISIEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLPPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSSLQVIKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNENKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSRPVYVDVCDDDGEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWGG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTTFTAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFFFSSGFFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGGFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVTTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEGSLASWTONLKELQTMKADLTRHVLVEDUMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSEAAEIDDKLNKINDRWGHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQDD LQRDIEQHSAGVESVFNICDVILHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB
			RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK YLWQG\LFQLYLDEAGRGHSFSHGAALTAPKQGQELMAKALES LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGYPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSFLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLPPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSSLQVIKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNENKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSRPVYVDVCDDDGEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	}		NQREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
1			FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
			YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
	}		DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
1			WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS
l			PSCPEHHYKQMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
ì			LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
1			LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
1			LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
į	<b>k</b>		SAKNRROKAHVTDPKADPRALLECRRELMQLEKELVEROPOVDM
ł			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
1 .			ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLLLACLL
Ĺ	<u> </u>		PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
			TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
1			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
1			TQRFLSQHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
1	<u> </u>		IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
	f		RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
i .			PSPCAVWLAGGMAGA I SWGTATPMDVVKSRLQADGVYLNKYKGV
1			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRGDHAVTSP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
l		200	RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
I			SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
			FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
1			ARRIRRTDVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
ł i			ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
			PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
			KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
			NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
1			AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
1			VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
6142	116	602	DEFVFDVWGVIGDAKRRGL
	110	002	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNOENDEKDEKEOVANKCEDLALDLANGEVCVDDCARDD
			LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
	İ		REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
[			\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTOVPHFLLED
ł l	ļ		LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN
{	1		SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
]	İ		FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
j			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
j	İ		QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
į į	· •		YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
1 1			FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
	į		TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
]			QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
]	-		YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
1 1			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
	1		GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
L			TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
aı	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon. /=possible nucleotide deletion,
	sequence	Dogumen	\-nossible nucleotide insertion)
	sequence	<u> </u>	LIKINKAAGESSTTSTSWEGNRASOTLSFOETALLKAVLVAGL
ł		1	VDNUGKTIYTKSVDVTEKTACIVETAOGKAQVHPSSVNRDLQTH
1	i	1	CWILLYOFK IRVARVYI RETTLITPFPVLLFGGDIEVQHRERLLS [
l .			IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
1	Į.	1	LOIITELIKTENN
			SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
6144	1289	568	VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
}	}	1	VSASGGARHGGRGSGGFVICTIGF BBLT2VA(TLA) VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
1	1	1	VGDRTVTLGTWDTAGSERTEMISRTTTRGARGATT COUNTRY OF THE PROPERTY OF
1		1	FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
	1	1	QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
	1	}	DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
		1	GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
1	ł	<b>!</b>	DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
i	1		OGVATITOVEVDTVGMPETYOARLOOSFPGIEVTVKAKADALYPV
ŀ	1	Į.	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
1	1		/TKAWI.KEHVEPVE\GFP\OFVRF\SWRTAQTI\LEKEAEDVIR
1	1	i	EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
1	1	1	т.
		781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
6146	428	/81	R/YPGHEAHDQGG\WDAROSIIRKVVDPETGRTRLIKGDGEVLE
1	1	ĺ	EIVTKERHREINKQATRGDCLAFQMRAGLLP
			GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
6147	1	2304	GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
i	1	]	ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
1	l		DEMDRIATINAVITOFSARISATLQDRHERITKLAGVHALLRKL
ı	1	1	QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
	<b>\</b>		IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
1	ţ	1	EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
	l l	<b>\</b>	EELCEEFLAHARGRUEKEURNUEAEUGFSFFAFDUUGSPVFALV
	1	l .	SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
ŀ	•	ł	ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
	1	- 1	EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
ŀ	Ī	1	GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
Į.	l	1	CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
1	ł		RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
1		1	RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
1		1	VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
1		l	GCDMCTWASHGASSVARASVREPOGNKSPRMNTKRAGECLCPRS
1		Į.	CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
	Ĭ	<b>\</b>	CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
0148	3036	333	KSVKAVI,EDPMI.KFSGLYOETCSDLYVTCQVFAEGKPLALPVRT
1	1	1	SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
	1	1	PVGGTTVSI.FGKYGMFROGMHDLKVWPNCRSQMDQKPTKTPGRT
	1	ļ	SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
1	1	}	VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
1	1	1	LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
ı	1	j	LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
1			DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
1		1	DLPQGAKQALALIGAKWKYMIDVEDSLEDISSRI ING I VAKTAVAK
		1	LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
			ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
1	l		THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
1			KAMODESGNEKKKNERLOALLGDNEKMNLSDVELIPLPLEPQVK
- [	1		TPGTTPETATI.FKSAI.MPAOLFFKTEDGGKYPVIFKHGDDLRQD
- 1	1		QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV
	1		

C 650	T 20 - 32 - 5 - 5	· · · · · · · · · · · · · · · · · · ·	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
l	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			PVAEVLDTEGSIONFFRKYAPSENGPNGISAEVMDTYVKSCAGY
j			CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
	]	Í	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
1	1		SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANP I KNGKTSPASKDQRTGKKTSVQGQVQKGND
	1	}	ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
	,		GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
}	į.		GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAOO
	Į	1	POQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
	İ		VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
	f		STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
1		{	VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HOGL
[	Į.		S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
			LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
[	[		LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
	·		QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
1			TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
			QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
1			KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
1 1			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
1 :			KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
			GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
1			PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
1 1			GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
1 1			KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
1 1			LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
			NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
1 1			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1 1	i		TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
] ]	1		YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
1 1	i		AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
1	1		GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
1	ļ		ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
	1		WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
1 !	i		FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
1			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
1 1	1		ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
1 1			TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
} 1	ľ		SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
1 1			FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
1 1			AAIALMILAFLLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
j 1		ļ	WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
1		. ]	SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
Į. I		,	TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
1 1	j	1	ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
1 !	Į.	,	KEKTLARVCLCOKIDINUETEODOVDA OPPORTA OVOY
1			KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM
1 1	1		VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV
, ,	į	ļ	TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ĬD	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
l	amino acid	sequence	
	sequence		\=possible nucleotide insertion) LODVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
ł			
1	İ		APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
İ	1		SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
i			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
	1		SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
l	Į.		RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
	1		NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
	1		
			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
			RCOSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
į.			RQQSSVTVSEPLAPNQEEVRSIKSEIDSIIEVDSVAGEDQDDQS ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
İ			FIKKAEKKP*SNSGKQQKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
P122	869	121	YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
1			TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
	1	İ	P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
l	1	1	COKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
1			VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
0130	3,23	5504	VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
İ			ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
1	1 -	· ·	FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
}	ĺ		GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
	i		AIWEAAOFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
1	1		DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
1	į.		ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT
1	1		VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
1	1		IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
į.	1		DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
Ţ			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
1			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
1	1		IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
		}	PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
1		ı	QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
L	<u> </u>		QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
1			PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
1		1	RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREKEREKE
1		1	KERGKNKDRDKEREKDREKDKEKDREREREKEHEKDRDKEKEKE
1		1	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
1			HISERRERESTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
<b></b>			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53 .	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
		1	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
		1	IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
1	1	1	NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
		1	IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
60.00	<del> </del>	-	DVSVSCDCTTAYQPG
6160	1626	1790	AGAKFFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
L			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR

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SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
) NO.	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
- [	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
l l			ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
1	}		SLFYAEATPMLKTLSDATTKFVSENKNLPIENTIDCLSTMASVC
			RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
}			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
L			KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
1			KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
•			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
Í	•		GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
ŀ			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
į			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
-			ARPOSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
6162	1	586	LATCSFYDHALHLWEWEGN
1	_	200	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
ł			KKRSKSVTSSSSSSDSSASDSSESEETSTSSSSEDSDTDESS
ļ			SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
<b>.</b>			EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
			TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
			MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIELIRQR
			ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
			GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
1			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
]			LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
1			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
] ]			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1 1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1 1			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1 1			VOAKLGALELNORDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1 1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
, ,			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
6165	90	100	GGERFG
"-""		406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
[ ]			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
[ ]			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
j i	ł		WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
	[		YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
1			GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
) I	Ì		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
<u>L</u>	Į		KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
!	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
'	amino acid		Codon, /=possible nucleotide deletion,
l	1	sequence	\=possible nucleotide insertion)
	sequence		
Į.		1	PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMERMTTDIN
1			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
į	ł		HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
l	ł	1	PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
Ì		l	EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
ł	l .	1	VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
İ		i .	SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1		l	HFPOMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
}	1	į.	1
		<u> </u>	GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
I			LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVQNR
l			IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFQEAWTMP
1	1		FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
1			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
l .			EGNIGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
1	1	ļ	SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
	i	ł	GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
1	İ		NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
1	1	1	VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1	i	1	LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
1 .	l .	ì	VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
	1	}	HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
1		ł	LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
1	1	1	LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
İ	1		DRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWV
ļ	ì	i	VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
1	1		OPFSLKNLDK
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
9100	1 03	1 2322	GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
İ			ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
i	1		FUNDIF APVOAGATSAGADEASVVCAF FAGGETAGDACKTON
	1	1	DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
1	1		EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
1	1		PPGFVLKKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF
1			LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
1		1	ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
1			ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
1			EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
1 5207		1	AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFQRFVT
	1		PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEQDKSRDEDN
1		1	DEDEBRLEEEEQNEEEEVDN * KGRETVAPWKVPLEMRRATCFCE
1		1	
L			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
1	[	1	AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
1	1	1	VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
1	ĺ	1	TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
1		1	G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
1 ~	302	1	MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
l	i	1	SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
1			RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
ł	1	1	
L			NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
j			SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
1			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

<u> </u>		· · · · · · · · · · · · · · · · · · ·	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
Í	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
-	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	L	\=possible nucleotide insertion)
j			QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
	]	1	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
1			SDILRYLFPVPKDDSHRVITFANODDYISFRHHVYKKTDHRNVE
1			LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
	<u>i</u>		LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
1		i .	LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
ť			ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
	1	1	RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
ŀ	i		TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
j			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
l	1	ł	HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
			MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
1	1		MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
	<b>{</b>		LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
i i		33.	DALDDDAGDEDAGEONGTONDER GERNAMAAPVKGNRKQSTEG
}			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
1			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
-			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
1			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
1 1			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1	1		SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1 1	}		DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
1 1	1		KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1 1			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
1 1			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF FHLNTKL
6176	1040	402	
1 1	-010	204	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
	ļ		GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
	1		SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
1 1			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
6177	1400	000	RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
1 1	-300	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
1		ĺ	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
1	į		PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
6178	1022		VCPI
01/8	1027	254	STORGGI KGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
1	]		HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1 1	}	1	LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1		!	NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
1 1		ļ	CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
1 63 75			THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
1 1	1	. ]	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
	· I	ŀ	WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
L			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECON*
j l	1	ļ	SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
1	1	,	SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
		ſ	MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
	1	Į.	TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
	1	1	VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
	İ	•	HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
l	1	į.	LSNESOPTLOLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
l	1	1	KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
İ	1	1	KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
ł		1	PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
}	1		
l .			MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1			YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
1	<b>,</b>	1	VSLLELLHIYVGIESNHLLPRFLQLTERIIILFVVITSQEEVQE
1			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
1		1	IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
1		1	YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
ŀ	ì	1	KDRLWIOCSK*NTGSILVEKFLVF
6100	1769	1224	AS*IDYOLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
6182	1/69	1224	VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
1	Į.	1	VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
1		1	
1	İ		FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
l .	1		CWARAHSLTSSIPGAWITNFSLTMMVIFFLORRSPPILPTLDSL
i	1	1	KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
ì	1	1	YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
1		Į.	SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
1	į.	1	APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
ŀ	l	1	STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
			GSGCGGCGSSCGGCGSGCGGCGSGCGGCSSCGGCGS
1		1	RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
1	]	1	GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
1	ŀ	1	CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
ļ	ł	Į.	VP
			IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
6184	1	2191	EPPPPLOAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
1			EPPPPDAVLVANDSTURKFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
1	ı		FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
1	<b>{</b>		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
1		1	LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
1	i i		HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
1	1	l .	'QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
1	1		NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
1	]	1	PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
1		1	NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1		į.	TSOUVYGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1	(		DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI
1	1	1	NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
1			GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
1		Ī	GKEENISCOMPAPETMOPVIWIMISPYPAMÄAPPUA APPLADÃÃ
1		1	MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
1	1	Į.	FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
1			QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
	'	1	IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR
		1	HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
1			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
1	1		REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
1			GCQEAEMQTPRRLGWGWYHTLTLYLWEEK
L			VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA
6186	569	238	AIGIDSSMINIHGAEFWAKKTIKWAMUDCUMÖSKIDAAGINIA

SEO	Predicted	T 50	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
· ·	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
[	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
	1		KERKVKNKVKNKADTEEVFNNSPTNQEKMPTSAILPDFSGSVIS
	1	}	NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI
1	ſ		PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
			EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
	1	1	AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSP
i	1	ł	LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK
ł	ļ		VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
i	1		VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
6187	1701	771	PSGSRVGSRYD
		'' <del>'</del>	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1	1		AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
1			ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
1			LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
1		İ	AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1	ŀ		TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
}			A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA+GPRWASW
			NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
j	J		NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
			INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP
			RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
	i		PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
1			QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
1			PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
ļ	i		VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
L			AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
1			TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
1			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1			VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
			RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPOVHRD
			AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR
1 1	1		GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLOLLDIAGNO
	1		LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
1 1	j	•	KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
6190	66		EEEEDEVEEEETR
1 1	90	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
į i	ŀ	Ì	GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
	ļ	į	VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
[ ]		[	CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
, ,			SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
į į			PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLBGNCIK
( l			KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLOTIFSVS
}	, ]		TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
			YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
6191	1212	1513	VAPNGQLTLTTPIHNYKA
		1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
1	1	1	MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
6192	3		QDYMFSLISGS
	,	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1	I	į	KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
J		Í	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
ı			RCSNHLQDKIQKLYERKIKEGMDMNYIIORKKEFRNPSIYEKI.I
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

	<del></del>		<u> </u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
<del></del>			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAOKRKSKW
1	İ	Į.	DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1		į	IVKKAKQ
C102		950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
6193	3	950	l e
i	j	l .	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
ļ	1	1	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
1	ļ	1	RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1	ļ		QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
1	į.	1	AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1	i	1	DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1	Į.	i	IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
į.		Į	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
	1		PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
j		1	RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1	1	j	QPCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
	1	ı	AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1	i e		DSAIPVTTIAOPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1	l .	İ	
		l	IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
	ł	Į.	YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
		1	PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
1		· ·	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
1	į	1	QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
ļ.	1	ì	HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
Ì	İ		FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
1	f	1	MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
ļ	į.	1	NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
ļ		1	NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
0257	1	1 012	PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
ļ	1	Į.	ROIEIQFAQGDRKTPGOMKSKERHPCSPSDHRRSRSPSQRRTRS
İ	i	l .	1 =
1		i e	RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
1		I .	SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
i i	1	1	RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
L		1	YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
1		1	RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
1		Į.	REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL
1		1	LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
1		1	GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
1			SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
1		1	TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
1	1	1	AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
1		i	DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
1	1	1	YGGEEKVYIATOGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
Ī	1	1	EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
1	1	1	GLKHYWFTSWPDOKTPDRAPPLLHLVREVEEAAQQEGPHCAPII
1		1	- · · · · · · · · · · · · · · · · · · ·
1		1	VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
			MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
1			TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
1	1	1	BSPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
1	1	}	YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD
1	1	1	VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEQ	Predicted	Decate and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
J	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion
<b></b>	sequence		\=possible nucleotide insertion)
1	1		FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
1	•		NKRYTCEQAARHPWIAGDTALNKNIHESVSAOIRKNFAKSKWRO
į	1	l	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
6200	702	96	HAL*
1 3200	1 /02	30	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
1		ļ	WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
1			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
1			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
1			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
J			RKRILGSASPEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
L			DGSQGFKORR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
1			DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
J	}		KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASQHPA
			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYOERMNKGER
1	]		LNQDQLDAVSKYQEVTNNLEFAKELORSFMALSODIOKTIKKTA
			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
1		•	PILSEEELSLLDEFYKLVDPERDMSLRLNBQYEHASIHLWDLLE
			GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
1	l l		SAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFTS
			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
1			NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
ł			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
	1		LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFKMNAPVP
1	1 1		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
1	1		TYHGSPDQSHQVTGNHQQPPQONTGFPRSNOPYYNSRGVSRGGS
	}		RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTOSOFSAD
1	1 1		RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPOM
6204	2933		NTQQVN
0204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
1	i	•	PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
ļ	1		RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
l	1		CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
			ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
ļ			YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
	1		HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
1			AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
<b>(</b>	ľ		EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
]			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
	<u> </u>		SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIOLSLOESGLA
			LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
			LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
	f		AGQDPNINDNLLGNIMAWFHDMNPOSIALIPPATTEISADSOLP
	•		CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
6205			PGGGKQHPQAW
0203	1	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
	}		SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
	1	1	KROKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLOEON
	f	1	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
<u> </u>	<u>-</u>	- <del></del>	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN

	•		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 2	\=pcssible nucleotide insertion)
	Bequence		YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
į.	1	i	
<b>!</b>	1	]	IBLLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
Į	1		QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
ļ.		1 .	DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
ì		į.	LDIF
6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
6200	1 10	1412	APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
İ		1	
	ì		LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
1	1	1	IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
Į.	Į.	1	FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
1	ļ	1	ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
į.	ŀ	1	VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
1	1	1	TNCNPSLLSIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
1	1	1	
ł	1	1	FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
l	1	1	RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
	1		KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
1	1	l .	GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1	1		SVVCKYFORGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
1	1	1	SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
i .		1	GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1		1	
	1	i	VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1	1		HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1	i		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1	1	1	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1		j	GRREEPOROKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
í	1	4	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
			TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
6208	2924	1471	
I			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
			SVVCKYFORGYCIYGDRCRYEHSKPLKQBEATATELTTKSSLAA
1	1	· .	SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
1	1	}	GOPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1	j	1.	VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
i		I	HEKDMELSFAVORSKDMVCGICMEVVYEKANPSERRFGILSNCN
1	l	1	HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
ì	1	1	
i	1	1	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
I	1	1	GRREEPOROKVGTSSRYRAORRNHFWELIEERENSNPFDNDEEB
l	i		VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEENSVTHHEVKCQGK
ì	i	1 .	PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
1	1	1	KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKRAQGK
1	I	1	TOONRKLTDFYPVRRSSRKSKABLQSEERKRIDELIESGKEEGM
1		ł	
ī	1	1	
I .			KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
		1	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL
			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
6210	3761	387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEWRLTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGMMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGMMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGMMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHCGWGKHNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCFTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
6210		387	AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGMMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG SGPIWFDDLICNGNESALWNCKHCGWGKHNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK

SEO	Predicted	1 500 500	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ı	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	- Squece		\=possible nucleotide insertion)
İ	ŧ	İ	FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
1 .			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
	i		SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
i	ı		IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
		,	HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
	1		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
1	i		GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
1	į		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
i			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
1			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
1			ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
6211	3761	20-	EMNSCLNADDLDLMNSSGGHSEPH
1 0222	3,01	387	1 FGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
ł			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
1	j		SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
1			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
1	1		WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
			LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
1			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
) ]	j		SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
1	j		IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
1 1	1		HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
	Ì		RPTIPEESAVACIESGOLRLVNGGGRCAGRVEIYHEGSWGTICD
į j	1		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
	1		GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1 .1	1		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
1 1	1		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1. [	j		WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
1 1			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
1 1	İ		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
1			VGILGVVBLATFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	
1 - 1	_	*****	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
	}		RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
1 1			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
1 1			QKNNCVMPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI.
	•		SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
1 1	ļ		VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
1	1		DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
1 1			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
6213	1		GPSGPSGPSTSSTSKSSSGSGNPTRK
0213	-	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
į (		1	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
1	1	į	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	ļ	. 1	QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
L			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
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DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL	1			YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
	1	1	1	AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
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Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence codon, residue of amino acid sequence 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  6222  2 2116  MAREBARLHUMPATSELLORSALTIRO TOTALEURINE SEPARTICA ACID, FEDYGLEFMREGIVTATEQUE SEARPYOTT SEPARTICA ACID, FEDYGLEFMREGIVTATEQUE SEARPYOTT SEARCH
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to first amino acid residue of amino acid residue of amino acid sequence  6222  2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
residue of amino acid sequence amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)  6222 2 2 2116 MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQ PRRNPAWSLQAGRLFSTQTAEDKEFPLHSIISSTESVQGSTS EFQAETKKILDIVARSLYSEKEVFIRELISNASDALEKLRHK SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNIGT RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVY SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIMMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP. FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA FEDYSGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMPAGTRNITYLCAPNRHLAEHSPYYEAMKKKDTEVLFF EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPACLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRIEFDGLAVULQQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVQDIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVQDIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVQDIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVQDIYENAMIAAGLVDDPRANVGRLNELLVKALEI DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGGRUNDELIVKGALTING RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYYTT
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dinino acid sequence Codon, /=possible nucleotide deletion,    -possible nucleotide insertion    -possible nucleotide insertion   -p
Sequence   -possible nucleotide insertion
MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQ PRRNPAWSLQAGRLFSTQTAEDKEFPLHSIISSTESVQGSTS EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKIRHK SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNIGT RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVY SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP FDVSRELGSSVALYSRKVLIQTKATDILPKNLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA FEBYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRNQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EFGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI  6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
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EFQAETKKILDIVARSLYSEKEVFIRELISNASDALEKIRHK SDGQALPEMEIHLQTMABKGTITIQDTGIGMTQEELVSNIGT RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVY SAAPGSLGYQWLSDGSGVPEIAEASGVRTGTKIIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIMMMPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP. FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE. PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA. FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS. EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF. EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA. CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLE. AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLR. EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI BAARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG. RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
SDGQALPEMEIHLQTMAEKGTITIQDTGIGMTQEELVSNLGT RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVY SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIMMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP, FDVSRELGSSVALYSRKVLIQTKATDILPKNLRFIRGVVDSE, PLNLSRELLQESALIRKLRDVLQQRLIKFFIDGSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF- EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI RLYDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVY SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFV EQFDELTLLHLRFFDKKKLISVETDIVVDHYKEEKFEDRSPA CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI RLYDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCK SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIMMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP FDVSRELGSSVALYSRKVLIQTKATDILPKNLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF: EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA CLSEKETEELMAWMRNVLGSRVTTVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI ROMARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIMMMDPKDV WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLRYESSALPSGQLTS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF: EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAL CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI BAARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
WOHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKP FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFIDQSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSQQLTS: EYASRMPAGTRNIYYLCAPMRHLAEHSPYYEAMKKKDTEVLF EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAL CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI 6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSE PLNLSRELLQESALIRKLRDVLQQRLIKFFIDGSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSQLITS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF- EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA- CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI BAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRRNFDEAAKVLKFRCEERQHSDSCYKLGAYYVT
PLNLSRELLQESALIRKIRDVLQQRLIKFFIDQSKKDAEKYA FEDYGLFMREGIVTATEQEVKEDIAKLLRYEESALPSGQLTS: EYASRMAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF' EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA: CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI  6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFRCEENQHSDSCYKLGAYYVT
FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTS: EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLF- EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA- CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEI AARHFLMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRJ- EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI  6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVT
EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFO EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAL CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEO AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRO EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEO 6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFRCEENQHSDSCYKLGAYYVT
EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPA CLSEKETEELMAWMRNVLGSRVTTVKVTLRIDTHPAMVTVLEI AARHFLRMQQLAKTQEERQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI 6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFRCEENQHSDSCYKLGAYYVT
AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRI EPGLAQLLVDQIYENAMIAAGLVDDPRANVGRLNELLVKALEI  6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTX
6223 3 715 DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTX
DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGG RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTX
RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTG
RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTG GGIJTODI.KAAARCFI.MACEKPCKKSI.AACUNUGI I.AUDCOLAU
GGDTODLKAAARCFLMACEKDGKKGTAACUMUCT.LAUDCOMM
CORDI CUA DE L'ALTER A CONTRACTOR
GQPDLGKARDYYTRACDGGYTSSCFNLSANFLQGAPGFPKDMI
ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNI QQVHKEQQKGVQPLTFG
6224 1 133 LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHE
6225 3259 938 LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDI
QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPELIRRLE
GEVPWGEERRRRPGPCAGIYAEHVLRPKNIGLAHQRQQQLQFS
QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIE
SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVII
KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVC
RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERT
TGEK?YECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGY
NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHORTHSGE
PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSOKS
LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFV
KDCGRGF1QKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNK
LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQC
KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKT
SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGF
WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSK
KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNK YYSKHLKRHLREKRFCTGSVGEASS
6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDG
IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227 2581 890 MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQAR
NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLT:
YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDF
AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAPANET!
NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSN
VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSI
PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVQ
QQANNSPPVAQASVGQQTQPLPPPPPPQPAOLSVOOOAAOPTRWI
APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEXLRSIN
NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNI
RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAC
VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRI
TQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQ

·		·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<u> </u>	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
	İ	'	CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
1			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
	]		QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
l			DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
1			SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
İ	1		EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
ł	Į.	1	RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
İ		į.	ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
ļ			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
Ì			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
	1		RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQ1QASQEKQ
1			QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
6229	1571	560	ELCQGLSLPQWRLRWVQAQGALQKLCS
0223	15/1	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG NAATSLTANPDATTVNIEDPGETPKHOPGSPRGSGREEDDELLG
	1		NDDSDKTELLAGOKKSSPFWTFEYYOTFFDVDTYOVFDRIKGSL
[			
ļ			LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
]			VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
1			ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
)			AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
l			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
l	1		SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
			TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
İ		ł	SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
}	l e		KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
1			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
l		J	LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF
ł			SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK
	1		AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
l			PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
		<b></b>	AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
1	1		YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
1	1		KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
1			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
I		j	IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
]		1	PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
[		[	LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
l	1		APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
			FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
		1	INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
ļ <sup>,</sup>		[	IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
l	1		THNIALLREVIINSRPVKGDISTKPLSDVYPDGFKGHMLTKSEK
1			NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
l	1	1	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
		1	QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
	1		TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
6233	1	2654	MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
1 2233	1 *	2654	HSTRENLNAGNPNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

SEO	Predicted	Predicted end	1 Amino and 1
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
İ			LACSRTYFFGATHVPYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
1			LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
1			TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
l			LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
	Ì		VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP
			EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
1	1		ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF
1			SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
1			EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
1			AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
Į			MYYRQIMDSSECFHAAHFQRYLSSALEAQQNRSARQSAYIRKKT
ł			RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
	1		IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPENLRSRYL
1	[		MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIOS
1			SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
	1		EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
	1		KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
į			NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF
	<u></u>		ELKP
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
1	į i		DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
1	1		ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
			DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
1.			KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
	ĺ		LTKDGVDLMESYVDRTGDVQTASYCMI.QGSPLDVLKDERVQYWI
1			ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVPVSCNFCG
1			KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
1			ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
	ļ		CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV OP
6235	1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ
			DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATO
1			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
	ŀ		DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
			SSGFVGGFLLGLAS
6236	1	703	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
1		•	NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
j	ĺ		NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
			SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT
1 '			LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
			DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
1 1	1		LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL
į į	1		GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
6238			CKK
0236	ż	4666	ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
.	ļ		CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
j I		,	YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
1 1	1	J	TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
1 1	i		KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
	ł		INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
, ,	I		MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS
			DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
] [	ļ		LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI
·		t	TOO A SEASON OF THE PROPERTY O

Predicted   Predicted in uncleotide   Cocation   Coca				
Notestide   Cortesponding to first	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortisponding to first   amino acid   mi	_			
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence  Dryesidue, T-Threomine, N-Nasparagine, p-sesidue of amino acid sequence  Dryesidue of amino acid sequence  Dryesidue of amino acid sequence  Dryesidue nucleotide deletion,	NO:	nucleotide		
to first amino acid residue of amino acid olityfordistyrep		location	corresponding	
amino acid residue of amino acid sequence solve of amino acid sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide sequence (Codon, /=possible nucleotide deletion, /		corresponding	to first	
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide de		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence    Codon, /-possible nucleotide dieletion,    -possible nucleotide insertion    DTYESSKVYTISSPVGIRMENPILSVEGODILGTASPENERN     IPLIGSYRSFIFLKERNENPISSPRESVEGODILGTASPENERN     IPLIGSYRSFIFLKER     IPLIGSYRSFIFLKE     IPLIGST     I	l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence    Codon, /-possible nucleotide deletion,  -possible nucleotide disertion    DTYESSKVTIRSPVQIRMISVPLSVYEROFILDIGFASPEREFN   IPLIGSYRSFIFLKEREDENYOKEGE   DFFEII INDIGALKKKCRS   KNISKESFILNIVPEKUNITSLSVYSEROGULPYIMILMPPILL   RILLPYKIAYIEDEISSVFILSEGERSGOLTCAGLALKKKCRS   KNISKESFILNIVPEKUNITSLSVYSEROGULPYIMILMPPILL   RILLPYKIAYIEDEISSVFILSEGERSGOLTCAGLALKKKCRS   KNISKESFILNIVPEKUNITSLSVYSEROGULPYIMILMPPILL   FSTORMEPFINNKUQLMVTDELSNOFSIDTVGSHGAVKCKUK,   MDYGVAVIILSSENTITIVITFPYFMIKNKIKSLIVIAVEEGIND   KNISLDLEGCIPPHEYASSKLLIQVERSEDPPKRIVHKUGKKCKS   MDYGVAVIILSSENTITIVITFPYFMIKNKIKSLIVIAVEEGIND   KNISLDLEGCIPPHEYASSKLLIQVERSEDPPKRIVHKUGKKCK   HELVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPCKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCKKS   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCK   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCK   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCK   HERVOYNOSSLSELEDSLEPKKAVYTYTADPUGSRILKWRCK   STRICK HERVOYNOSSLSELEDSLEPKKAVYTOTATERSPEKTION   STRICK HERVOYNOSSLSELEPKKAVATOTATERSPEKTION   STRICK HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVOYNOSSLSELEPKKATASSLOCKATION HERVO	ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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VVWETKPKKKARMKEMSVRITELLEREFKETTESPSEDEKVIQL DTMYPVELTPTGHNIKLLQPPVLALRRNYLPALKVEVNTSAHGS SFRIQIYRIQIQNQIHGAVEPPVFYVRVRPKSVTMDSAPREPTD VSIVMSAGHSQISRIKTFKVLIQBEDDRLDLGFIYALTIDLMIE ARTVERTEVELFHKDLEAFKERTKATSLVDQSQVSLYEYPHISP IKLHLSVSLSSGREBAKDSKQNGGLIFVISINLLKSIGATLID VQDVVKLAFFELNVGPTTTSDLQSEVIRIYSKQALKQMYVLIL GLDVLGNPFGLIREFSEGVERFYFYEPYQGAIQGFEEFVEGHALG LKALVGAVGCLAGARSITTGAMGAMATHDEDVYQKREAM NKQPAGFREGITRGGKGUVSGPVSGTTGIVTRYIKGAQKGGAAG FFKGVGKGLVGAVARTPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTNOMLOKKIGFYREHIMTHSSSSDD DDDDDDDDDDDDDDDDDDDDDDDLDNH KPGMGRGSGGRFPLLLGLLVAVATVHLUICFYTKVEESFNLQA THDLLYHMQDLEGYDHLEFFGVVPRTFLGPVVIAVFSSPAVVIA SLEMEKFYSQLIVKGVULGLGVIFTGLGVEVRHFGGAWARTH PCWTAMQPHLMFYCTRTLPWLALPVULALAARLRHEWARFI WLSAFAIIVFRVSLCLPLGLLLLALAGNRKVSVVWALAHHAVPAG ILCLGLTVAVDSYFWRQITWPEKKVLMYNIVINKSSNWGTSPLL WYFYSALPRGLGCSLLFIFLGLUDARKTHSTVLAGFKAKYSIL PHKELRFIIVAFFMINITARGCSYLLNNYKKSWLYKAGSLLVI GHLVNNAYSATALVYGHFNYPGGVAMQRHHQLVPPQTDVLLHI DVAAAGTGVSFFLQVNSAMVPUKGVQPGTGMLAYTHLLMFA COLLALVROPHRVLASVVGTTGVSLNLTQLFPFRVLLGFFKLYSLL DVAAAGTGVSFFLQVNSAMVPUKGVQPGTGMLAYTHLIMFAA PGLLALVROPHRVLASVVGTTGVSLNLTQLFPFRVLLGTFKLIVLL ERLPPS  6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHP DPLSSGSRSSLKSAGGTGFSLGGLGSIRSEGTTSTSVKSLAMG TRINGSLSYDSLLTPSSPDFSSVGAGGPEDPPLGTTSPFLSARL AQQREARHPRLVPTGPTHRSPSPVRTOMLSRHIVASLQEREKL LRQSPPLFGREEBEGGGGGGGGTGTGTGGHAPRTSSSSDDSKRSP LCKFPLGRPAPVPRFGRPDGLRGRGVGSPEEPTAPYLGRSNYS SQKAQPGVSBTEEVALQPLIFREVQVLKTTYSKSRQFKSLGS ASPGGGPPLSSPTRGGKKVVSGVGTTYELSV  FYNGLEPPLGPPICTEGREGGGAVAVERTITYLLRIAGIKDETLQANVR EILALIGYVDPVKGRGIRILSIDGGGTGGVALQTLTRKLVBLTQ KVPHGLPPYLGGVTSGALAFHTDFLCCTT KVPHALGPPICTGVTKMSSWSHAPYDGGTMEN LLKDRMGSALMIETTANP TCPKVAAVSTIVNRGITPKAFVFRNYGFFGINGMSALMIETTANP TCPKVAAVSTIVNRGITPKAFVFRNYGFFGINGMSALMIETTANP TCPKVAAVSTIVNRGITPKAFSDVTRTVTYTSLAKTGGCQYKM MQAIRASSAAPGTYAETALGGGDTGGTHLADANGSALMMETARNP TCPKVARVSTIVNRGITPKAFSDVTRTVTIVLGGGGTGCKINAATT	1	1		
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AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGPPLSSPTRGGVKKVSGVGGTTYEISV  6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1	1		
LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEFGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV  6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSGTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	I	l	1	
LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYELSV  6241 3 1341 RNAEEKKRLSLQREKIJARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLBLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMIECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE		1	ì	
SQKAQPGVSETEEVALQPLITPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTTEISV  6241 3 1341 RNAEEKKRLSLQREKILARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLBFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	İ			
ASPGPGOPPLSSPTRGGVKKVSGVGGTTYEISV  6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEPPEGKGVAVKERIIPYLLRLQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFFGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	ŀ		1	
6241 3 1341 RNAEEKKRLSLQREKI IARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKER I PYLLRLRQI KDETLQAAVR EILALIGYVDPVKGRGIR ILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDY I CCVSTGAI LAFMLGLFHMPLDECEELYRKLGSDV FSQNVI VGTVKMSWSHAFYDSQTWEN ILKDRMGSALMIETARNP TCPKVAAVSTI VNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLINNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCEN I PLDESRNEKLDQLQLE	1			
RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLINNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1	I	] ·	
RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLINNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	6241	3	1341	RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ  KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV  FSQNVIVGTVKMSWSHAFYDSQTWENILKORMGSALMIETARNP  TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM  WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC  LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD  TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1	_	1	RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHF9INSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1 .	i	1	
FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFFGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1	I	1	
TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1			
WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC LWPDVPLECIVSLGTGRYBSDVRNTVTYTSLKTKLSNVINSATD TEBVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	i			
LWPDVPLECTVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD TEBVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	I	1		
TEBVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE	1	1	1	
	1	1	}	LWPDVPLECIVSLGTGRYKSDVRNTVTYTSLKTKLSNVINSATD
GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP	1			
	1	1		GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

SEQ	Predicted	Predicted end	I amino and a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	residue of	residue of	S=Serine, T=Threonine, V=Valine.
ļ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion) FFSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
1		1	SSEDIDQMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
			GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ
1		ľ	NOHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
			VLDLPLPPPPPEPLSQEEEEAQAKADKIKLALEKLKEAKVKKT.V
			VKVHMNDNSTKSLMVDERQLARDVLDNLFBKTHCDCNVDWCLYE
i			IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAUF
1			KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
6243	1509	614	KDVCSIFKSFASENNGKI
		014	RSASRFSGCWSRDSTCCCCCPSTCWSRSSASCPRARWPPSSAPAT
1			TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA AGTPSPTIMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
			MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
1 .			SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
i			RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
6344			GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNOPSELSK
ł			FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAVE
6245	81		EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
1	"-	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
	. [		ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
1 .			KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
	. 1		EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP
1			RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
			NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMOYTGLDEST:
			MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
6246	1177	350	PRG
''''	-1,,,	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV
			QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS
1 1			HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
			PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ
i i	ļ	. :	KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
			LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
			PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFI.
-			YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
			SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
			LOAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
		ĺ	QVTAIFICIGVPTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL
		i	AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
1	1		IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL
1	1		GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
	İ		IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
1	ł	1	LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
6248			SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
0240	56	1773	VPPPRMMAAVPPGLE?WNRVRIPKAGNRSAVTVONPGAALDLCI
[	ļ	. [	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
1	ĺ	ł	ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
- 1		İ	SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHI.GLQEFII
	•	Í	LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF

C C C C	Dec di at = 3	1 5 - 12 - k - 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	ļ		KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
	Į.		FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
	1		TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
	1	1	ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
	i	Į	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
	1	l .	ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
	1		SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
	1		LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
		1	YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
	1	i	LINEQSPRASEETLLGISKKAKOMKINVQNNVDLGQPVKNKRVF
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
	1		VIGTPHAKSFVORFREAESFTOLSEEIQMAVVWCRSKKLKAOAI
	1	}	FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
	1		TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
	l		ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
		1	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKOLETVLDD
			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
		•	SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
	1		EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
i			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
	1		LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
1			VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
		1	PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
		1	KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
			KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			1
6252	27	1897	EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
0256	1 "	1 2031	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
		1	
			PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLEVAEAEEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKI COADIVEAVDIASAAKHFDLNLROFGPYRLNYSRTG
1		1	RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
•			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
		1	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
		]	TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
•			KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
	i	1	GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPABLIC
			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
	1		SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
	<u> </u>		ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
		}	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
		1	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
		1	KLPHSKAKTRSRLEVAEAEEEETSIKAARSELLLAEEPGFLEGE
ţ		1	DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEO	I Decoding a		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
1			TGFLTYLDVSVGKIVAALNARAGRLDVMSONPYNAVIHLGHSNG
1	ł	ŀ	TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHOL
Ì			KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
1			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
1			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
6254	155	1139	ALDRFVR
	1 133	. 1139	HALGRRGGSQELSAAACGCFALRLRAPGSGRPALAPGAAAFAGL
4			GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH
1	]		SHEQSDRGEGVEVVQNEPFEDPHHGNGQFTEKRVYLNSKLPSWA
			RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
1			SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
1			HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
			VCNQHSSPVDDIESHAQTST
6255	1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT
			VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS
1			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
l			LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTI
ļ			GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYQASFDADSATLR
1 .			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
			RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
1 .			VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
			PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
1	1		VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
			EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
) )	Ī		RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPQNLIAQSQSG
1	I		TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
1 1			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
1			FIDPKKIKVFVLDEADVMIATQGHQDQSIRIORMLPRNCOMLLF
1 1	•		SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR
ľ	}		DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA
] ]	•		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
			INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM
6257	210	615	NILNRIQEHFNKKIERLDTDDLDEIEKIAN
		0.25	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI
	j		TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
l l'	•		KA KA
6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
1	. 1		NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
	1	l	TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
		į	KA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
	1		SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
	ŀ	•	SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI
	·		NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSOIGETVCK
İ			YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
		Į.	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
	}	Ī	KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
L			GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

SEQ	Predicted	Predicted end	Duine agid coment containing signal negative
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ			KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHORTHTGEKP
			YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
1			IVHORTHTGEKPYKCNECGKTFCEKSALTKHORTHTGEKPYECN
i	i		ACGKTFSQRSVLTKHQRIHTRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
	1 2002	1.50	RFVEDSFDPNINPTIGASFMTKTVOYONELHKFLIWDTAGOERF
1	1		RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELROHGPPNI
1	]		1.
			VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	
	1	1100	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
1			SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
1			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCEIA
1	1		QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1	1		EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA EIARKLQEEELLATOVDMRAAQVAODEEIARLLMAEEKKAYKKA
1			KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA
	1	ļ	
6262	2	1759	RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
1 0202		1/39	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEETL
			GSTRLVSQGLEALRSBHQAVLQSISQTIECLQQGGHEEGLVHEK
i	ļ	İ	ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGOLRO
1			YDEDGHTSBEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
į.		j	TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
	1		GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
	}		NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
	ł		PNVARTKNNLASCYLKQGKYAEAETLYKEILTRAHVQEFGSVDD
1	f		DHKPIWMHAEEREMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
	ŀ		NTTLRNLGALYRRQGKLEAAETLEECALRSRRQGTDPISQTKVA
}	1		ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
	<b>j</b>		SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
1	<u> </u>		IEVRRCSMPSVICEHTKQFQTISEESNQGSLLTVPGDTSPSPKP
l			EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
			APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
1			PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
1			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANOEPGILOO
1			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
1	!		IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
l .			SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
1			AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
	1		QSTQPEMHKYGQLVKVELEENAEDDKTENQIPQRMTRNKANTMA
1			NOSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
[			VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
i			ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
1			DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
			REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
1			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
1			QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
1			VNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
1			TOPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
1			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNONDSWIFTLAVLL
1	[		SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
1			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
	l		Land of the Author Should be desired and the Land Light

CEO	I D 32 - 6 - 3		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
4	to first	to first	b=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	Sequence		\=possible nucleotide insertion)
	1		SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
	l l		ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
i	1		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
1	1		LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
İ	j		DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
I	1		QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1	1		EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
6265	143		CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI .
0203	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
1			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	]		WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
	1		SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
1	i :		ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
1	1 1		SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
	1		ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	j		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
1	!		LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
1			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1	1 .		YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
1			QTDQILTEKEKEIEVECVKABSAQASAKMVEEMQIKYQQMMEEK
j	l · · l		EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
	i		GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
1		•	ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
Ī	1		PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
	l I		GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
1	i i		SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
1 :	! !		LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
1	1		RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
1			NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKOPGNTAPNLIFLAVSPEEKESWINALNSA
[		•	ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
			VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLOEPVTFODVAV
[ ]	ļ		DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
[ ]			PNSDIPEERPAPSLKVQESSRDCALSSTLEDTLOGGVOEVODTV
	. 1		LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLOKIDNPE
1 1	,		SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHO
1 1		ĺ	KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
, ,			IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTOHORVHS
ļ l		į	GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCODCGKAFRO
j 1	1	ļ	SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
<del> </del>			KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
] [	ļ		TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
1 1	1		GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
ļ			FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYOEOMRDSVAR
1	1	!	IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP
	ì	į	TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
	ļ	j	WHWALYLIEKGEYEAALTIYDTHILPSLOANDAMLDVVDSCSMI.
	1	!	YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA
L			HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALVEAE

SEO	Predicted	Drodiahad	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G≈Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Ī	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			DGNPDRVLELLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
	l .		SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMO
6270	23	2086	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYKKA
]	1		FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
1	1		GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
1	İ	:	KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
1			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
I	ı		EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
ļ	}		YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQMS
Į	ŧ		DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKOLDOG
Į	į		NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKELPEW
1			SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIOPE
			EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
ł			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
	Ì		VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
1			NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
6271	32	1050	EGAANVNVRGEKDEQTKEVKEAKKKDK
02/2	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTGA
			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHH
1			IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA
i			AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
1	1		AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
			MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
i .			ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRIEGVLERQGAPPAAGQGGALVELIPTPGGLAL
			VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ
1			QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI
			SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
1 1			HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
1 1	1		ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME
6274			LAHVEHYAEVRDNTYCVLPT
02/4	56	1142	AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
	1		VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
1 1			LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
1	ŀ		DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
1			AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
	]		LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
1 1			ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
1 1	1		QSLHRVFOKS
6275	20	565	SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
	l		GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
			KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
			EEDTEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
	j	1	KCHVM
6276	797	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
[			SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
1			VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
			LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL
}			LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPO
			GYHKDLLAHVGRN

SEQ Predicted Predicted end Amino acid segment containing	
The segment containing	signal peptide
MARIANTE, Cacysteine, DeAsp.	artic Acid, E=
NO: nucleotide location Glutamic Acid, F=Phenylalanin corresponding H=Histidine, I=Isoleucine, K=	e, G=Glycine,
corresponding to first L=Leucine, M=Methionine, N=As	Lysine,
to first amino acid P=Proline, Q=Glutamine, R=Arg.	paragine,
amino acid residue of S=Serine, T=Threonine, V=Valin	inine,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=U	ne,
amino acid sequence Codon, /=possible nucleotide	Aclorica
sequence \=possible nucleotide insertic	on)
6277 4600 2744 MAFRTEMGLYYSYFKTIVEAPSFLNGVWM.	MNDKI.TEVDI.VINE
LKRFNLYPEVILASWYRIYTKIMDLIGIQ	CKICWTVTIGEGLSP
TESCEGLGDPACFYVAVIFILNGLMMALFI	FIYGTYLSGSRLGGI.
VTVLCFFFNHGECTRVMWTPPLRESFSYP	LVLOMLLVTHILRA
TKLYRGSLIALCISNVFFMLPWQFAQFVLI	TOIASLFAVYVVGY
IDICKLRKIIYIHMISLALCFVLMFGNSMI	LTSYYASSLVIIWG
ILAMKPHFLKINVSELSLWVIQGCFWLFGT	TVILKYLTSKIFGIA
NDAHIGNLLTSKFFSYKDFDTLLYTCAAEI	DFMEKETPLRYTKT
LLLPVVLVGFVAIVRKIISDMWGVLAKQQT	THVRKHQFDHGELVY
HALQLLAYTALGILIMRLKLFLTPHMCVM	SLICSRQLFGWLFC
KVHPGAIVFAILAAMSIQGSANLQTQWNIV	GEFSNLPQEELIEW
IKYSTKPDAVFAGAMPTMASVKLSALRPIV	NHPHYEDAGLRART
KIVYSMYSRKAAEEVKRELIKLKVNYYILE	ESWCVRRSKPGCSM
PEIWDVEDPANAGKTPLCNLLVKDSKPHF1	TVFQNSVYKVLEVV
6278 3 823 ILFRLVLLSLVYLLNSVATEERKPAEVLIV	1000011717100017
IRILLEYCQQVDNIPSVTTDMLTRLSDLLK	VENCECOLUT CAC
ALQVVGLKTITTKNLALSSRCLQLIVHYIE	UTDAUEEADI DOVO
YSMLRHFDHITKDYHDHIAEISAKLVAIMD	SI BUKI I SKARDENKO
PVPSACFRNICKQMTKMHEAIFDLLPEEQT	OMLFLRINASYKLU
LKKQLSHLNVINDGGPQNGLVTADVAFYTC	NLOALKGLKDLDLN
MAEIWEQKR	
6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYG	AOHPPFDPLLHGTL
LRSTAKMPTTPVKAKRVSTFQEFESNTSDA	WDAGEDDDELLAMA
AESLNSEVVMETANRVLRNHSQRQGRPTLQ	EGPGLQQKPRPEAE
PPSPPSGDLRLVKSVSESHTSCPAESASDA	APLQRSQSLPHSAT
VTLGGTSDPSTLSSSALSEREASRLDKFKQ	LLAGPNTDLEELRR
LSWSGIPKPVRPMTWKLLSGYLPANVDRRP EHYYDSRNDEVHQDTYRQIHIDIPRMSPEA	ATLQRKQKEYFAFI
LFIWAIRHPASGYVQGINDLVTPFFVVPIC	DILLUPRATEIFER.
GVPAEVLCNIEADTYWCMSKLLDGIQDNYT	ETUDCIONAMANIE
ELVSRIDEQVHRHLDQHEVRYLQFAFRWMN	MITWALATINAVAMITE
LWDTYQSEPDGFSHFHLYVCAAFLVRWRKE	LLEEKDFOELLLFI.
QNLPTAHWDDEDISLLLAEAYRLKFAFADA	PNHYKK
6280 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRG	AGLRRSEEEEEDE
DVDLAQVLAYLLRRGQVRLVQGGGAANLQF	IOALLDSEEENDRA
WDGRLGDRYNPPVDATPDTRELEFNEIKTO	VELATGOLGLRRAA
QKHSFPRMLHQRERGLCHRGSFSLGEQSRV	ISHFLPNDLGFTDS
YSQKAFCGIYSKDGQIFMSACQDQTIRLYD	CRYGRFRKFKSIKA
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHI	CNIYGEGDTHTALD
LRPDERRFAVFSIAVSSDGREVLGGANDGC	LYVFDREQNRRTLQ
IESHEDDVNAVAFADISSQILFSGGDDAIC	CVWDRRTMREDDPK
PVGALAGHQDGITFIDSKGDARYLISNSKDQ	
EGMEASRQAATQQNWDYRWQQVPKKAWRKLI GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKT	THE THE PERSON TO THE PERSON T
LTNHKACVRDVSWHPFEEKIVSSSWDGNLRI	AAIDDDGHIAKK
PESECASAPAPVPQSSTPFSSPQ	MATE AND TEANING
6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGA	GLRRSEEPPPPD
DVDLAQVLAYLLRRGQVRLVQGGGAANLQFI	OALLDSERENDRA
WDGRLGDRYNPPVDATPDTRELEFNEIKTQV	BLATGOLGIRRAA
QKHSFPRMLHQRERGLCHRGSFSLGEOSRVI	SHFLPNDLGFTDS
YSQKAFCGIYSKDGQIFMSACQDQTIRLYDC	RYGRFRKFKSIKA
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHIO	
	NIYGEGDTHTALD
LRPDERRFAVFSIAVSSDGREVLGGANDGCI	YVFDREONRRTLO
LRPDERRFAVFSIAVSSDEREVLGGANDGCI IESHEDDVNAVAFADISSQILFSGGDDAICK PVGALAGHQDGITFIDSKGDARYLISNSKDC	YVFDREQNRRTLQ VWDRRTMREDDPK

050	Dec 22 - 1		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Ì	ļ	1	EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
l		į.	GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
		1	PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
	ŀ	1	FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
	ļ	ľ	VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAF
	l	1	RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
į .	j	İ	VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
1		1	GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILOHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
1			KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
[	[	1	AEFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
		1	TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
i	<b>!</b>	1	RNHNHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIQLFKSK
		1	VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
	1		KKKPEEOHNKSVHVAGLSWVKPGSVOPFSKEEKTVAT
6284	1	2879	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
}	1 -	1 20.5	ONLOVERENVOKRTFTRWINLHLEKCNPPLEVKDLFVDIODGKI
1			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
	1		VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS
			1
	<b>i</b>		LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
	ļ	1	KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
		1	RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
İ	<u> </u>	1	ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
l			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
l			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS
	1		LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
1			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
ļ		į.	CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
l	Ì	i	EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA
İ	1		EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA
[	1		EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
ſ	i	1	EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF
	1	}	YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
l	1		EEADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
1	1		LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
l	1		ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
			TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH
[		1	IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
l	1		ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
l	1		GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
1	1		VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA
1			EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
1		1	NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAOLQTRFYTDNKKYAVDDV
1		1	PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGOFLRM
l	1		PLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIK
İ			GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD
l	1		
l			SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA
l	1		VDGSGTKFCSGSWDKMLKIWSTVPTDEBDEMEESTNRPRKKQKT
1		J	EQLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD
1	i		VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
•		1	
	1	1	KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

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NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-ct
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
6287	278	7.100	TTSHVGA
1 5207	276	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
Ì			APAKLQVQKILCDLLLPENLKEGLKESSWSSI.DCTKNDDDDDDDD
			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
ŀ	J		MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
1			NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
į			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
			QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
1			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
			YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1			MLDSGADYLHLDVMDGHFVPNITFGHPVVESI,RKOLGODPFPDM
1			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
1			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGOKEMEDMM
			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMTVGGGATM
6289	1		RSEDPRSVINLLENVCSEAAQKRSLDR
0205		743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
	1 .		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRFNGM
ł	ĺ		KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TIGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRMISRYTRKA
			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
1			DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
1			QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
j l	•		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
1 1		i	GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIFFV
1 1			LAPDHIDIEEGFHGKKSEAATEKOKLGYPPIAPFYCMKEDVIAV
1	1		VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSPSSCV
1 1	j.		LSELHPLVLPRVPQSKVLYITSNPMSLCOASRHOPMVNDLLVPG
1 1			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTTLSTRNWPNDAUERS
1	1		TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
1 1			RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
1	ì		PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
			QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
6291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
<b>1</b> [	1	1	PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG
1		1	AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST
		i	SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD
1	1		GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNDBK
] [		[	APITPHSGSTEKAETHEKVVERRENTAEALPEGFFDDPEVDARY
			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRIDDO
1 1	1	i	IGEIDEQIECYRRVEKLRNRODEIKNKI.KEILTIKELOKKEEPN
6292	1835		ADSDDEGELQDLLSQDWRVKGALL
	1032	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLITNAVV
]	ł	1	LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMT
		i i	LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVT.TVDN
1	į	i i	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIII.TFKGV
1		ŀ	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
6293	2382		AKEPPPPYVSA
			FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
		<b>!</b> .	VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
		<u></u>	DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence		\=possible nucleotide insertion)
1 .			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
	`		LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA
1 1			APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL
			LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
1			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
1 1			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
			NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT
			VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
1			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
1			LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
1 1			DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
j i			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1 1			RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
1			RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
1 1			EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
1			TRRLSSSESPQRDPPPPPPPPPPLLRLPLPPPPQQRPRLQEETEAA
			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
1 1			TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVVQSSSFGGE
			GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR
1 1			RRRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
1 1			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
1 1			ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
1 1			NMVIVKEFQRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS
1 1			FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
ł I			QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN
Į į			NESADDHETTONNESADDNNENPEDNNKNTDDNEENPNNNENTY
ł i			GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
1 1			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
1 1			SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
6296			DLEDVLQVPNGWANPGKRGKTG
0296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
1	[		EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTERDT
	-		LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
6297	1	922	KWALIHKRVRLSVFGARWGRIYFGK
	-	244	QRAAAAS PSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
	1		VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
<b>,</b>	1		VYRLPWTWKCSKLIMKSIHAGINAVAAILAIISVVAVFENHNVN NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
	1		MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
	1		FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEO
			GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGORSTM
6298	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
]	ļ		PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLSFLNRPDLPNLA
	İ		YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
	!		YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
[	1		WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM
			KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
	ļ		LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
	i i	i	QLLVYTIDDLIDKLSTIVN

Sto	SEQ	Predicted	- D	
No: nucleotide location corresponding to first chick to first amino acid residue of amino acid residue of amino acid sequence solvent chick to first amino acid sequence solvent chick to first chick to first amino acid sequence solvent chick to first chick to first amino acid sequence solvent chick to first chick to first amino acid sequence solvent chick to first chick to first chick to first chick to first solvent chick to first so	_		ž	Amino acid segment containing signal peptide
Location corresponding to first amino acid amino acid amino acid amino acid seducore content of the state of amino acid sequences sequences seque	ı			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid sequence sequence sequence 5299 512 814 814 814 814 814 814 814 814 814 815 815 814 815 815 814 815 815 814 815 815 815 814 815 815 814 815 815 815 814 815 815 815 814 815 815 815 814 815 815 815 814 815 815 815 814 815 815 815 815 814 815 815 815 815 814 815 815 815 815 814 815 815 815 815 815 816 817 817 817 817 817 817 817 817 817 817				Glucamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of anino acid anino acid sequence solvent anino acid sequence sequence sequence sequence sequence solvent sequence sequ	- 1			H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence acid of a	1		1	b=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence  6299 \$12				P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence \[ \text{\codon} \] \[ \te	I			S=Serine, T=Threonine, V=Valine,
sequence       Sequence				w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6300  121 692 APPSINSS VENDES SEPTIONS PRODUCTIVE CONTROL OF SEPTION OF SEPTI	1		sequence	Codon, /=possible nucleotide deletion,
SIDAMDISA FISOPYKPETPIELES PHICATYSOVEVPE ILGEYO MECEVOLANINI  6300  121  692  ARPSCINGENCYPARCITES PHICATYSOVEVPE ILGEYO MECEVOLANINI  ASPSCINGENCYPARCITES PHICATYSOVEVPE ILGEYO LVIGSLEPALLES PHICATYSOVEVPE SPECTOR PROGRAM AGSPS IPMSS VPYGSODS VHSSPEDGGGGREPRVGS FIGHE LVIGSLEPALLES PHICATYSOVER SENDERGEMENT AGSPS FIGHE TYTHEDVLS KDAGSCAICLEELQOGDT TARLPCLCTVHKGC IDE WEWNRSCOPENS BORD STARLPCLCTVHKGC IDE WEWNRSCOPENS BORD STARLPCLCTVHKGC IDE GASCATILLKENSSGSDWANDCRSKEMBOSCHTTS PVSGFW IPSQYCLIFCNDPONRGLYTP  1804  6302  490  745  1961  1963  1961  1963  1961  1963  1963  2061  1963  1964  1964  1964  1966  1965  1966  1966  1966  1967	6299			\=possible nucleotide insertion)
6300 121 692 APSICRSORVPARATESPRILIVSRAAAPSAGPMCANROCARA AOSPSIINSSSYPYGSODSVIBSPEDGGGGDRPWCSFGGRAR AOSPSIINSSSYPYGSODSVIBSPEDGGGGDRPWCSFGGRAR AOSPSIINSSSYPYGSODSVIBSPEDGGGGDRPWCGSFGGRAR LUIGSLEPAHLSPHMEGGCFCVCSEFYSDSEMDLHLIMCLTKPR ITTHEDVLSKDAGGCAICLEELQGGDTIARLFCLCTYHKGCIDE WFEWRSCFEHPSD 6301 616 284 GKFVPVNNEPPGPLEFPKYLRCYRCLLEFTELGCLLGSDICLTP AGSSCITLHKKNISGSODYWSDCRSKEDGSNTRTSPVSGFW IPSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQYCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLYTP 1PSQXCFLDFCMDPONRGLTTMTREADCHORECOPP 1PSCXCFTCMDPONRGLTTMTP 1PSQXCFLDFCMDPONRGLTTMTREADCHORECOPP 1PSCXCFTCMDPONRGLTTMTP 1PSQXCFLDF	1	342	014	ECDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
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AGPPS INDSSVPYIGSGDEVISSEPDGGGGDRPVGGSPGGPR LVIGSLPAHLS PHMPGGPKGPVCSKFVSSDEMDLHLMCLTKPR TYNEDVLSKDAGGCG1 LGEEUQGGDTIALPCLCTYHKGCTDE WEVWRSCPEHPSD  6301 616 284 GKPVPVNNEPPQDLE PFKYLRCYRGLLETKELGCLLGSDICLTP AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW 1FSQYCELDFCXDPQNRGLYTP 6302 490 745 1FGFLHLFHNEHSFLVGALFAHVFFSSSGGSVALUSDPCLLS FVLINLCUPGLRPLDELIYAGKLKYRAT SEELDHALINBMTSL FVLINLCUPGLRPLDELIYAGKLKYRAT SEELDHALINBMTSL 6303 2 1951 YNNEYGGGLLWGSWGERFGGALSSEWMPPDTKEREGHYSOL WYYLEGGVWRACCWTPAGNSCCDTPTYKTRADDROBCX KVDLVSFLSSPTMGNDSSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARTENDADROBCX KVDLVSFLSSPTMGNDSGCTDTVARSCHJFFTKSSEKFFFKK SKILSKVEKFLTWVNKRMDERASGSSSSIDMGHDASTGDSEED PSHKKRCHTUNKRMDERAGGSSSSSIDMGHDASTGDSEED PSHKKRCHTUNKRMDERAGGSSSSSIDMGHDASTGDSEED PSHKKRCHTUNKRMDERAGGSSSSSIDMGHDASTGDSEED MSWKKGDDLLETNNTEPEKCGSSSSSIDMGHDASTGDSEED PSHLARGENDADROBCX VSGSTKCDVVVDARCGGGGNTIGFALTGGNAVLDTLSPERGSDLAAT VSGSTKCDVVVDARCGGGGNTIGFALTGGNAVLDTLSPERGSDLAAT VSGSTKCDVVVDARCGGGGNTIGFALTGGNAVLDTLSPERGSDLAAT VSGSTKCDVVVDARCGGGGNTIGFALTGGNAVLDTLSPERGSDLAAT VSGSTKCDVVVDARCGGGGNTIGFALTGGNAVLDTLSPERGSDLAAT VSGSTKALTGADAATATATATATATATATATATATATATATATATATA	6300	121		
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KVDLVSPLSSFIMGNNDSGTSDKÖHBEILGGISNIKLNSEEVT QSQLDSCTSHDGHQQLSEVSKRECPASGQSEPRINGTNEESNS SGNTNTDPPAEDSQKSGANTSKDRPHASGTDGDESEDDPPEHK PSKLKKSHELDIDENFASDFDDSGSLLGERYGSGQKYGGINFS HRQVEYLEKRVKLKSKYLDMRRGIKMKHIFFTRESEKPFTKK SKILSKVEKFLTWYNKPMDEASGSSSSEDMOHDASTSCDSEEQ DMSVKGDDLLETNPEPEKCOVSSAGELETENFERSKLDLATV PDEODCYTGEVPDSRQAETEABVKKKNKKKNKVMCLPPEIAA VPELAKYWAGRYRLFSRFDDGIKLDREGMFSVTFEKIABHIAGS RNNAEVYGIADKLEFICGOPLLLASFLKADVVFLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSGHFSTVHVVLKEE ARNAEVYGIADKLEFICGOPLLLASFLKADVVFLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSGHFSTVHVVLKEE BEVGDGTEGOPLNKKKTITAYFGDLIRRPASET  HRARVDRSFESFGGDLRHFGRVRRDITLSGHFRLSTCHVVLLKE BEVGDGTKDLGHPCHGSSIGTGSEVVTLVSPLPGSDMAALPA WRATSGITLMPHTAEGROLLGAENRALTGGQABDPTLASGAYO WPGSVEKLQGSVVCDAFTLLSSGTGQAPPWITDHDVQMLRL AQGEVVDKARVPAHGQULQVGFSTBAALQDLSSPRLSQLCSGGL CGLIKRPGDLPEVLSFHVDRVLGGRSELBYARRFHISPLLPYRY TDGGARRVIWWAPDVQHLSDPDDNSLALGWLQYQALLAHSCN WPGGAPCPGTHHTEWARLALFPFLLQVHDRLDRYCGGFEBEPSD PCVEERLREKCRNPASELRIVHLSSDPSHLVYIDNAGNLOHP EDKLNFRLLEGIDGFSESAVKVLASGCLQNMLLKSLQMDPVFWE SQGAQCLKQVLQTLEQRGQVLLCHHICKHHILTFRDEDD  6305 99 420 MMIWRGRSTYRPPRRSVEPPELIGPMLENDEPGQEEPPTES RDPAFGGRREDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQCKILTKSSQFWAPS RDPAFGGRREDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQCKILTKSSQFWAPS  6306 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHRCATRVPNDCLGEALINGDVMREATDFSEADKSALMD SSDSOVIPGSHSEBRALHASEEEGEGGKAQSSLGVIPLMRVVQ SVHHTTRKSSTTLREGWVVHYSNRDTLRRHYWRLDCKCITLPQ NNTTNRYYKEIPLSFLITPSEADKSALMD SVHHTTRYSTTLREGWVHYSNRDTLRRHYWRLDCKCITLPQ NNTTNRYYKEIPLSFLITPSEADKSALMD APGHAPHRQASLSISVSNSQIQENVDLATVYQIFPDEVLGSQGF GVYGGKHRKTGROWVAVVIINLKPPTKQBSQDFPDVRC GVYGGKHRKTGROWVAVVIINLKPPTKQBSQDFPDVRC TKPLITOTLIVALGHMENTSTPEKVVVWHSLANGDFPQVKLC DFGFARIIGEKSFRTSVVGTPAYLAPEVLLLASADPFPQVKLC UMYVSLSGTPFFREDEDINDQIQNAPMPAPSPHSHISAGAID LINNLLQVMRKRYSVDVSLSHPWLOSVOTVLLLASAGDFPQVKLC VIMYVSLSGTPFFREDEDINDQIQNAPMPAPSPHSHISAGAID LINNLLQVMRKRYSVDVSLSHPWLOSVOTVLLLBELBCKMREP				YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
GSQLDSCTSHDGHQQLSEVSSKRECPAGGGEPRINGTNEESINS SGNTNTDPABEDGKSSGANTSKORPHASGTDGESEEDP PEHK PSKLKRSHELDIDENPASDPDGGSLLGFKYGGGKYGGIPNFS HRQVRYLEKNVKLKSKYLDMRRQIKMRKHIFFTKESEKFFFKK SKILSKVEKFLTWVNKPMBEBASGESSHDNGHDASTSCDSERD DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV PDEODCVTGEVPDSRQASTEAEVKKKNKKKNKNKNDLPBIAA VPELAKYMAGRYRLFSRPDDGIKLDREGWFSVTPEKIAEHIAGR VSGSFKCDVVUDAFCGVGNTIQFALTGMRVAIDIDPVKIALA RNNAEVYGIADKIEFICGDFLLLASFLKADVVPLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNIVYFLPRADIDQVAS ARAFTFDIRTMMSPDGFEIFRLSKKITNIVYFLPRADIDQVAS LAGPGGQVEIGNFLNNKLKTITAYFGDLIRRFASET BERGGGVEIGNFLNNKLKTITAYFGDLIRRFASET DEVEDPGTKDLIGHPOHGSPTGTSEVVTLVSPLPGSDMAALPA WRATSGLTLWPHTAEGROLLGAENRALTGGQAEPPTLASGAYQ WPGSVEKLQSSVWCDATLLSSSRTGQAPPWITDBUVMLRLL AQGEVVDKARVPAHGQVLQVGFSTERALQDLSSPRLSGLCSGGL CGLIKRRGDLPEVLSFHVDRVLGLRSLPAVARRFHSPLLPYRY TDGGARPVIWAPDVGHLSDPBEDQNSLALGMLOYQALLAHSCN WPGQAPCGIHHTENARLALFDFLLQVHDRLDRYCCGFEPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPSSAVKVLASGCLQNMLKSLQMDPVWE SQGGAQGLKQVLQTLEGRGCVLLGHIQKHNLTLFRBEDP 6305 99 420 NMIWRGGSTVFRPFRRSVPFERSDFEIGPMLEFGDEPDGEPDGEPFTES RDPAPGGGREEDGGAASTQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFRWPERGR 6306 1 1874 PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHRCATRVENDCLGRALINGDVPREATDFSBANKSALMD ESSDSGVIPSHSENALHASEEGEGGGKADSLGVIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLRKRHYWRLDCKCITLPQ NNTTNRYYKEIPLSEILTVESAQNFSLLVPFOTNPICFEIVTANA TYFVCEMPGGTPGGPSGGGAARGMCTAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENDIATVYGIFPBEVLGSGQF GVYGGKHRKTGRDVAVKUJDRIPPTGFESQLRNEVALIGSLAR HRGIVALECMFETPERKFVVMBELHGDMLEMILSSEKGRLPPRL TKFLITQILVALRHLHFKNIVHCLLKEPRVLLASADPFPQVKLC DRGFRRIIGEKSFRRSVVCTFAYLAPEVLLOKGYNRSLDMWSVC VIMYYSLSGTFFFREDEDINDQIQNAARMYPASSPWSHISAGAID LINNLLQVKMRRRYSVDKSLDHAGEOGYNGSCLMWGFE				KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSERVT
SCNTHTOP PAEDS OKS SCANTSKORPHASCTICGESEED PP EHK PSKLKRSHELDI LDENPASDFDOSGLLGFYKSGOKYGG (1 PNFS HROVEY LEKNVELKSKYLDMRRQ IKMKNKHI FFTKESEKP FFKK SKILS KVEKFLTWVNKPMDEEASGESS HONGHDASTSCOSEGS DMSVKKGDDLLETNNPEPEKGOSVSSAGELETENY PROBSILATV PDEODCVTQEV PDSRQASTEAEVKKKNKKKNKKNKKVOLPPEIAA VPELAKYMAQ RYRLFSR PDOEIKLDREGMESVTPEK LAEHIAG? VSQSFKCDVVDA PCCVGGNTI QFALTGMRVI AIDID PVKIALA RNNAEVYGIADKI EFICED PLLLASFIKAD VVPLSP PWGGPDVA TARTFDIRTMSPDOFFIFIKKSKITMN IVY FLPRRADID QVAS LAGPGGQVEIRQNFINNILKTITAYFGDLIRRPASET HRARVDRSRESS FGGDLR PROFINING KRITNITY FPROBLID QVAS WARATSGLILWPHTAER ROLLGAENRALTGGQQAED PTLASGAYQ WPGSSVELQGSVWCDAFTLLSSFTGQAP PWHTDBUD QVMLRL AQGEVVDKARVPAHGQVLOVGFSTEAALQDLSS PRLSQLCSQGL CGLIKR PGDLDEVLS PHVDR VLGRRSL PAVARR FHSPLLPYRY TDGGAR PVI WWAPDVQHLSD PDEDQNSLALGMLQ VQALLAHSCN WPGQAP CPGTHHTEWARLALFDFLLQVHDRLDRYCCG FEP EPS D PCVEERLREKCRNPASIRLY HILVRSSD PSHLVJ IDNAGNLOHP EDKLNFRLLEGIDGF PESAVKVLASGCLOMMLLKSLQMD PVFWE SGGAQCLKQVLOTLEGRGCULGHIQKHUNLLKSLQMD PVFWE SGGAQCLKQVLOTLEGRGCULGHULKHNLTLFRDEDDP 6305 99 420 MMTWGRSTYRFR PRRSVPP PELIGFMLE PGDEEPQQEEP PTES RDPAPGGREED GGAAD TO VPDLEADLQ ELSQSKTGDECGDGPD VQCKLTIKSSDYRMP EGG SGGAQCLKOVLOTLEGRGCULGHULKHSLGVCKOTTLPQ WCKLTIKSSSCJKMP EGG SVSTGMERGON SVRHTTRKSSTTLREGWVHYSNKDTLRRHWRULDCKCTTLPQ NNTTNRYYKE IDLSELTLYESAQN PSLVPPETUPHCPEIVTANA TYFVGEMPGGT PCGP SGQAEAAR WETA IRQALMPVILQDAPS APGHAPHRQASLSISVANSQLGENVDLATVYGI FPDEVLGSGOF GVYGGKHRKTGRDVAVKU IDLST PTROBSCLRIPE ILVRANA TYFVGEMPGGT PCGP SGQAEAAR WETA IRQALMPVILQSLRS HPGIVALECM FETPER VFVWMEKLHGDMLENT LSSEEKGRLPERL TKLLTOTLIVALRHLHKRIV LEFT PTROBSCLRIPE ILVRANA TYFVGEMPGGT PCGP SGQAEAAR WETA IRQALMPVILQSLR HPGIVALECM FETPER VFVWMEKLHGDMLENT LSSEEKGRLPERL TKLLTOTLIVALRHLHKRIVALDELFERUNDLAGAN FRANFASSOKLUP VLUGSLRWGE UTMYSLSGTFFFENDED IND OLGARAAR MYPASS PMSHISAGAID LINNLLQVKM RKRYSVDKSLSHPWLOEVOTHLAGRENGE	1			QSQLDSCTSHDGHQQLSEVSSKRECPASGOSEPRIGGTNEESING
PSKLKRSHELDIDENPASDFDDSSLLGFKYGSGOKYGGIPNSS HRQVEYLEKRVKLKSKYLDMRRQIRMKNHIFTKESEKPFFKK SKILS KVEKFLTWVNKPMDEEASQESSSHDNHDABTSCDSERQ DMSVKKGDDLLETINPEPEKCOSVSAGELETENYEROSILLATV PDEODCVTOEVDSRQABTEABWKKKNKKKWGLEPEIAA VPELAKYAAQRYRLFSRFDDGIKLDREGMFSVTPEKIAEHIAGR VSOSFKCDVUVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALAA RNNAEVYGIADKIFFICGDFLLLASFLKADVVPLSPPWGGPDYA RNNAEVYGIADKIFFICGDFLLLASFLKADVVPLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNYVFIPRNADIDQVAS LAGFGGQVEIEQNFINNKKTTAVFGBIJRRPASET AGFGGVEIEQNFINNKKTTAVFGBIJRRPASET DEVGDPGTKDLGHPHOHGSPIGETOGEVVTLVSPLPGSDMAAJPA WRATSGITLWPHTABGROLLGABURALTGQQAEDPTLASGAYQ WPGSVEKLQGSWCDABTILSSSRTGQAPPHLTDHDVQMLRLL AQGEVVDKARVPAHGQVIAOVFSTEAALQDLSSPRLSQLCSQGL CGLIKRPGDLPEVLSFHVDRVLGGRSLPAVARRFHSFLLPYRY TDGGARPVIWAPDVQHLSDPEDDNSLALGMLQYQALLAHSCN WPGSQFCPGHHTENARLALFDFLQVUBDLDRYCCGFPEPESD PCVEERIREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE SQGAQGLKQVLQTLEGGGQVLLGHIQKHNITLRRDEDP  6305 99 420 NMIWRGRSTYRPRPRRSVPPPBLIGPMLEPGDEEPQGEPPTES RDPAPQGREEDGGAAETQVPDLEADLQELSQSKTGDECGDSPD VQGKILTKSEQFKMPEGR  FPRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCARVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESSDSGVIPGSHSENALHASEEEEGGGKAQSSLGYTPLMRVVQ SVRHTTRKSSTTLRFGWVVHYSNKDTLRKRHYWRLDCKCTTLFQ NNTTNRYYKEIPJSEILITVESAQNFSLVPPGTNPCHCETIVTANA TYFVGEMPGGTPGGPSGQGABAARGMETAIRQALMPVILQAPS APGHAPHRQASLSISVSNSQIQENVVILANCHPTKQESQCRNEVAILQSLR HPGIVALECMFETPEKYFVVMEKLHGGMLEMILSSEGGRLPERL TKPLITQILVALRHLHFKUTCOLKDEDVLLASADPFPQVLC DFGFARIIGEKSFRSVVCTPAYLAPEVLLNQGYNRSLDMWSVC VIMYYSLSGTFPFRIDEDINDQIQNAAPMYPASPWSHISAGAID LINNLLQVKMRKYSVDNSLSHPWLOGKQVULDLIRELGEMGTEB	1			SGNTNTDPPAEDSOKSSGANTSKORPHASGTDGDFSPEDDDENK
HRQVEYLERNYLLKSYLDMRRQIKMENNHIFFTKESEKPFFKK SKILSKVEKFLTWNNKPMBEASQESSSLENGHDASTSCDSEEQ DMSVKKGDDLLETNNFEPEKCQSVSSAGELETENYEROSLLATV PDEODCYTQEVEDSRQAETEAEVKKKNKKNKKVKGUPEIAA VPELAKYMAQNYRLESFFPDGIKLDREGMEYSTYPEKIABHIAGS VSOSFKCDVVDAFCGVGGNTIGPLIAGFLKADVVFLSPPWGGPDYA RNNAEVYGIJADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFLNNKLKITLAYFGDLIRRPASET DEVGDPGTKDLGHPOHGSFIGETROGEVTLVSPLPGSDMAALPA WRARSGITLWPHTAEGRDLLGAENRALTGGQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETILSSSRTGGQAPPWLTHDVVMLKE AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSGGL CGLIKRPGDLDEVLSFHVDRVLGLRSLSPAVARRHSPLDYRY TDGGARPVIWAAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIHHTEWARLALFDFLLQVIBRJENGVCGFEPEESD PCVEERLREKCRNPAELRUHILVRSSPPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE SQGAQGLKQVLQVIOTLEGRGQVLLGHIQKHNTLTPRDEDP  6305 99 420 NMIWRGRSTYRPRRSVFFPELIGPMLEPGDEEPQGEEPPTES RDPAFGQEREEDGGAAAETQVPDLEADLGELSQSKTGDECGCDPD VQCKLITKSSCFKMPEGE RDPAFGQEREEDGGAAAETQVDLEAGLGSKTGDECGCDPD VQCKLITKSSCFKMPEGE SSGGSVLSKGPKMPEGE SSGGSVLSKGPKMPEGE SSGGSVLSKGPKMPEGE SSGGSVLSKGPKMPEGE GVYGGKHRTKSSTTLREGWVYHYSNKDTLRKRHYWRLDCKCTTLFQ NNTTNRYYKSTDLEGGDYDGSGGAGAARGWETAIRQALMPVLLQDAPS APGHAPHRQASLSISVSNSQIQENVLTATVQIFFDEVLGSGGF GVYGGKHRKTRGRDVAVKVDKLRFPTKGSQLGRENDLAGSLG HPGIVNLECMFETPEKYFVVMEKLHGDMLEMILSSEKGRLPERL FKLITOILVALRHLHFKNVLDCLKCPSLVDSGGF GVYGGKHRKTGRDVAVKVDKLRFPTKGSQLGNENLALGSLR HPGIVNLECMFETPEKYFVVMEKLHGDMLEMILSSEKGRLPERL FKLITOILVALRHLHFKNVLDCLKCPSLLDASADFPQVKLC DFGFARIIGEKSFRSVVCTPATLAPEVLLNQGYNRSLDMWSVC VIMYYSLSCTFPFRIEDEDINDQIQNAAPMYPASPWSHISAGAID LINNLLQVKRRKYSVDKSLSHPWLOGKYQNLDLRELEGGMGFE	ì		•	PSKLKRSHELDIDENPASDFDDSGSLLGERVGSGOVVCGIDNEG
SKILS KVEKFLTWINKPMBEEASGESSIEDNEHDASTSCDSEEG  DMSVKKGDLLETNINPEKCOSVSSAGELETENYERDSLLATV PDEODCVTQEVPDSRQAETEAEVKKKKNKKKKKKKKGLPPEIAA  VPELAKYMAGRYRLFSRFDDGIKLDREGFFSVTPEKIAEHIAGR VPELAKYMAGRYRLFSRFDDGIKLDREGFFSVTPEKIAEHIAGR VSQSFKCDVVDAFCGUGGNTTQFALTGRAVTAIDIDVKIALA RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA TAETFDIRTMMSPDGFEIFFLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFLINKLKTITAYFGDLIRRPASET  LAGPGGQVEIEQNFLINKLKTITAYFGDLIRRPASET  BEVORDFGTKOLGHPOHGSPIQETOGSVVTLVSPLPGDMAALPA MRATSGLTLWPHTAEGRULLGAENRALTGGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVGMLEKL AQGEVVDKARVPAHGQVLQVGFSTRAALQDLSSPRLSQLCSGGL CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLFYRY TDGGARPVIWMAPDVQHLSDPEDDONSLALGWLQVQALLAHSCN WPGGAPCPGTHHTEWARLALPDFLLQVUBDLDRYCCGFPEPESD PCVEERIREKCRNPAELRLVHTLVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIGGFPSKVVLASGCLQNMLLKSLQMDPVFWE SQGAQGLKQVLQTLEGRGQVLLCHIQKMLTLFREDEP  6305 99 420 MMIWGGSTVRFPRFRSVPPPELIGPMLEFGDEEPQGEEPPTES RDPAFGGREEDQGAAETVALAGGCLQNMLKSLQMDPVFWE SQGAQGLKQVLQTLEGRGQVLLCHIQKMLTLFREDEP  6306 1 1874 PTRPSKVKVPHTELHSYTRPTVCQACKLLKGLFRGGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESSDSGVI PGSHSENALHASEEEEGGGKAQSSLGYI PLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDLRKRHYMRLDCKCTTLFQ NNTTNRYYKEIPLSELITUVSAQNFSLVPPGTNHCHCEIVTANA TYFVGEMPGGTPGGPSGGAEAARGMETATRQALMPVILQAPS APGHAPHRQASLSISVSNSQIQENVVILANGLPGTVLOAPS APGHAPHRQASLSISVSNSQIQENVVILANGLPGTVLOAPS APGHAPHRQASLSISVSNSQIQENVVILANGLPGTVLOAPS APGHAPHRQASLSISVSNSQIQENVVILAGAGPPPQVKLC GVVYGKHKRTGRDVAVKVIDKLRFPTKGSSQLRNEVALIQSLR HEGIVALECMFETPEKFVVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALARHLHEKVUTOLKDEMVLAAPSLOMWSVC VIMYVSLSCTFFPRIDEDINDQIQNAAPMYPASPWSHISAGAID LINNLLQVKMRKYSVDNSLSHBWLOGKYQTNLLASADPPPQVKLC DFGFARIIGEKSFRRSVCTPAYLAPEVLLNQGYNRSLDMWSVC VIMYVSLSCTFFPRIDEDINDQIQNAAPMYPASPWSHISAGAID LINNLLQVKMRKYSVDNSLSHBWLOGKYQTNLLASLEGGMGEB		ł .		HROVRYLEKNVKLKSKYLDMRROTKMKNKHTEETVEGEVDERVY
DMSVKKGDDLLETNNPEPEKCOSVSSAGELETEN VERDSLLATV PDEODCYTOEVDESDAGETEAEVKKKKKKKKKKKURGLPPEIAA VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR VSQSFKCDVVVDAFCGVGGTTIQFALTGMRVIATDIDPVKIALA RINNAEVYGIADKIEFICDFLLLASFLKADVVPLEPPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEONFLANKLKITITAYFGDLIRRPASET HRARVDRSRESPGGDLEHPGRVRRDITLSGHPRLSTGHVVLLRE DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA WRATSGLTLWPHTAEGRDLLGABRRALTGGQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETILSSSRTGGAPPWLTDHDVQMLRLL AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY TDGGARPVIWMAPDVQHLSDPDBDQNSLALGWLQYQALLAHSCN WPGGAPCPGIHHTEWARLALFPELLQVHDRLDRVCCGFEPEPSD PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP EDKLNFRLLEGIDGFPESAVKVLASGCLQMMLLKSLQMDPVFWE SQGGAQCLKQVLQTLEQRGQVLLGHIQKHMLTLFRDEDP  6305 99 420 MNTWRGRSTYRPPRPRRSVPPPELIGPMLEPGDEEPPQEEPPTES RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQCKLITKSSCJFKWPEGR  6306 1 1874 PTRPSKVVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESSDSGVIPGSHSENALHASEEEGEGGKAQSSLGYIPLMRVVQ SVYHTTRKSSTTLREGWHYSNKDTLRRHYWRLDCKCTILPQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGABARAGWETAIRQALMPVILQDAPS APGHAPPHQASLSISVSSQIQENVDIATYVQIPPDEVLGSQF GVYYGGKHRKTGRDVAVKVIDKLRPPTKQESQLRNEVAILQSLR HEGIVALECCHFETEKVFVVMEKLHGDMLEMTLSSEKGRLPERL TKPLITQILVALRHLHFKNIVHCDLKPENVLLASADDFPQVKLC DFGFARIGEKSFRRSVGTPAYLAPEVLLNQGYNRSLDMWSVC VUMYVSLSGTFPPREDEDINDQIGNAAEMYPASPWHSIGSAGAID LINNLLQVKMRKYKSVDKSLSHPWLOEYOTWILDLEREHGMGFF	i			SKILSKVEKELTWYNKPMDEFASOFSSSUDNSUDASTOSTOR
PDEODCYTQEVPDSQAETEABUKKKNKKNIKKUNGLPBEIAA VPGELAKYWAQRYALFSRPDGIKLIDREGWFSVTPEKIAEHIAGR VSOSFKCDVVVDAFCGVGGNTIQFALTGMRVIATDIDDVKIALA RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPMGGDPYA TAETTDIRTMSPDGEFIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET  1 1438 HRARVDRSRESFGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE DEVGDPGTKDLGHPGMSPIQETQSEVVTLVSPLPGSDMAALPA WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ WPGSVEKLQGSWWCDAETLLSSRTGQQAPPMLTHDVVMLRLL AQGEVVDKARVPAHGQVLOVGFSTEAALQDLSSPRLSQLCSGGL CGLIKRPGDLPBVLSFHVDRVLGLRRSLPAVARFHSPLLPYRY TDGGARPYIWMAPDVQHLGDPBEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPPEPSD PCVEERLREKCRNPASLRIVHILVRSSDFSHLVYIDNAGNLQHP EDKLNFRLLGEIDGFFSAVVVLASGCLOMMLLKSLGMDPVFWE SQGGAQGLKQVLQTLEDGCQVLLGHIQKHNLTLFRDEDP  MTWRGRSTYRPFRPRRSVPFPELIGFMLEFGDEEPQGEEPPTES RDPAPGGGREEDQGAAETQVPDLEADLQELGSQSKTGDECGDGPD VQGKILTKSSQFKMPEGR  6306 1 1874 PTRPSKVKVPHTELHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD ESSDSGVIPGSHSNALHASEBEEGEGGKAQSSLCYIPLMRVVQ SVRHTTRKSSTTLREGWVHYSNKDTLRKRHYWRLDCKCTLPQ NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGGPGGGABAARGWETAIRQALMPVILQDAPS APGHAPPHRQASLSISVSQIQENVDIATVYQIFPDEVLGSQF GVVYGGKHRKTGRDVAVKVIDKLRPTTKGESQLNEVAILQSLR HEGIVNLECCHFETEKVFVVMEKLHGDMLEMTLSSEKGRLPERL TKFLTTQILVALRRLHFKNIVHCDLKGPNTVLLASRADFPQVKLC DFGFARIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVC VIMYVSLSGTFPFNEDEDIINDQIGNAAFMYPASPWHILSSAGAID LINNLLQVKMRKYKSVDKSLSHPWLOEYOTWILDLRSLEGKMGFF	1			DMSVKKGDDLI.ETNNPFPFKCOSVSSAGELETENVERDOLI AMIL
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NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA TYFVGEMPGGTPGGPSGGAEAARGWETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSSQF GVVTGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRRRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER	[	ł	l	CUBUTTER COTTE PROMINENCES
TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF GVVYGGKHRKTGRDVAVKVIDKLRFFTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFFFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER	1			MATTER CHARLES OF THE
APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSSQF GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER	1 1	ľ		THE LINE I KELPLSELLTVESAQNFSLVPPGTNPHCFEIVTANA
GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADDFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER				TIT VGEMPGGTPGGPSGQGAKAARGWETAIRQALMPVILQDAPS
HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADDFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYMRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER	] ]	.		APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF
TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVILINQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOGYOTWLDLRELEGKMGER	, 1	. 1	İ	GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER	į l	· [	1	HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER	<b>!</b>		İ	TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER	[	i	l	DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNOGYNRSLDMWSVG
LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER	ļ J	į	Ì	VIMYVSLSGTFPFNEDEDINDOIONAAFMYPASPWSHISAGAID
YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPODHDMOG	1 1	İ	ļ	LINNLLQVKMRKRYSVDKSLSHPWLOEYOTWLDLRELEGKMGER
	<u> </u>			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMOG

CPO	Prodictod	Predicted end	There are a second contributed as and a second
SEQ ID	Predicted beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	amino acid	
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG
1			QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
		1	VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
i	1	1	TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
ł		ļ	SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
ł			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
	1		GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
1	1		VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
	1		GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
1		1	PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
	1	i	DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
		<u>L</u>	QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
1		1	LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
1	1	1	PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
İ	1	İ	WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL
}	ł		VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
1	į.	1	VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
i	1		KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
1	1	1	PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
	<u> </u>		YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
L		l	KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
	1	]	AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
Į.			IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
ł		ł	KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
1			VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
1	1		CIPKIQSMIEDANKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
	1	1	LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
1	1		ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
1		1	PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
1			MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
J	j	1	KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI
L	<u></u>	<u> </u>	KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
I	i		GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
	1		RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
1		}	VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
1			DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
l			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
1		i	GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD
			VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
l	1		YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
1 .	1		FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
1	1		RLNEQREODRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
}			TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
1			FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
	1		TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
1			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
1	1		QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
L	<u> </u>		

:5

SEQ	Predicted	F 6 32 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
]	sequence		\=possible nucleotide insertion)
		<del></del>	SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
ł	1		LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
1		•	TEPVTSMTIJEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
1	1		QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
1			MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
	1		AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
1			RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFOEF
1			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIOGEEEANDVWKAAF
1			FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVT
	ĺ		TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKOSVK
1			YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCPSDPTSK
i			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
1			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
ĺ			LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
<b>!</b>			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA
			IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI
1 1	İ		VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
1 1	4		HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
	i		VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLODTVFLGP
1 1	I		GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH
<del> </del>			LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
1 1			MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEOAKKES
1 1	1		EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
[ [	ļ		ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEOYOKAA
] .	ļ		EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
6317	102	839	MHCVNHAKQSMLEKGG
		650	PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
j !	ľ		FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
] [		i	TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
1		i	QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
	]		PAITAAKQNTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
] [	]	· -	LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
1	1		LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
	İ		VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
1		ļ	ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
		Ī	DVASLEHTKOWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
		ļ	EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
			ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT
			ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWOAOPGATEES
		1	CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
			SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV
	<del></del>		

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del></del>		TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
1	1	1 ****	RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
1			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			EDKLWDI INVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
1	ļ	ļ	PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
1			MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
6321	1418	341	FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
1	7470	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
1	1		RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1			VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
J	j	]	FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1		ĺ	NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
1			IPGGMVDPGEKISATLKREFGEEALNSLQKTSAEKREIEEKLHK
i		i .	LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
1	1	ļ	LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
6322	2047	1083	EADCHAL NORTH YOUNG TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF T
1	2017	1003	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
1	1		WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
1	1		AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
	}	•	FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
i	1		RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
1	1		
	}		VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALOA
1	<u> </u>	020	PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
1			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
	l		LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
1	1 .		MALSVIATHRGLRSSASILVAEPHDWNTERPOVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
1	l .		RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1	1		PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
1			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTQPGVHGP
1			WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1	]		PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
1			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
1	j l		RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
I	]		KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
1			EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
l	]		SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
			EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
1			KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
1			KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
1			SRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRRHO
1			RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
1		•	RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWRDRSR
1			TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
1			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
1	ļ		VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
1	ĺ		GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
	·		1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
(	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			QAWGGVGQEASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
1	· .		DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
ľ	1		GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
	į.		LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
			LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
}			RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
	ł		SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
	į.		RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
1			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEBEMHTDAKIRAENGTGSSPRGPGCSL
			RHFACEQNLLSRPDGSASFLQGDTSVLAGVYGPAEVKVSKEIFN
i			KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
i	1		TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
	ł		SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
	ĺ		ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
1			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
	•		RGDIERKSLAINEEFVSIFKEVKEELESISEDVQAMSNCCQDMT
			SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT
			SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA
1			GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
1			PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE
1 .			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
			YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
1			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
1			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
<b>1</b>			EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
1			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
			LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR
		<u> </u>	SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
1			PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
1			KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
1			EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
1			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
			NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
6331		· · · · · · · · · · · · · · · · · · ·	TYESCLIN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
1 1			LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
[	<b>!</b>		RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA
- <u>  </u>			IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
; I			NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
j			SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
; I			SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
1 1	. 1		BLRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
		*	VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
<u></u>			KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
1 1	ľ		QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
1 1	ļ		GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
L			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS
			· · · · · · · · · · · · · · · · · · ·

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SEQ	Predicted	Predicted end	Umino paid goment as being a series
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Coden /-negrible runlestide deleti-
į.	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
<u> </u>	Sequence	<u> </u>	
1	}	l	GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK
1	]		CPWKEYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYQNTIVAG
	•		SLITKSNLHAMIKAEESSKQEECTTTSTAPVPTTEIPTTMSTMA
1	į.	Ì .	AAEAAAAVVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1	i		EVTSIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
I	ļ	1	EETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL
	1	1	KEKRVPSNASWEQAMKMI INDPRYSALAKLSEKKQAFNAYKVQT
-			EKK
6334	. 17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHN1LSKR
			GFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK
I			ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD
!		1	QVVEDLNSREQETCQPVHVVNVDIQDNHEEATLGAFLICELCQC
	<del>                                     </del>		IQHTEDMENRIDELLQEFEEKSGRTFLHTVCFY
6335	82	529	AARAR PGVLCCRLLGAALGDQSRVEMSYI PGQPVTAVVQRVEIH
l			KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
1		ł	GPAEIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
			LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
1.	j		LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
ļ	1	1	ADFWLTEKDLIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
1	i	1	MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
			NHSSHTAQTPGI .
6337	76	524	EGIQMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
i			ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI
I		1	PAFEMVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ
L	<del> </del>		TDYBEGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
i		İ	GLRLALLLLGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNY
l		1	KNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLED
İ		l	KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
İ	ł	ŀ	ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
•		Í	DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
1		l	AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
[		İ	DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIIWI
1			DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE
(222	1		DLPSAEELEDWLEDVLEGEINTEDDDDDDDD
6339	245	1813	NRCDRGGGGQAERQAGQGCRTQGAGPGFGFGHSFFSQGAMKAFH
]		j	TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
1	1		VTESPQRVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE
ı			SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY
İ	1	1	LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
		<b>!</b>	VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL
1		ł	KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL
J		l	VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
		1	DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR
1		İ	TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
1		1	GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM
<u> </u>			NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
6340	2	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS
		1	SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF
1		1	PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
1	i	I	EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR
ł .	1	1	
			HPHTEHVQQTFRTEIKI
6341	2	645	l ·
6341	2	645	HPHTEHVQQTFRTEIKI

SEQ	Predicted		
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid F=
	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	corresponding	corresponding	H=H1Stidine, I=Isoleucine, K=Lysine
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
j	residue of		S=Serine, T=Threonine, V=Valine,
į.	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	sequence	sequence	Codon, /=possible nucleotide deletion,
	Degacace		\=possible nucleotide insertion)
- 1			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
6342	2	1102	VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
0012		1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
	1	1 .	KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
	}		TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
	1		DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
1	1	İ	QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLTGOKEAKRWG
1	1		TAHGSIVPYQAFKTKDGYIVVGAGNNOOFATVCKII,DI,PEI,TDN
i	Į.		SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
1	į		PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKEK
6343			MSEARPFPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDOHETH
0343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESOFTLSKCIDAV
l			MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
ı	l i		GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGOHT
1	1		ETLLAGSLAKALCYIHRMNKEVKDNOEMKSRILVIKAAEDSALO
ı			YMNFMNVIPAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
	]		PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNI.
1	1		IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKLK
6344	2508	147	VSA
1	1 2300	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
i			QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
ĺ	ł .		QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
i	ļ <u> </u>		PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
1	] · [		VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
i	l ·		TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
1			PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
1	i		LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
	i		PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
1			VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
	1		LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
1			ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
1			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
1 1	ľ		PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
[ [	į		DHFITVDAVGCFEGDEEEBEDDEDEEEIEVEEBLCKQVRSRDIS REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
1 1	ļ		SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
L!	<u> </u>		TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
ļ <i>i</i>	1	l	HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
	1	f	ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
[			IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
l i	1		EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
	Į.		QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
l		ļ	RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
	1	į	QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
}	l l	1	QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
	i		QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
ľ	1	i	LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA
i i		ł	ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
İ		į	ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
j	j	I	VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
l		:	TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
			RV3MDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
]		1	SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
- 1	1		DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
		1	DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
<u> </u>		<del></del>	VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
	i		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
ĺ	<b>.</b>		TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
1	<b>!</b>		TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
	1		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
	}		GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
	Ì		HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
]	<b>.</b>		DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1	f		GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
1			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
1	Į į		IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
ı			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
i			PNTALTPPTPLVGLYSLWQELTPDYSMESHORDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
1			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
1			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
i			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
1			DVDG
6347	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTOKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
•			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
ì			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
1			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
} .			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
]	1		RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
[ i			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
1			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
	ĺ		CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
1	1		ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6348		3655	DVDG
0340	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
[			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
; [			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
j i			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
j [			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
!!		•	EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
j 1			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
į l			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
<b>L</b>	<u>-</u>		LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

1D beginning nucleotide location corresponding to first amino acid acid acid acid acid acid acid acid	SEQ	Predicted	Predicted end	
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence estate of the first amino acid residue of amino acid sequence estate of the first sequence estate of the first of	1 -		ľ	Amino acid segment containing signal peptide
Corresponding to first amino acid electide d	NO:			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequ	i	1		Gracianic Acid, F-Phenylalanine, G-Glycine,
to first amino acid residue of residue of amino acid anino acid sequence  Securine. The Three mine is a sequence  Securine. The three mines is a sequence  Securine. The three mines is a sequence  Sequence				I-Leugine M Mattieri
### Particle of amino acid sequence   S=Serine, T=Threndine, V=Valline, M=Typtophan, Y=Typcosine, X=Unknown, *=Stop Codon, /=possible nuclectide deletion, /=p	1			P-Proling O.Clubanine, N=Asparagine,
amino acid sequence    Sequence		amino acid	,	S-Serine T-mbroomine, R=Arginine,
amino acid sequence    Codon, /-possible nucleoid Single deletion    -		residue of		W-Truntonham V Waline,
ECATTCSNSIGPTSSNOPHER/KTKTTFEDR/KDSTLIGSSSIVER EDAVHITEMESDDEEEEKGPVSPRALGESEEEVPGESNDEG YSTLSITPEMLASYKSYSSTFISLEGOVGANDGRIRHDOWN KENHEATGPRISRELLDEKGPBVLODSLDRCYSTPSGCLEUTUS COPYRSAFYVLGQRVGIANNDEIEKYGDEDOPSCPPLESG ELLDEKGPBVLODSLDRCYSTPSGCLEUTUS COPYRSAFYVLGQRVGIANNDEIEKYGDELDPSCPPLESG ELLDEKGPBVLODSLDRCYSTPSGCLEUTUSCOPYRSAFYLLEQGRVGLAV BELLDEKGPBVLODSLDRCYSTPSGCLEUTUSCOPYRSAFYLLEQGRVGLAV DMDEIEKYGEVEDQDPSCPRLSGELLDBEKGPUSGBLENGER PBVLQDSLDRCYSTPSGCLEUTDSCOPYRSAFYLLEQGRVGLAV DMDEIEKYGEVEDQDPSCPRLSGELLDBEKGPUSGBLENGER PBVLQDSLDRCYSTPSGCLEGHDSCOPYRSAFYLLEQGRVGLAV DMDEIEKYGEVEDQDPSCPRLSGELLDBEKGPUGBSLDRCYST TPSGCLELTDSCOPYRSAFYLLEQGRVGLAVBMEIEKYGEVED DDPSCPRLSGRELLDBEKEPVLQOSLGRCYSTPSGTLEDHDLOG PYSSAVYSLEEQYLGLALDVDRIKKDGEEEDGOPPCRESGEL LEVVSPBVLQDBLORCYSTPSGCLEGHDSCOPYGSFTALBEER VGFSLDVGEIEKKGKKRRGRSKKERRGRKGEEGDOPPCP RINSMLMEVEREPVLQDSLDCYSTSPWTSGVLEIDLOG PSSAVYSLEEQYLGLALDVDRIKKDGEEEDGOPPCRESGRL LEVVSPBVLQDGLORCYSTPSGCLEGHDSCOPYGSFTALBEER VGFSLDVGEIEKKGKKRRGRSKKERRGRKGEEGDOPPCP RINSMLMEVERPEVLQDSLDCYSTSPWTSGVLEIDLOKGPRES KLABGLKQABELRQYKVLVHSGCRELTQLREKLARGRDARSSLN EILDALLTPEDPDLSQGGDLGGLGGAGCRCADHUCKLSEEND DDDEDVQVZVABKVQRSSSPRBMCKABEKEVPEDSLBEKLTTGS NSHGPCDSNGPHKNIKTTEEDEWNSTLVUNGTRSSHDECQDALN LIPVGGTSSATNVSMVVSAGPLSGEKAANNILEINELPPOLA EKKOCPFNILKEKCSLTQLALGALLATOPEDFSGCGOLLGGGLAGGCCLADGHUNGK LSPENDNDDDBDVQVEVABKVQKSSSPRBMCKABEKEVPEDSLBE ECATTCSNSHGPVDSNOPHRNIKTKITEEDEWNGTUNGTESSHDEV EDAVH I PPRISDDEEEEKGPVSPRILOGSEEBEVPGBSUBE CATTCSNSHGPVDSNOPHRNIKTKITEEDEWNGTUNGTSSSHVBB EDAVH I PPRISDDEEEEKGPVSPRILOGSEEBEVPGBSUBG VSTLS I PPBMLASYSKYSSTFISLEGQVCAMDIGHRNDQVK KEDHBATGFRLSFELLDEKGPFVLQDSLDRCYSTPSGCLELTDS COPYRSAFYVLEQQRVGLAVMBGEIRKGCREGDOPPCPLERISELELDEKGP PSSAVYSLEEQVIGGLALDVRDREIRKGCBEDONPCC BLABEKTSPELLDEKGPFVLQDSLDRCYSTPSGVLLEPDLGQ PSSAVYSLEEQVIGGLALDVRDREIRKGCEBEDOPPCPLERISEL LEVVERPVLQDSLDRCYSTPSGCLLEDTSSCHPLEPDLG PPSSAVYSLEEQVIGGLALDVRDRIEKYGPSLEPDLG PPSSAVYSLEEQVIGGLALDVRDRIEKYGPSLEPDLG PPSSAVYSLEEQVIGGLALDVRDRIEKYGPSLEPDLG PPSSAVYSLEEQVIGGLALDVRDRIEKYGRSEPDLECATTCS NSHGPCSNOPHRINKITTERSGELDENGSCHOLG	i	amino acid	ſ	Codon /possible x=Unknown, *=Stop
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GINGLALDVORITKOOGEEEDGGPPCCRISRELLEVVEPEVLOG  SIDRCYSTYSSCLEDGYDSCOPYGSTABERHUFGSLDUGETE  KKKKKKRKRKRRRSKKERRSKKERRSCEEDGNPPCPRISRELLDEKG  PRIVLODSLDRCYSTPSCLELDTSCOPYRSAFYILEGGRAVGLAV  DMBEIEKYGEVEEDGDPSCPRISGELLDEKEPEVLOGSLDRCYS  TPSGCLELTDSCOPYRSAFYILEGGLAVDMEIEKYGEVEE  DQDPSCPRISRELLDEKEPEVLQDSLORCYSTPSCYLELPDLGG  PYSSAVYSLEEDYLGLALDVORIKKUGEEEDGGPPCPRISRELLDEKG  VGFSLDVOGEIEKKGKKKRRGRKKKERRGKKEGEEDGNPPCP  RIMSHLMEVEEPEVLQDSLDICYSTPSSCLEOPDGCOPYGSSFYALEEKH  VGFSLDVOGEIEKKGKKKRRGRKKKERRGKKEGEEDGNPPCP  RIMSHLMEVEEPEVLQDSLDICYSTPSSCLEOPDGCOPYGSSFYALEEKH  VGFSLDVOGEIEKKGKKKRRGRKKKERRGKKEGEEDGNPPCP  RIMSHLMEVEEPEVLQDSLDICYSTPSWFELDDFFKEE  KLAEGLKGABELRQYKVLVHSOGEELTQLREKLEGGRDASRSLN  BEILGALLTDFEPPKSGOQDLOGGLAECHAGHLVOKLSFENDN  DDDEDVQVEVAEKVQKSSSPREMKKEEKEVEEDSLECATTCS  NSHGCDSNOPHKNIK HITTEEDEVINGUORLAGECHAGHLVOKLSFENDN  LIPVEGTTSSATNVSMVVSAGPLSGEKAAINILEINEKURPQLA  EKKOOFRINLEKCEFLOLACFLANGODLAGECRLAGHLVOKLFMEN  EROFKEEKLABGLKQAEELRGYKVLVHSGEBELTQLEKLREGR  DASRSLABEHLQALLTPEPPBKSGOODLOGGLAGECHAGHLVOK  LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEKEVEEDSLE  ECATTCSNSHGPYDBOPHRTKTITTUORESHDECQUACHUOK  KEDHBATGPRLSREILDEKGPEVLQDSLDRCYSTPSGCLEITDS  COPYRSAFYVLBQQRVGLAVMMDEIEKVGEVEEDOPSCPNISHE  ECATTCSNSHGPYDBOPHRTKTITTEDEDVOSODLAGECRLAGHLVOKLFMEN  KEDHBATGPRLSREILDEKGPEVLQDSLDRCYSTPSGCLEITDS  COPYRSAFYVLBQQRVGLAVMMDEIEKVGEVEEDOPSCPRISRELLDEKG  ECATTCSNSHGPYBOPHRTKTITTELEDQUTGOPYSSAFVLEE  GYALALDUDRIKKOGEEEBGCPPCPPRISRELLDVGEIE  KKGGKKRRGRRSKKERRGRKEGEEDONPPCTRLSRELLDEKG  PEVLODSLORCYSTPSGCLEITDSCOPYRSAFYILEGGRAVELEE  QYALALDUDRIKKOGEEEBGCPPCPPRISRELLDVGEIE  KKGGKKRRGRRSKKERRGRKEGEEDONPPCTRLSRELLDEKG  PEVLODSLORCYSTPSGCLEITDSCOPYRSAFYILEGGRAVELOWE  DODDSCCPRLSRELLDBLAGVTTSSHLIDDFGHYRSVEY  TPSGCLELTDSCOPYRSAFYILEGERGRAGEGEDOPPCPCRISRELL  LEVVEPEVLODSLORCYSTPSSCLEGDPSCOPYGSSFYALEEKHUGE  DODDSCCPRLSRELLDBLAGVTTSSHLIDVFGMYIPPO  PYSSAVYSLEGQYIGLALDUDRIKKGCETLOTHSMILRGERGABGSIL  LEVVEPEVLODSLORCYSTPSSCLEGDCOPPCGREGRE  LEVVEPEVLODSLORCYSTPSSCLEGDLOSCHEGEGGPCOPPCGREGRE  LEVVEPEVLODSLORCYSTPSSCLEGDLOSCHEGEGGPCOPPCOPPLISRELL  LEVVEPEV	ł	1	j	ELLDEKEPEVLODSI GRCYSTPSGYLEL DDL CODYSCAVYCE DR
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DIMDLIEKYQEVEEDQDSCPREGEILDEKEPEVLQESLDRCYS  TPSGCLETIDSCOPYRSAFYILEQORVGIANDMEIEKYQEVEE DQDPSCPRISRELLDEKEPEVLQDSLGRCYSTPSGYLELEPLIGO PYSSAVYSLEBQYLGIALDDURINGREEDQDGPPCPRLSREIL LEVVEPEVLQDSLDRCYSTPSSCLEOPDSCOPYGSSFYALESKH VGFSLDVGEIEKKGKKKRRGRKSKERGKEGEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSWYFELDPSFQHYESVFY SFEEBHISFALYVDNRFFTLTVTSIHLVFQGVIFFO  AGAEKCFVTLLACFLAKQONKYKYECKOLIKSMLKNELQFKEE KLAEQLKQAEELRQYKVLVHSQEREITQLREKLREGRDASRSLN BILQALITPDEPPKSQGQDLOEQLAEGCRLAQHLVOKLSFENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLENCAITCS NSHGPCDSNOPHRIN KITFFEDEVALDRCHSKYKPECKOLIKSMLKNELQFKEE EKKOPFRILKEKCFLTQLACFLANQQNKYKYEECKOLIKSMLRNEL ERQFKEEKLAEQLKQAEELRQYKVLVHSQEREITQLREKLREGR DASRSLMEHLQALLTDDEPDKSQGQDLOEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQASAPREMPKAEREKEVPEDSLE ECAITCSNSHGPYDSNQPHKRTKITFEEDKVDSTLIGSSSHVEW ECHTOLIT LENESDEEPEKGPPOSJENGER ECAITCSNSHGPYDSNQPHKRTKTIFFEDKVDSTLIGSSSHVEW ECHTOLIT LENESDEEPEKGPPOLSDECKTEVPDSSWDEE ECAITCSNSHGPYDSNQPHKRTKTIFFEDKVDSTLIGSSSHVEW ECHTOLIT LENESDEEPEKGPPOLSDECKTEVPDSSWDEE ECAITCSNSHGPYDSNQPHKRTKTIFFEDKVDSTLIGSSSHVEW ECHTOLIT LENESDEEPEKGPPOLSDERCYSTPSGCLELTDS COPYRSAFYULBQQRVGLAVNMDEIEKYQEVEEDQSWDEG YSTLS IPPEMLASYKSYSSTPHSLEEQQVCMADICHIRHWDVK KEDHBATGPRLISELLDEKGPEVLOSDELGCYSTPSGCLELTDS COPYRSAFYULBQQRVGLAVNMDEIEKYQEVEEDQSWDEG SLDRCYSTPSGCLEDDFSCPPLSGFLILDGFSFAVLEEPDCSWDEG EKKGKKRGRHSKKRRRGRKEGEEDQNPPCPRLSFELLDEKG PEVLQDSLDRCYSTPSGCLELDKGPEVLGELDEKTSELDEKG PEVLQDSLDRCYSTPSGCLELDKGPEVLGELDKEPSVLGELDCF TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCFRLSELLDEKGPEVLGELDKRCFSTPSGYLLEDLOQ PYSSAVYSLEQYLGLALDVDRIKKDQEEEDQCPPCRLSFELL LEVVEPEVLQDSLDRCYSTPSGCLELDKRCPSTPSGYLLEDLOQ PYSSAVYSLEQYLGLALDVDRIKKDQEEEDQCPPCRRSREIN LEVVEPEVLQDSLDRCYSTPSGYLEPDLOQ PYSSAVYSLEQYLVALNSGERELTQLEKCHRSGRASRSIN EHLQALLTDEPEDRSGQDDLOQLAEGCRLAQHLVQKLSPENDN DDDEDVVEVAEKVQKSSSREWGRAEERGKREGEGDQNPCCP RLMSMLMEVEEPEVLQDSLDRCYSTPSMYTEPDDSFOHRSKYF SPEEBIHSFALVVONFFFTILVTSLLLVFROMENSFELDFKEE NSHGPCDSNQPHKIKKTITTDJEEVLKSPDSASRSIN EHLQALLTDEPDRSGGODLOQLAEGCRLAQHLVQKLSPENDN DDDEDVGVVAEKVQKSSSREWGRAEERGVYEDGLEECAITCS NSHGP	1			PEVLQDSLDRCYSTPSGCLELTDSCOPYRSAFYILEOOPVCLAV
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PYSSAVYSLEEQYLGLALDVORIKKDOEEEDOGPPCPRISREL LEVVEPEVLODS LDRCYSTPSSCLEOPDSCOPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRKGRESKKERRGKEGEEDONPPCP RINSMLMEVEPEVLQDSLOTYSTPSMYFELDDSPOHYRSVFY SFEERIISPALYVDMRFPTLTVTSLELVFQMGVIFPO AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMLENELQFKEE KLAEGLKQAELRQYKULVISQEELTQLIEKKLEGRDASRSLN EILQALLTDEPDKSQGQDLQEQLAECGRAGHLVOKLSPENDN DDEPDVQVEVAEKVQKSSSPROKAEEKEVPBGLLEKCATTCS NSHGPCDSNQPHKNIKITFEEDEVNSTLUVDRRSSHDECQDALN LIPVFGPTSSATNUSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKULVISGGRELTQLREKLREGR DASRSLNEHQAALTTDPEDPKSQGQDLQEQLAEGGRLAQHLVQK LSPENDNDDBDUQVEVAEKVQKSSSPREMPKREKEVPEDSLEE ECATTCSNSHGPYDSNQPHKNIKTKITFEEDKUSTLIGSSSHVEW EDAVHI IPENSDDEEEEKGPVSVPNLOBSEEBEVQDSWDGG VSTLSI IPPEMLASYKSVSSTSTEEQQVCMAVDIGRHRMQVIK KEDHEATOPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAAVMMGEIEKVGEVEEQDDPSCPRISR ELLDEKBPEVLQDSLGRCYSTPSGYLELDLLGOPYSSAVYSLEE QYLGLALDVDRIKKDQBEEBDQGPPCPRISRELLEVVEPEVLQD SLDRCYSTPSSCLEOPDSCQPYGSSFYALEEKHVGFSLDVCGI KKGKKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLEDTSCOPYRSAFYILEQQRVCLAV DMBEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLQSUCRULAV DMDEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLQSUCRULAV DMDEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLQSUCRULAV DMDEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLQSUCRULAV DMDEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLQSUCRULAV DMDEIEKYGEVEEDQDDPSCPRISRELLDEKCPEVLGSUCRUMDEIEKYGVEE DQDPSCCPRISRELLDEKCPEVLQDSLGRCYSTPSGYLELDPLOQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRISREL LEVVEPEVLQDSLDRCYSTPSGCLEEDDSCQPPCGSFYALEEKH VGFSLDVGGIEKKGKGKRRGRSKKERRGRKGGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSGYRELDLFOX GFSLDVGGIEKKGKGKGKRGRRSKKERRGRKGGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSGYRELDLFOX GFSLDVGGIEKKGCGKARGRSKKERRGRKGGEEDQNPCP RLNSMLMEVERPEVLQDSLDRCYSTPSGYRELDLFOX GFSLDVGGIEKKGCGKARGGRSKKERRGRKGGEEDQNPCP RLNSMLMEVERPEVLQDSLDRCYSTPSGYRELDLFOX GFSLDVGGIEKKGCGKARGGRSKKERRGRKGGEEDQNPCP RLNSMLMEVERPEVLQDSLDRCYSTPSGYRELDLFOX GFSLDVGGIEKKGCGKARGGRSKKERRGRKGGEEDQNPCP RLNSMLMEVERPEVLQDSLDRCYSTPSGYREDLOX GFSLDVGGIEKGCGCARADHLUSKLSPENDN DDEDDVQFVARKVCLARG	1		•	DQDPSCPRLSRELLDEKEPEVLODSLGRCYSTPSGYLELDDLGO
LEVVEPEVLOBSLDRCYSTPSSCLEOPSCOPYCSSTYALEEKH VGFSLDVGEIEKKGGKKKRGRKSKERRGKEGEEDONPPCP RLMSMLMEUEDPEVLQDSLDLCYSTPSWYFELDDS FQHYRSVFY SFEERHISSALVVONRFPTLTVTSLHLVFQMVIFPO  AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMLENELQFKEE KLAEQLKQAEELRQYKVLVHSQCRELTQLEKKLREGRDASRSLN EILQALLTTDEPDEVSQGQLOEQGLAEGCRLAGHLVOKLSPENDN DDDEDVQVEVAEKVQKSSSPREMKKAEREVPEDSLEKCAITCS NSGGPCDSNOPHKNIKITPEEDEVSTLVVDRESSHDECQDALN ILPVFGPTSSATNVSMVVSAGPLSGEKAINILEINEKLRPQLA EKKQGFRILKBKCPLTQLACFLANQQNKKYEECKDLIKFMLRN ERQFKEEKLABCLKQAEELRGYKVLVHSQCRELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLOEDLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVGKSSAPREMYRAEKEVPEDSLE ECAITCSNSHGPYDSNOPHRKTKITFEEDKVDSTLIGSSSIVEW EDAVHIIPSNESDDEEEEKGFVSPRNLDGSEEBEVPQESMDEG ECAITCSNSHGPYDSNOPHRKTKITFEEDKVDSTLIGSSSIVEW EDAVHIIPSNESDDEEEEKGFVSPRNLDGSEEBEVPQESMDEG COPYKSAFYLLGQQRVGLAVMOUTGRIRMDQVK KEDHEATGPRLSRELLDEKGPEVVSDLDCSTSTSGCLELTDS COPYKSAFYLGQQRVGLAVMOUTGRIRMDQVK KEDHEATGPRLSRELLDEKGPEVVSDLDCSTSTSGCLELTDS COPYKSAFYLGQQRVGLAVMOUTGRIRMDQVK KEDHEATGPRLSRELLDEKGPEVVSDLDCSTSTSGCLELTDS COPYKSAFYLEGQRVGLAVMOUTGRIRMDQVS KKDHEATGPRLSRELLDEKGPEVVSDRJDERCSTSTSGLELDEKG ELLDEKRPEVLQDSLGRCYSTPSGYLELPDLOQPYSSAVYSLEE OVALGLALDVORIKKQDGEEEBQPPCPRLSRELLDEKG ELLDEKRPEVLQDSLGRCYSTPSGYLELPDLOQPYSSAVYSLEE OVALGLALDVORIKKQDGEEBGPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYKSAFYILEOQRVGLAV DMDEIEKYGSVERBOOPSCPRLSGRLLDEKGPEVLQDSLDRCYS TPSGCLELTIDSCOPYKSAFYILEOQRVGLAVDMDEIEKYQEVEE DOPSCPRLSRELLDEKGPEVLQDSLGRCYSTPSGYLELDELOG PYSSAVYSLEEQYLGLALDVDRIKKQDEEEDQGPPCPRLSREL LEVVEPFEVLQDSLDRCYSTPSGYLELDLOG PYSSAVYSLEEQYLGLALDVDRIKKQDEEEDQGPPCPRLSREL LEVVEPFEVLQDSLDRCYSTPSGYLELDLOG PYSSAVYSLEEQYLGLALDVDRIKKQUEEEDQGPPCPRLSREL LEVVEPFEVLQDSLDRCYSTPSGYLELDLOG PYSSAVYSLEEQYLGLALDVDRIKKQUEEEDQGPPCPRLSREL AEAGLKAGRGKKKRGRRSKKERRGRKGGEGDQNPCC RINSMLMEVEEPSVLQDSLDCCYSTPSGYBSTALEEKK VGFSLDVGGIEKKGKKKRGRRSKKERRGRKGGEGDQNPCCP RINSMLMEVEEPSVLQDSLCCCLIKGMLNGCHYSTECKCULLIKSMLRNECHDAS AGAEKCFVTLACFLAKQQNKYKYBECKLUTLSSKLECHLIKGUR NSHGPCDSNOPHNIKITTPEDPDVSCQDLOGLGERLACHLUVAK BAGECTSANDHLQALLTPDEPDVSCQDLOGLGERLACHLUVAK BAGECTSANDHLQALLTP				PYSSAVYSLEEQYLGLALDVDRIKKDOEEEEDOGPDCDBLSDBL
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ALMSMIMEVEEPEVLQDSLDICYSTPSWFELDBSFQHYRSVFY SFEEEMISFALVDUNRFFTLTVTSLHLVFQMSVIFPO AGAEKCFVTILACFLAKQQNKYKYEEKDLIKSMLRNELQFKEE KLABQLKQABELRQYKVLVHSQRRELTQLREKLRSGRAASSLIN BURDALTTDEPDKSGQDLQEQLAEGCHAGHLVOKKSPENDN DDEDDVQVEVABKVQKSSSPREMQKAEREVPEDSLEKCAITCS NSHGPCDSNQPHKNIKITFEDEVNSTLVVDRESSHDECQDALN ILPVEPPTSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQOFRNIKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN DASRSLNEHLQALLTTPDEPDKSGQDLOEQLAEGCRLAQHLVQK ERQFKEEKLAEQLKQAEELRQYKVUVHSGERELTQLREKLEGGR DASRSLNEHLQALLTTPDEPDKSGQDLOEQLAEGCRLAQHLVQK KEDHENDNDDDEDVQVEVABKVQKSSAPREMPRÄEEKEVPEDSLE ECAITCSNSHGFYDSNQPHRKTKITFEDKVDSTLIGSSSHVEW BEAVHIIPENBSDDEEEERBVPSRNLOESEBBEVPQESWDEG YSTLSIPPBMLASYKSYSSTPHSLEEQQVCMAVDIGRHRNDQVK KEDHEATGPRISTELLIDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLUQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSGE ELLDEKEPEVLQDSLGRCYSTPSGVLELPDLGQPYSSAVYSLEE UKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELDDSCPPTSPSTLEELDDLOEGE EKKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG DASSAVSLEELLDEKEPEVLQDSLDRCYSTPSGVLELPDLGQ PYSSAVYSLEEQYIGLALDVDRI KROQEEEDQPSPCPRLSRELL LEVVEPEVLQDSLDRCYSTPSGCLELIDEKSPEVLQESLDRCYS TPSGCLELTDSCOPYRSAFYILEQQRVGLAVDMDEIEKYGEVEE DQDPSCRRLSRELLDEKEPEVLQDSLDRCYSTPSGVLELPDLGQ PYSSAVYSLEEQYIGLALDVDRI KROQEEEDGDPPCPRLSRELL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCCPYGSSFYALEEKH VGFSLDVGETEKKGKGKRRGRRSKKERRGRKEGEBONPPCC RINSMLMEVEEPEVLQDSLDRCYSTPSSCLEQPDSCCPYGSSFYALEEKH VGFSLDVGETEKKGKGKRRGRRSKKERRGRKEGEBONPPCC RINSMLMEVEEPEVLQDSLDRCYSTPSSCLEQPDSCCPYGSSFYALEEKH VGFSLDVGETEKKGKGKRRGRRSKKERRGRKEGEBONPPCC RINSMLMEVEEPEVLQDSLDRCYSTPSSCLEQPDSCCPYGSSFYALEEKH VGFSLDVGETEKKGKGKRRGRRSKKERRGRKEGEBONPPCC RINSMLMEVEEPEVLQDSLDRCYSTPSNCHELDFKPHYSVFY SFBEEHISFALVYUNRFFTITVTSLHLIVFOMGVIFPG  AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLEQFKEE  LAEQLKQARELRQYKVLVINSQERELTQLREKLREGR NSHGPCDSNQPHNIKTTFEEDEVNSTLVVDRESSHDECQDALN LLPVPPGPTSSATNVSMVSAGPLIGGEKAAINTLBINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLNM ERGFKEEKLAEQLKQAEELRQAKUVHGGREILTGLREKLREGR DASSKLNEHLQALLTDDEPBYGGOODLOEOLAEGCRLAOHLVOK		]		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDONPPCP
3 3679  AGAEKCPYLLACFLAKQONKYMYEEKOLI KSMERNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLRREGRASRSLN EIILQALLTPDEPDKSQQDLQEQLAEGCRLAQHLVOKLSPENDN DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLEEK-LATICS NSHGPCDSNQPHKNIKITFEEDEVINSTLVVDRESSHDECQDALN LIPPVEPTSSATNVSMVVSAGPLSGEKAANHLVDRESSHDECQDALN LIPPVEPTSSATNVSMVVSAGPLSGEKAANHLVELTREKLRPQLA EKKQOFRILKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVOK LSPENDNDDDEDVQVEVABKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNOPHKRIKITFEEDEVDSTLIGSSSHVEW EDAVHI IPENESDDEEEEEKGPVSPRNLQESEEEEVPQCSWDEG YSTLS IPPEMLASYKSYSSTFHSLEEQQVCWAVDIGRHRWDQVK KEDHEATGFRISTRELLDEKGPSVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMWDEIEKYQEVEEDQDPSCPPLSR ELLDEKEPSVLQDSLDRCYSTPSGVLELDDLGQPYSSAVYSLEE QVLGIALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPSVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKKKKRGRRSKKERRGKEGEEDQNPPCPPLSRELLDEKG PEVVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEXYGEVEEDDDSSCPYRSAFYILEQQRVGLAVDMDEIEXYQEVEE DQDPSCCPRLSRELLDEKEPSVLQDSLDRCYSTPSGVLELDPLOG PYSSAVYSLEEQVIGLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPSVLQDSLDRCYSTPSGCLEUTDSCQPYGSSFYALEEKH VGFSLDVGGIEKKGKKKRGRKRKRRGREGEEDQNPPCP RLNSMLMEVEEPSVLQDSLDICYSTPSGYLELPDLOG PYSSAVYSLEEQVIGLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPSVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGGIEKKGKKKRKRRKKRRRGREGEEDQNPPCP RLNSMLMEVEEPSVLQDSLDICYSTPSMYTELPDSPOHYRSVPY SPEEBHISFALYVDNRFFTLTVTSLHLVFOMGVIFPO AGAEKCFVTLACHCAPLAVAGEKERCROASRSLN EHLQALLTPDEPDRKSQGQDLOEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAERVQKSSSFREMGAEEKEVPBDSLEECATITCS NSHGPCDSNOPHKNIKITFEEDEWNSTLVVDRSSSHDECQDALN LLPVPGPTSSATNVSMVYSAGPLSGEKAAINLLBINKELRFQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQVKUVHSQERELTQLREKLREGR ASKLOPHLJALLTPDEPDKSGGODLOELAEGCLLAAMINUKLFRUMM ERGFKEEKLAEQLKQAEELRQVKUVHSGERELTQLREKTRUML				RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYPSVFV
KLABÇLKQABELRQYKULVHSQERELTQLREKLERGERDASRSLM EILQALITPDEPDKSQQQDLQEQLAEGCRLAQHLVOKLSPENDN DDDEDVQVEVAEKVQKSSSPENGKAEEKBYPEDSLEKCATTCS NSHGPCDSNQPHKNIKITFEEDEWNSTLVUPRESSHDECQDALN LIPVPGPTSSATNVSMVVSAGPLSGEKAANNILEINEKLRPQLA EKKQOPRNIKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKSEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEGLAEGCRLAQHIVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHKRIKITFEEDKVDSTLIGSSSHVEW EDAVHI I PENESDDEEEEKERPVSRRNLGSSEEEVPQESWDEG YSTLS I PPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRNDQVK KEDHBATGGRLSRELLDEKGPEVLQDSLDECYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMNDEIEKYQEVEEQDDPSCPRLSR ELLBEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVVSLEE QYLGLALDVDRIKKDQEEEEDGOPPCPRLSRELLEVVEPSVLQD SLDRCYSTPSSCLEQPDSCQPYRSAFYILEQQRVGLAV DMBEIEKYQEVEEDQDPSCPRLSRELLDEKGPEVLQDSLDRCYSTPSGLALDKE EKKGKKKRRGRRSKKERRRGKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMBEIEKYQEVEEDQDPSCPRLSGELLDEKEPSVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPSVLQDSLGRCYSTPSGYLELPDLCQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPSVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLINSMLMEVEEPEVLQDSLDICYSTPSSMYFELPDSFQHYRSVFY SFEEBHLSFALYVDNRFFTLTVTSLHLVPROMVIFPQ  GAGAKCFVTLLACFLAKQONKYKYEECKDLIKSMLRNELQFKEE KLAGQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQQDLQEQLAGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQXAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKTFTEEDEVNSTLVVDRESSHDECQDALN LILPVPGPTSSATNVSMVVSAGPLAGGCRLAQHLVQKLSPENDN DASRSLNEHLQALLTTPDEPDKSQCDLQGOLAGCGRLAGHLOKLRPQLA EKKQQFRNLKEKCFLTQLACFLARQONKYKYEECKDLIKFMLRR	6349	3	3686	SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPO
EILQALITPDEPPKSQQQDLQEQLAEGCRLAQHLVOKUS.PENDN DDDEDVQVEVAEKVQKSSPREMOKAEEKEVPEDSLEKCAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAANNILEINEKLRPQLA EKKQCPRNLKEKCFLTQLACFLANQQMXKYEECKDLIKFMLRN ERQFKEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPPDKSQGQDLQEGLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPNESDDEEEERGPVSPRNLQESEEREVPQSSMDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHBATGPRLSRELLDEKGPEVLQDSLDECYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGCLELTDS QYLGLALDVDRIKKDQEEEEDGPPCPRLSRELLEVVEEFEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGPSLDVGEIE KKGKGKKRRGRRSKKERRGKEGEDQNPPCPRLSRELLDEKG PEVLQDSLLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE QDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGVLEIPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEDONPPCP RLINSMLMEVEEPEVLQDSLDRCYSTPSGVLEPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDONPPCP RLINSMLMEVEEPEVLQDSLDRCYSTPSGVLEPDLGQ PYSSAVYSLEDQYLGLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDONPPCP RLINSMLMEVEEPEVLQDSLDRCYSTPSGVLEPDLGQ PYSSAVYSLEDQYLOLALDVDRIKKDQEEEEDQSPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDONPCCP RLINSMLMEVEEPEVLQDSLDRCYSTPSGVLECHOLKSMLRNELQFKEE KLAGQLKQAEELRQYKVLVHSQERELTQLRECRDASRSLN EHLQALLTPDEPDFRSQQDLQEQLAEGCRLAQHLVVKLSPENDIN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVEDSLEECAITCS NSHGPCDSNQPHKNIKTTFEEDEVNSTLVVDRESSHDECQDALN ILPPGPTSSATNVSMVVSAGPLSGCRLAQHLVVKLSPECKDLIKFMLRN ERGFKEEKLAAGLKQAEELRQYKVLVHSQGRELTQLREKLREGR	""		3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
IDDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEKCATTCS NSKGPCDSNOPHNIKITTEEDEVNSTLVVDRESSHDECQDALM ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQCPRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAELRQYKUVHSGERELTQLREKLREGR DASRSILNEHLQALLTPDEPDKSQQDDLQEQLAEGCRLAGHLVQK LSPENDNDDDEDDVQVEVAEKVVKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNOPHRKTKITTEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEFEEKGPVSPRNLOESEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHBATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAFYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDGEIE KKGKGKKRGRRSKKERRGKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSSCLEUDSCQPYGSSFYALEELDEKG PEVLQDSLDRCYSTPSSCLELDBKGPEVLQDSLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELDGLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNFPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNFPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNFPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNFPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGKEGEEDQNFPCP RLMSMLMEVEEPEVLQDSLDICYSTPSSCLEGPSCDTLICYSPC VGFSLDVGEIEKKGGGRDAGLAGCTLAQHLVQKLSPEND DDEDVQVEVAEKVQKSSSFREMQKAEEKEVPEDSLEECATTCS NSKGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGGTSSANNYSMAGPLSGERAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYEECKDLIKMLRN ERQFKEKLAEQLKQAELRQYKVLVHSGGRELTQLEKKLEGGR		· 1		KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
NSHGPCDSNOPHKNIKITIFEEDEVNSTLVUDRESSHDECQDALN ILPVPGFTSSATNVSAGPLSGEKAAINILEINEKLRPQLA EKKQFRNLKEKCFLTQLACFLANQONXYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLINEHLQALLTPDEPDKSGGQDLQEQLAEGCRLAGHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSIGPYDSNQPHKTKLTIFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEKGFVSPRNLQESEEBEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHRATGPFLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDELEKYQEVEEDQDPSCPRLSR ELLDBKEPFVLQDSLGRCYSTPSGVLELPDLGOPYSSAVYSLEE QYMGIALDUDRIKKDGEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGETE KKGKGKKRRGRSKKERRGGKEGEEDQNPPCPRLSRELLDEKG PEVVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYLLEQQRVGLAV DMDELEKYQEVEEDQDPSCPRLSGELLDWFDEPLGQ PYSSAVYSLEEQYFGSAFYLEQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPFVLQDSLGRCYSTPSGVLELPDLGQ PYSSAVYSLEEQYLGLALDUDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKKKRGRRSKKERRGRKEGEEDONPPCP RLINSMLMFVEEFEVLQDSLDICYSTPSNYFELPDSFQHYRSVFY SFBEHISFALVYDNRFFTTLTVTSLHLVFQMGVIFPO RLINSMLMFVEEFEVLQDSLDICYSTPSNYFELPDSFQHYRSVFY SFBEHISFALVYDNRFFTTLTVTSLHLVFQMGVIFPO KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSGQDUAEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSFREMQKAEKEKPEDSLEECATTCS NSHGPCDSNQPHKNIKITTEEDEVNSTLVVDRESSHDECQDALN ILPVPGFTSSATNVSMYSAGPLSGGRAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEEKCKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSGQDLOGOLAECGRAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR	1			DDDDDDGGGCRLAQHLVQKLSPENDN
ILIPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKOPFRNIERKEFTTQLACFLANQONXYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQEERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSQGQDLQEGLAEGCRLACHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHOPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEKGPVSPRNLQESEEBEVPQESWDEG YSTLSIPPENLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHBATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELDPLQQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLDEKG ELLDEKEPEVLQDSLGRCYSTPSGYLELDPLOGPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQOPPCPRLSRELLDEKG KKGKCKKRRGRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSRELLDEKGPEVLQPSLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSRELLDEKGPEVLQPSLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQCPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQDPSCQPYSSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDCYSTFSWTELDPSFOHYRSVFY SFEEHIJSFALYVDNRFFTLTVTSLHLVFOMGVIFPQ AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSIN EHQQALLTPDEPPKSQGQDLQBOLABGCRLAGHLVQKLSPENDN DDDBDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECCATTCS NSHGPCDSNQPHKNIKITTEEDEVWSTLVVDRESSHDECQDAIN ILEVPGFTSSATNVSNYSAGPLSGEKAAINILBINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLABCLKQAEELRQYKVULVHSGERELTQLREKLREGR	i	[ ]		NEUGRODENORUSINATION
EKKQOFRNLKEKCFLTQLACFLANQONXYKYEECKDLIKFMLRN ERQFKERKLABQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGODLQEQLAEGGRLAGMIVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAERKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEKGPVSPRNLQESEEEEVPQESWDEG CAPYRIST PPENLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHBATGPRLSRELLDEKGPEVJCPDSLDRCYSTFSGCLELTDS CQPYRSAFYVLEQQRVGLAAVNMEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQDDSCQPYGSSFYALEEKHVGFSLDVGGIE KKGKGKKRRGRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV MDEIEKYQEVEEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEQQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDONPPCP RLNSMLMEVEEPEVLQDSLDTCYSTSMYFELPDSFQHYRSVFY SFEEBHISFALYVDNRFFTLTVTSHHLVFCMGVIFPQ RLNSMLMEVEEPEVLQDSLDTCYSTSMYFELPDSFQHYRSVFY SFEEBHISFALYVDNRFFTLTVTSHHLVFCMGVIFPQ KLASDLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGODLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITTFEEDEVNSTLVDRESSHDECQDALN ILPVPGFTSSATNVSNVVSAGPLSGEKAAINILBINEKLRPQLA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSGRELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSGGODLOGOLAGEGRIAAUHVOKL	1	{		TLDVDCDTCCATTUCATUCATUCATUCATUCATUCATUCATUCATUC
ERGFKEEKLAEQLKQAEELRGYKVLUHSGERELTQLREKLREGER DASRSLMEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAGHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEKEKPVEDSLLE ECAITCSNSHGPYDSNGPHRKTKITTEEDKVDSTLIGSSSHVEW EDAVHI IPENESDDEEEEKGPVSPRNLQESEEBEVPQESWDEG YSTLS IPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRIRWDQVK KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDBKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLDEVSPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLEDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYIGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHV VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHV VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDONPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEBHISFALVYDNRFFTLITVTSLHLVFQMGVIFFQ KLAEQLKQAEELRQYKVUNSQERELTQLREKLREGRABSELN DDDEDVQVEAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVDRESSHDECQDALN LIEVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPGLA EKKQGFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAELLRQYKVLVHSQERELTQLREKLREGGR EKKQGFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAELLRQYKVLVHSQERELTDLREKLREGGR DASRSLMEHQALLTPDEPDKSGGODLOEGLAEGCRLAGHLVOKLS	1	1		EKKOOFPNI. KEKCEL TOLAGEL NOONGUURI DE CHE
LSPENDNDDDEDVQVEVAREKVQKSSAPREMPKRAEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHBATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLEEDLOGPYSSAVYSLEE ELLDEKEPEVLQDSLGRCYSTPSGYLEEDLOGPYSSAVYSLEE SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSSCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGBIEKKGKGKKRGRRSKKERRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEBHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ  6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQPKEE ELQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSFENDN DDDDLVQVEVAEKVQKSSSFREMQKAEEKEPPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILFVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRILKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVUVHSGERELTQLREKLREGR	ł	<b>!</b>		EROFKEEKLAFOLKOAFELPOYYULUUGOEDEL GOLDENKIMLRN
ECAITCSNSHGPYDSNQPHRKTKITFEEDKUDSTLIGSSSHUEW ECAITCSNSHGPYDSNQPHRKTKITFEEDKUDSTLIGSSSHUEW EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPEVYLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDDPSCPRLSGELLDEKSPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEKH VGFSLDVGEIEKKGGKKRRGRRSKKERRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHIISALYVDNRFFTITVTSLHLVFQMGVIFFQ  6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRADARSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDEDGVVAEKVQKSSSFREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNIKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQEEEITQLREKLREGR	1	1		DASRSLNEHLOALLTDDEPDKGOGODLOEGLAEGGREARING
ECATTCSNSHGFYDSNQPHRKTKITFEDKVDSTLIGSSSHVEW EDAVHI I PENESDDEEEEKGPVSPRNLQESEEBEVPQESWDEG YSTLS I PPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHBATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGVLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKRRGRRSKKERRRGREGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKRRGRRSKKERRRGREGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDCXTFPSMYFELPDSFQHYKSVFY SFEEEHISFALYVDNRFFTLTVTSLHLUVEOMGVIFPQ RLNSMLMEVEEPEVLQDSLDCXTFSMYFELDDSFQHYKSVFY SFEEEHISFALYVDNRFFTLTVTSLHLUVEOMGVIFPG KLAEQLKQAEELRQYKVLVHSQGRELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPRBMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGFLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR BKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR	1	}		LSPENDNDDDEDVOVEVAEKVOKSSADDEMDVAERVENDERS
EDAVHI I PENESDEEEEERGPVSPRNLOESEEEEVPQESWDEG YSTLS I PPEMLASYKSYSTFHSLEEQQVCMAVDIGRHRWDOWK KEDHBATGFRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRI KKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVMDBIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEGPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTDLREKLREGR				ECAITCSNSHGPYDSNOPHRKTKTTFFEDKIDSTLIGGGGIUEW
KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLEITDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRISR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVCEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVCLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVCLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYIGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKKKRRGRRSKKERRGREGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGDDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSGGDDLGEGGRLAOHLVOK		1		EDAVHI I PENESDDEEEEEKGPVSPRNLOESEERFVDOEGWDEG
KEDHEATGFRILSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRILSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBQDDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEB DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRGRRSKKERRGKEGEEDQNPPCP RLNSMLMEVEBPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPQ RLNSMLMEVEBPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPQ KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVOKLSPENDN DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLECCAITCS NSHGPCDSNQPHKNIKITFBEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSGGODLOEOLAEGCRIAOHLVOK	ŀ			YSTLSIPPEMLASYKSYSSTFHSLEEOOVCMAVDIGRHRWDOVK
CQPYRSAFYULEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELEDUGQPYSSAVYSLEE QYLGLALDUDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGBIEKKGKGKKRRGRRSKKERRRGKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFFQ AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQEREELTQLREKKREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGGDLOEOLAEGCRLAOHLVOK	1 1	ŀ		KEDHEATGPRLSRELLDEKGPEVLODSLDRCYSTPSGCLFLTDS
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SEQ   Predicted   Dredicted end   Dredicted end   Dredicted   Dred	d, E= ine, -Stop -SSHVEW -SSWDEG EWDOVK
No: nucleotide location corresponding to first amino acid residue of amino acid sequence    Codon, /=possible nucleotide deletion, restriction	Stop SSHVEW SWDEG
corresponding to first amino acid residue of amino acid sequence    Comparison   Corresponding to first amino acid residue of amino acid sequence   Codon, /=possible nucleotide deletion,	Stop SHVEW SWDEG
corresponding to first amino acid residue of amino acid sequence	SHVEW SWDEG
amino acid residue of amino acid sequence  ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSS  EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQE  KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCL	SHVEW SWDEG
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion)  ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSS EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQE YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHR KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCL	SHVEW SWDEG
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sequence   -possible nucleotide insertion	SWDEG WDOVK
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PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQR	VGLAV
DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESL	DRCYS
TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKY	OEVEE
DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLEL	PDLGO
PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPR	LSREL
LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQFYGSSFYA	LEEKH
VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQ	NPPCP
RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHY	
SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ	
6351 1291 319 REARRITERSQLGRMLVVEVANGRSLVWGAEAVOALRER	LGVGG
RTVGALPRGPRQNSRLGLPLLLMPEEARLLAE IGAVTLV	SAPRP
DSRHHSLALTSFKRQQEESFQEQSALAAEARETRROELL	EKITE
GQAAKKQKLEQASGASSQEAGSSQAAKEDETSDGQASG	EOFEA
GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLD	WRVOS
KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFL	VYPGD
PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLL	LCSPQ
PDGKVVYTSLQWASLQ	
6352 235 923 WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQ	GRSAP
AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVG	QGAPG
LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQ:	PPPEE
PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQ	YPDVP
TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANE	LRADP
DDCVYIVVD 6353 65 672 PRACACA T DEAD ADDRESS OF THE CONTROL OF THE	
THOAGATEEARARPED VQAAEEEREMUUPUSAS RVFCG	RILSM
VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQ	QMSER
FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSH	IPEAS
FLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSL	SPGFE
DLSHVQPGSPAINGRSQTDDEEMTGE  6354 965 510 PSLRPMEPTRDCPLAGGAESATLEMGATDVCDLPDVDDV	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	QEVFC
HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARA	AVHVE
SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDV	TUHQA
LLRLPQYQTDLLLTFNQPP  6355 158 1662 RGSSAAFRGSGLPGAMTPDVLDHGMGPGLLTPDPGTPPG	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GFSLD
WDGKVSEIKKKIKSILPGRSCDLLQDTSHLPPEHSDVVIV	VGGGV
LGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVO	GICQ
QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPS	
LASEKDAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWII	NTEGV
ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTT	RFVSS
SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVIN	NAAGA
WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPC	
ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLE	EVDHD
FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGV	<b>JVGPH</b>
PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTII	JUSPF
6356 354 633 TGLTSSCLDLOWMMTPTTPDMGPPSCUTTGTTDPPPPPTT	
13D13SCBFDQVMM1RR1RDMGRFSSV1VS11DEEEEE1E	
ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKG	FTLID
NQFK	

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTOGOGDRALS
		1	RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
}		İ	QPVEEKVGAFTKIIEAMGFTGPLKYSKWKIKIAALRMYTSCVFK
		ł	TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKOEGRSGKYM
- [			CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY
ì			DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL
6358	2009	1040	DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
0330	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
·			AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
,			EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
1	<b>j</b> .		QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTB REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
			DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
1	'		MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
L.			GAFVLVLYDELKKVI
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
	l		GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL
Į.	ł ·		PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIOPVHKAESSTDSS
}	1		GPLEEAEEAPQLMRTKSDASCMSORRPKCRAPGEAORIRRHRFS
			INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLOVLTLLLNKFRV
1			EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
			LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT
6360	1	345	MKFQALRLTMLQRLEQLVEAK
1	· •	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
1	j		RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVGSC.
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ
	1		FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
			APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
			NSTGIWDIQETVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF
1 1	i		GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLIG
1			ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF
1	į.	•	LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHIJVSW
1 1			PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYOAAFLSO
1	j.		ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
1	i		ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM
			TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG
6363	21	1201	VPYRVLEHTKKE
		~~~	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
] [	i		NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTIGVVLD
] [	}		SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
}			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
	1		TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
	ĺ		RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
<u> </u>		1	RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG
		[	DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
[			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
		1	NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
		ĺ	SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
į į			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAOYYLPDGS
			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

Deginning   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coctation   Coct	- 000	T Billias In . S	( No. 32 - 5 3 3 - 3 3	[ ]
No: nucleotide location corresponding to first amino acid residue of seven point of the first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequen	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding   cofirst   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   amino acid   cesidue of   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company   company			B .	
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Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence		I .	1	
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TLEQYMMRAPADALEVI PMALSENSGMNPIGTMTEVRARGYKEM NPAGET DCLHKGTNDMKQQHVIETLIGKKQQISLATGMYRMILK IDDIRKPGESEE GRREGAHSSTFWLLSTFLIGKKQQISLATGMYRMILK IDDIRKPGESEE GRREGAHSSTFWLLSTFLIGKAVAMLCKEQGITVLGLNAVFDLV IGKPNVLETVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG MLYVRWRINGTOPPAFTEVDNPASFADSMLVRAVNYNYYSLNA WLLLCPMWLCFPDWSMCSCPLIKSIDNVILAGANDFCLIGLIC QALCSEDGHKRRILTLGLGFLVIEFDPASNLUFFRVGFVARRVL YLSSVGVCVLLTPGFQADASHITKKLIAAVVLGILETNTLRCV LRSGEMRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI RYYREAVRLNPKYVIAMNNLGNILKERSALGSEELLSLAVQIQ PDPAAAMMNIGIVORSLKRFEARGSYSTALHHRRKYPDCYYNL GRLYADLNRHUDALMAWRNATVLKPEHSLAWNMILLLDNTGNL AQAEAVGREALELI PINDISLMFELSLAWNMILLLDNTGNL AQAEAVGREALELI PINDISLMFELSLAWNMILLLDNTGNL KENYGLIRKKLEIMQKKAV 1934 SIGFFVMLVLSILLYTCEMFODSVAFEDVAVSETOERWALLDPS CKHYGLIRKKLEIMQKKAV GRAFYFLNLCLIHRRIHTGKYKYKCKGCKKAFSYLDSPQ SKHXACTKEKPYDGKECTEFT ISHSCIQRRRWHSGDGPYKCKY GGKAFYFLNLCLIHRRIHTGVKPYKCKQCGKAFTRSTTLPVHER THTSVANDAGKEGGGARFSFSSEIRHKRSHTGEKPYECKQGKV FISPSSIQYHKMTHTGEKPYECKQGKAFKCSSHLQKHGRTHTG EKPYECRQCGKAFRSTSDLHERTHTGDKPYEKCKVGGKFFTCSSIR YHERTHTGEKPYECKCKAFISNYINYHERTHTGEKPYGCKQG GKAFIRASSCREHERTHTINR 6369 1 327 PSPAKLNIPSSWFRTAGALFLRPPDLTMAVFHDEVSIEDFGYDE STYPYP-CPGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DOPVCGETTYPTFRGFGSLCHRFCRSAACTVTRTTHGSPREDTGT PRSSEMMFQDSVAFEDVAVSFTQEEWALLDSPGKNLYRDVWQET PKNLTSYGKTWKVUN IDESYKNPKKLYGKAFSYLDSFGSHDAKCTKERFYDG GRRCTTFFTTFGGFSSLCHRFCRSAACTVTRTTHGSPREDTGT PRSSEMMFDDSVAFEDVAVSFTQEEWALLDSPGKNLYRDVWQET PKNLTSYGKTWKVUN IDESYKNPKKCKAFSYLDSFGSHDKACTKEKPYD GRKCTETTJSHSCIQRHEKTHTGLERRECTERSHCTHTHTAN TGHKSSTYPYCPCCGGKAFRCSSLIJKMRCTKEKPYDCKQC ESPQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLMTHTRAD TGHKSSEYDFYGGNPYNKECKKAFSYLDSFGSHDKACTKEKPY DGKSCTETTJSHSCIQRHEKVAFSYLDSFGSHDKACTKEKPY DGKSCTETTJSHSCIQRHEKVHSGOGFYCKSCGKFFFSSIQTHM THTGEKPYECKQCGKAFRCSSHLOKHGRTHTGEKPYECKGGKA FRCTSSIDLQHEKTHTEDKYPCCKOGGRPCASCJCLHERTHSC	1			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK IDDIRKPGESEB  GREGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVPDILV IGKFNVLEIVQKVLHHOKSLENLGMLRRGGLFFRMTLLTSGGAG MLYVRWRIMGTGPDAFTEVDNASGADSMLVRAVNYNYYSLMA WLLLCPWMLCFDWSMCGIPLIKSISDMSVANVNYYSLMA WLLLCPWMLCFDWSMCGIPLIKSISDMSVALAALNECLIGLIC QALCSBCGHRRRILTLIGLGFLVIPFLPASNLPFRYGFVVAERVL YLPSVGYCVLLTFGPGALSKHTKKKKLIAAVVLGILFINTLRCV LRSGEWRSEGLFRSALSVCPLNARVHTNIGKNLADKGNQTAAI RYYREAVRLNPKVVHAMNIGNILKERRELQEAELLSLAVQIQ PDFAAAMMIGIVQNSLKRFEAAEGSYSTATKHRRKYPDCTYML GRLYADLNRHVDALNAWNARTVLKFEHSLANNUMIILDTGNI. AQAEAVGREALELIPRIDHSLANVLISKSQKYKESEALFLKA IKANPNASYHGHLAJLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  1934 SIGFFWMILVSILLYTCERFODSVAFEDVAVSFTQEEMALLDFS GRAILYBLVANGHUSSLAVGTWORDETKMPRRNLSLMRE KLCESKESHIGGESFRQIADDMLNRKTILFGITPCESSVCGEVGT GHSSLNTHIKADTGHKSSRYGEVGRAVFTRSTTLPVHER KLCESKESHIGGESFRQIADDMLNRKTILFGITPCESSVCGEVGT GHSSLNTHIKADTGHKSSRYGEKGAFGCSHLQKRGHTHTG CKAPTYFLNLCLIHERIHTGVKPYKCKQCGXAFTRSTTLPVHER THTGVNADECKECGNAFSFFSIRRHKRSHTGERFYECKQCGKV FISPSSIQVIKMTHTGVERFYCKQCGKAFFCSSLIGKRHTHG EKPYECRQCCKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSLRHERTHTGEKPH ECKQCGAFFYFSSLHHERTHTGEKPYECKQCGKGFRCA SQLQIHERTHSGEKPHECKECKVFKYFSSLRHERTHTGEKPY ECKGCGAFFYFSSLHHERTHTTGEKPYECKQCGKGFRCA SQLQIHERTHSGEKPHECKECKVFKYFSLRHERTHTGEKPY ECKGCGAFFYFSSLHHERTHTTGEKPYECKQCGKGCG GRAFIRASGCREHERTHTINR  6369 1 327 RPVPSKLNPRSGRPTAGADLRPPPLTMAVFHDEVEIEDFQYDE DSTYFYFPCGONFSITKEDLENGEWALLDPSQKALYRDVMQET FKMLTSVGKTWKVQNIEDEKKAPSYLDSFGSHIKACTKEKPY DGKSCTETFTFTSHSCIQRHRWMISGDDPVKCKECKSEKEHCG ESPRQIADDMLNRKTLPGTTPCESSVCCGCKOFTGSSLINTHTRAD TGHKSSEYQEKGRNPYNNECKKAFSYLDSFGSHBKACTKEKPY DGKSCTETFTSHSCIQRHRWMISGDGPVKCKCGCKFFCASCULHERTHSG URRETTSSCLQRHRWMISGDGFWKCFCCGKAFFTLMLCL HERIHTGKVPYKCKQCGKAFFRSTTLPVHERTHTGWADDECKE CGNAFSFPSEIRRHKRSHTGERPYECKQCGKVFISSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKIGRTHTGEKPYECRQCGKAFFCCSLQCHAFTRASC			1	**
IDDIRKPGESEE  GNKEGAHSETFWULLSIFLGAVAMLCKEQGITVLGLNAVPDILV  IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTEGGAG  MLYVRWRIMGTGPPAFTEVDNPASFADABMURAVNYNYYSIMA  WLLLCPWILCFDWSMCCIPLIKSIBDWRVIALAALNFCLIGLIC  QALCSEDGHKRRILTLGLGFLVIPFLPASNLPFRVGFVVAERVL  YLPSVGYCVLLTFGFGALSVCPLNARVHYNIGKNLADKGNQTAAI  RYYREAVRLINPKYVHAMINIGKILKERRELGEAEELLSLAVQIQ  DPPAAAMMNIGIVONSLKRFBAEGSYRTAIKHRKYPDCTYNL  GRIYADLNRHVDALNAWNATVLKPEHSLANNNIIILDHTGNL  AQABAVGREALEI IPRDHSLHRSLANNVLGKSGYKYKESEALFLKA  IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT  KENYGLLRRKLBLMQKKAV  3IGFFVMILVSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDFS  QKALYRDVMQETFKNLTSVGKTWKVQNIEDEYKMPRINLSLMRRE  KLCESKSSHGGSFNOLADDMINKTLDEITFDCSSVCGEVGT  GHSSLNTHIRADTGHKSSBYQEYGENPYNKECKKAPSYLDSPQ  SHDKACTKEKPYDGSECTETFISHSCIGRHRVMHSGDGPYKCKY  GRAPFYEINLCILHERLHTGVKPYKCKQGGAFTRSTTLEVHER  THTSVNADBCKECGNAPSPSSEIRRHKRSHTGEKPYECKQCGKV  GYAFFYEINLCILHERLHTGVKPYKCKQGGAFTRSTTLEVHER  THTSVNADBCKECGNAPSPSPSEIRRHKRSHTGEKPYECKQCGKFFRST  SQLQILERTHSGKPHECKECKVFKYPSSLRIHERTHTGEKPY  EKPYECRQCGKAPRCTSDLQRHEKTTEDKPYGCKQCGKGFRCA  SQLQILERTHSGKPHECKECKVFKYPSSLRIHERTHTGEKPY  EKPYECRQCGKAPFTSSLLHHERTHTGVKPYECKVCGKAFTCSSSIR  4 YHERTHTGERPYECKHCGKAFTISNYIRYHERTHTGEKPYCKQC  GKAPIRASSCREHERTHTING  5369  1 327  RPVPAKLNPRSWPRTAGALPLPPPLTMAVPHDEVEIEDFQYDE  DSTYYPYPCGOINFSTIKEDLENGEDVATCPSCSLIIKVIYDK  DGFVCGGTVPAPSANKELVKC  ESPMQIADDMLNKRTLEGITPCESSVCECVTGTGISSLNTHRAD  FUNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHCG  ESPMQIADDMLNKRTLEGITPCESSVCECVTGTGISSLNTHTRAD  TGHKSSEYQEYGENPYENKECKKAFSYLDSFOSIBMACTKSKPY  DGKCTETFISHSCIQRHRWMISGODPYKCKFCGKAFFLINLCL  HERLHTGVKPYECKQCGKAFTRSTTLPVHERTHTGWNADEX  GRAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM  THTGEKPYECKQCGKAFTCSSLLQKHGRTTTGEKPYECRQCGKA  FRCTSDLQRHEKKHTETDKOPCKQCGKGFRCASOQULHERTHSG  CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM  THTGEKPYECKQCGKAFTCSSLLQKIGGTTTGEKRYECRCGGKF  FRCTSDLQRHEKKHTETDKOPCKQCGKGFRCASOQULHERTHSG	1			
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IGKENTLEIVQKVLHKURSLENGGMLFRAVNYNYYYSLNA MLYURWRIMGTOPPAFTEVDNPAS FADSMLVRAVNYNYYYSLNA MLLLCPWMLCFDWSMCCIPLIKSISDWRVIALAALMFCLIGLIC QALCSEDGHRRRILITLGLGFLVIFFJASKLFFRVOFVVAERVL YLPSVGYCVLLTFOFGALSKHTKKKKLIAAVUGIJEFINTIRCV LRSGEWRSEGQLFRSALSVCPLNAKVHYNIGKNLANKGNOTAAI RYYREAVRLNPKYVHAMNNIGNILKERNELQEAFELLSLAVQIQ PDFAAAWMNIGIVONSLKRFRAAEGSYRTAIKHRRKYPDCYYNL GRIYADLNRHVDALNAWRNATVLKPERISLAWNNNIILLDNTGNL AQAEAVGREALELIPNDHSHATSLANVLGKGKYKESEALFLKA IKANPNAASYHGNIAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLLRKLELMQKKAV  6367 287 1934 SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNILYRDVMQETFKNLTSVCKTWKVONIEDEXKNPRRNISLMRE KLCESKESHHGESSFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNYHIRADTGHKSSEVQEYGENPYRNKECKKAPSYLDSFQ SHDKACTKEKPYDGKECTEFFISHSCIQRHVMHSGBGPYKCKF CGKAFYFENLCLHERHHTGVKPYKCKQCKAFTRSTTLPVHER THTGVNADECKECGNAPSFPSEIRRHKRSHTGERPYECKQGKV FISFSSIQYHKMTHTGEKPPECKQGKAFRCGSHLQKHGRHTHT EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQGKFRCA- SQLQIHERTHSGEKPHECKECKKVFKYFSSLRIHERTHTGKPH ECKQCGKAFRYFSSLHHERTHTGDKPYGCKQCGKGFRCA- SQLQIHERTHSGEKPHECKECKKVFKYFSSLRIHERTHTGKPH ECKQCGKAFRYFSSLHHERTHTGDKPYGCKQCGKGFRCA- SQLQIHERTHGEKPYECKCGKAFTSSLG KYNTYPSSLT KYNTYDK- THRETHTGEKPYECKCGKAFTSSLG KYNTYTHESEPPTGT  6368 1 327 RPVPBAKLNPRSWPRFTGGALPJRPPPLTMAVPHDEVBIEDFGYDG DSSTYFFYPCPCGDNFSITKEDLENGEDVATCPSCSLIKVIYDK DQFVCGETVPAPSANKELVK  6369 1 1745 AGCCRDTRFPTPRGGGSLCHNFCRSAACTVYRTTHGSPREDTGT PRSREMBFQDSVAFEDVANSFTQBEWALLDPSQKNLYRDVMQET PKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHCG ESPAQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSFYQEVGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKSCTETFTISHSCIQRHRVMHSGGBPYKCKFCCKAFFTSLILVILADE CGNAFSFPSEIRRHKRSHTGEKPYCKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFFCSSHIQKHGRHTHGEKPYECKQC GGNAFSFPSEIRRHKRSHTGEKPYCKQCGKVFTISFSSIQYHKM THTGEKPYECKQCGKAFFCCSHLQKHGRHTHGEKPYECKQC GGNAFFSPSEIRRKKTHTEDKYPYCCKQCGKGFTEASGLGIHERTHSS	1	ľ	ł	IDDIRKPGESEE
MLVYRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYSIMA WLLLCPWWLCFDWSMGCIPLIKSISDWNVIALAALNFCLIGLIC QALCSEDGHRRRILTLGLGFLVIFFLPASMLFFRVGFVVAERVL YLPSVGVVLLTFGFGALSKHTKKKKKLIAAVVLGILFINTLRCV LRSGEWRSEBGLFFSALSVCPLNAKVHYNIGKNLADKGNGTAAL RYYREAVRLNPKYVHAMNNIGNILKERNELQEAEELLSLAVQIQ PDFAAAWNIGIVONSLKRFEAAEQSYRTAIKHRKYPDCYYNL GRLYDLNRHVDALNAWRHATVLKPEHSLAWNNIILLDHTGKL AQAEAVGREALELIPNDHSIMFSLANVLGKSQKYKESEALFLKA LKANPNAASYHGNIAVLYHRWHDLDLAKKHYEISLQUDTASGT KENYGLRRKLELMQKKAV  6367 287 1934 SIGFPVMLVLSILLYTCEMFQDSVAFEDVASFTQEEWALLDFS KENYGLRRKLELMQKKAV GKNLYDVMOSTFINLTSVGKTWKVONIEDEYKNPRNLSLMRE KLCSSKSHHGGSSPNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSPQ SHDKACTKEKPYDGKECTEFFISHSCIQRRVMHSGGGFYKCKF CGKAFYFINLCLIHERTHTGVKPYKCKQCGKAFTRSTTLFVHER THTGVNADBCKECGNAFSPSEIRRHKRSHTGEKPYECKQGKKFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRHERTHTGEKPH EKKQCGKAFKYFSSLHHERTHTGKPYKCKCGKAFTCSSSIR YHERTHTGEKPYECKCGKAFTCSSSIR YHERTHTGEKPYECKCGKAFTCSSSIR YHERTHTGEKPYECKCGKAFTCSSSIR SCREBERTHTINR 6368 1 327 RPVPAKLNPRSWFRTAGALDTAPPTHAVFHDEVEIEDFGYDE DSTYFFYPCGGDNFSITKBLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  GKAPIRASCREBERTHTINR 6369 1 1745 AGCCRDTRFFTFRGFGSLCHNFCRSAACTVFRTHGEKPPGCKGC ESPNQIADDMLNRKTLPGITPCESSVCGEVGTIGSSLNTHIRAD TGHKSSFYQEYGENPYRNKECKKAFSYLDDFQGHDKACTKEKPY DGKSCTETFISHSCIQRHRWHSGDGPYKCKFCGKAFYF.NLCL, HERLHTGVKPYKCKQCGKAFTRSTTJPVHERETHTGNADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKFTSSSIQYHKM THTGEKPYECKQGKAFRCSSHQKKRTHTGEKPPECQGKA FCTSDLQRHEKHTHEDKRYCCKGCGKAFTCSSCJQJHERTHSS	6366	257	1898	
WILLCPWWLCFDWSMGCIPLIKSISDWRVIALAALMFCLIGLIC QALCSEDCHKRRILITIGLGFLUTPLPASNLFTPGFVVAERUL YLEPSUGVCULTTGFGBLSKHTKKKKLIAAVVIGILFINTIRCV LRGGEWRSEEQLFRSALSVCPLMAVHYMIGKNIADKGKOTAAI RYYREAVRLMPKYVHAMNNIGNILKERNELQEAFELLSLAVQIQ PDFAAAMMIGIVONSLKRFEABEGSYRTAIHHRKKYPDCYYML GRIYADLINRHUDALNAWRNATVILKEPHSLAWNNMIILLDNTGKL AQAEVAGREALEL I PRUBISIMFSLAWVLKSKGKYKSEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  316FPVMLUTSILLYTCEFFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDWQBTFKNLTSVGKTWKVONIEDEXKNPRNILSLMRE KLCESKESHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSFYQEYGENPYNKKECKKAFSYLDSFQ SHOKACTKEKPYDGKCTEFTJSHGCIQRHRWHSGDGPYKCKF CGKAPYFINLCLIHERIHTGVKPYECKQCKAFTRSTTLPVHER THTGVNADBCKECGNAPSFPSEIRRHKRSHTGEKPYECKQCGKV FISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRITHTG EKPYECRQCGKAFRCTSDLQRHEKTTETENPYCCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLATHERTHTGEKPH ECKQCGKAFKTSSLHIHERTHTGKPYPECKVCGKAFTCSSIR THERTHTGEKPYECKCGKFTSTSNYIRYHERTHTGEKPYQCKQC GKAPIRASSCREHERTHTINR 6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQYDE DSTTYFYPCCGDNFSITKBDLENGEDVATCPSCSLIIKVIYDK DGFVCGETVPAPSANKELVKC GKAPIRASCCREHERTHTINR 70 PKWLTSVGKTWKVQNIEDEXMRPRNILSLMREKLCESKSSHCG ESPRQIADDMLNRKTLPGTTPCESSVCGEVGTGHSSLITHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKSCTETFTISHSCIQRHRVMHSGDGPYKCKFCGKAFFFINLLCL HERIHTGVKPYKCKQCGKAFTRSTTLLPVHERTHTGVADAECKK CGNAFSFPSEIRRHKRSHTGBKPYECKQCKVFISFSSIQYHKM THTGEKRYPECKQCGKAFRCGSHLQKHGRTHTGEKPYECKQCGKA FCTSDLQGRECTTFTSHCJQKHCWHSTPSSIQYHKM THTGEKRYPECKQCGKAFRCSSLLQKHGRTHTGEKPYECKQCGKAF	1	1		IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
QALCSEIGHKRRILITIGIGFLVIPFLPASNIFFRVOFVVAERVL YLESVGYCVLITFGFGALSKITKKKLIAAVVIGILFINTIRCV LRSGEWRSEEGLFRSALSVCPLNAFVHYNIGNLADKGNGTAAI RYYREAVRLWPKYVHAMNICGNILKERNELQEAFELLSLAVQIQ PDFAAAWMIGIVONSLKRFEAAGGSYRTAIKHRRKYPDCYYNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL AQAEAVGREALELIPNDHSLWFSLANVLGKSQKYKESEALFLKA IKANPNAASYMGNLAVLYHRMGHLDLAKKHYEISLQLDFTASGT KENYGLLRRKLELMQKKAV  3IGFFVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHGGESFNQIADDMILNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSFVOEYGRNPYNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERHTGVKPYKCKQGCKAFTRSTTLFVHER THTGVNADECKECGMAFSFPSSIRRHKRSHTGEKPYECKQCGKV FISPSSIQVHKMTHTGEKPYECKCGGKAFRCGSHLQKHGRTHTG EKPYECRQCKAFRCTSDLQRHEKTHTEDKPYGCKQCKGFRCA SQLQIHERTHSGEKPHECKECKVFKYFSSLRIHERTHTGKFY ECKQCGKAFRYFSSLHIHERTHTGKPYSCKVCGKAFTCSSIR HYBERTHTGEKPYECKCGKAFTSNYIRYHERTHTGEKPY CKQCGKAFRYFSSLHIHERTHTGKPYPCKVCGKAFTCSSIR HYBERTHTGEKPYECKCGKAFTSNYIRYHERTHTGEKPYCCKQC GKAFIRASSCREHERTHTINR 6368 1 327 RPVPAKLMPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQVDE DSTTYFYPGCODNESIT TIEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC 6369 1 1745 AGCCRDTRFFTFRGFGSLCHNFCRSAACTVTRTHGSPREDTGT PRINLTSVGKTMKVQNIEDEYKMPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGTTPCESSVCGEVGTGHSSLITHIRAD TGHKSSEYQEYGGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFGKAFYFLNLCL HERIHTGVKPYVCKOCGKAFTRSTTLPVHERTHTGVADADECK CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKFFCASQLQIHERTHSC CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKFFCRSCQCKA FCTSDLQRHEKTHTEDKYPYCKQCGKFFCASQLQIHERTHSC			1	MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
Tylpsvgycvlitfggalskhtkkkkliaavvlglifintlrcv LRGGEWRSEEQLFRSALSVCPLNAKVHYNIGINLADKGNQTAAI RYYREAVRIBMEKYVHAMNIKUTILKERNELQEAEELISLAVQIQ PDFAAAMMINGIVONSLKRFEAEGSYRTAIKHRRYPDCYYNL GRLYADLINRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL AQAEAVGREALELIPINDISLMFSLANVLGKSGKYKESEALFLKA IKANPNAASYHGNLAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMGKKAV  6367 287 1934 SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVONIEDEYKNPRRNLSLMBE KLCESKESHHGGESFNQLADDMINRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSPQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF GGKSYFINLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADBCKECGNAFSFPSSIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCTSTLEPHER EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKFRCA SQLQIHERTHSGEKPHECKECKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYCKVCGKAFTCSSSIR YHERTHTGEKPYECKCCKAFTSNITYHERTHTGKPYQCKQC GKAFIRASSCREHERTHTINR RPVPAKLMPRSWPRTAGALPLRPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKEUVKC  6369 1 1745 AGCCRDTREPTPFRGFSICLMPFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FYNLTSVGKTMKVQNIEDEYKNPRRNLISLMREKLCESKESHHCG ESPRQIADDMLNKKTLPGTTPCESSVCGEVGTGHSSLITHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKSCTETFISHSCIQRHRVMHSGGPYKCKCGKAFFINLCL HERIHTGVKPYKCKQCGKAPTRSTLLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGVENDAECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGVENDAECKE FCTSDLQGRECTHETGEKTYCERQCGKA FRCTSDLQGRECTHTGEKTYGCKQCKAF	1	ł	i	WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
LRSGEWRSEQLFRSALSVCPLNAKVHYNIGKNLADKGNOTAAI RYYREAVRLNPKYVIAMNNLGIVORSLKRFEBAEGSYRTATKHRKYPDCYYNL GRLYADLNRHUDALNAWRNATVLKPEHSLANNNMIILLDNTGNL AQAEVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNASYHONLAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLRRKLEHMQKKAV  31GFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQLADDMLNRKTLPGITPCESSVCGEVGT GHSLINTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHOKACTKEKPYDGKSCTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADBCKECGNAFSPPSEIRHKRSHTGEKPYECKQCGKV FISSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGKFYECKVCGKAFTCSSIR YHERTHTGEKPYECKHGKAFISNYIRYHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGKFYCCKYCGCGKFRCAS GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTTYFYPCPCGDNFSITKBDLENGEDVATCPSCSLIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCROTRFFTFRGPSLCHNFCRSAACTVTRTIHGSPREDTGT PRSKEMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET PKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHCG ESFRQIADDMLNRKTLPGITPCESSVCCEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGKVPNADECKK CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKHTEDKPYGCKQCGKFRCASQLQIHERHTHSG	l	1	1	QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
RYYREAVRLINEKYVIHMINILGI LIKERNELGEAEELLSLAVOI Q PDPAAAMMINI GI VQNSLKRFEAAEQSYRTAIKHRKYPDCYYNL GRIYADLINRHUDALINAMRNATVLKPEHSLAMNINI ILLDNTGNL AQAEAVGREALEL I PINDHSIMFSILANVLGKSQKYKESEALFLKA IKANPNAASYHGINLAVLYHRIGHLDLAKKHYEI SIQLDPTASGT KENYGLLRIKLELMQKKAV  6367 287 1934 SIGFPVMLVLSI LLYTCEMFODSVAFEDVAVSFTQEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNI EDEYKNPRINLSLMRE KLCESKESHHCGESFNQI ADDMLINRKTLPGI TPCESSVCGEVGT GHSSLNTHI RADTIGHKSSENQEYGENPYRINECKKAFSYLDSFQ SHOKACTKEKPY DGKECYGENPYRINECKKAFSYLDSFQ GHSSLNTHI RADTIGHKSSENQEYGENPYRINECKKAFSYLDSFQ SHOKACTKEKPY DGKECYGENPYRINECKKAFSYLDSFQ GHSSLNTHI RADTIGHKSSENQEYGENPYRINECKKAFSYLDSFQ GHSSLNTHI RADTIGHKSSENQEYGENPYRINECKKAFSYLDSFQ SHOKACTKEKPY DGKECTETP I SHISCI QRHRWHTSGDGPYKCKP CGKAFYFINLCLI HER I HTGV KPYKCKQCGKAFTRSTTLPVHER THTGVINADECKEGNAFSFPSEI RRHKRSHTGEKPYECKQCGKV FISSSI QYHKMTHTGKFYPECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRYRSSLHHERTHTGDKPYECKQCGKAFTCSSIR YHERTHTGEKPYECKHCKKOKFYFYSSIR HERTHTGEKPH ECKQCGKAFRYRSSLHHERTHTGKPYECKQCKVFKYSSIR IHERTHTGEKPH ECKQCGKAFRYRSSLHHERTHTGKPYECKVFKYSSIR IHERTHTGEKPH ECKQCGKAFRYRSSLHHERTHTGKPYECKVFKYSSIR IHERTHTGEKPH ECKQCGKAFRYSSLHHERTHTGKPYECKVFKYSSIR IHERTHTGEKPH ECKQCGKAFRYSSLHHERTHTGKPYECKVFKYSSIR IHERTHTGEKPH DS=TYFYPPCPCGNFSITKEDLENGEDVATCPSCSLI IKVIYDK DPVCGETVPAPSANNELVKC  6368 1 327 RPVPAKLMPRSMPRTAGALPLRPPPLTMAVFHDEVBI EDFQYDE DS=TYFYP DCPCGNFSITKEDLENGEDVATCPSCSLI IKVIYDK DQFVCGETVPAPSANNELVKC  6369 1 1745 AGCCROTRFPTPRGPGSILCHNFCRSAACTVTRT HGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKALYRDVMQET FKNLTSVGKTWKVQNI EDEYKNPRRNLSLMREKLCESKESHCG ESFAQI ADDMLNRKTL PGITPCESSVCCEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYNRICKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCI QRHRWHSGDGPYKCKFCGKAFYFLNLCL HER I HTGVKPYKCKQCGKAFTRSTTLFVHERTHTGVNADECKE CGNAFSFPSEI RRHKRSHTGEKPYECKQCGKAFTGSTLJVHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKHTEDKYGCKQCGKFRCASQLQLHERTHSG		1	1	
PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL GRLYADLINRHUDALNAWRHATVLKEEHSLAWNNNI ILLDNTGNI AQAEAVGEALELI PINDHSLMFSLAWVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLBLMQKRAV  SIGFPVMLVLSI LLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADMLNKKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGEMPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKP CGKAFYFLNLCLIHERLHTGVKPYKCKQCGXAFTRSTLPVHER THTGUNADECKECGNAPSFPSEIRRHKRSHTGERPYECKQCGKV FISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQKHEKTITEDRPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFYYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYLRYHEETHTGEKPPQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKEUVKC  6369 1 1745 AGCCRDTRFFTPRGPGSLCHNFCRSAACTVTRTHGSPREDTGT PRIKESKEMMFQDSVAFEDVANSTPQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDESYKNPRRNLSLMREKLCESKESHICG ESFNQIADDMLNKKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKERPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFTSFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPPECQCGKA FRCTSDLQRHEKHTEDKPYGCKQCKGGFRCASQLQIHERTHSG		1	1	LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
GRLYADLNRHVIDALNAWENATVLKPEHSLAWNIMI ILIDNTGNL AQAEAVGREALELI PNDHSLMFSLAWVLGKSQKYKESEALFLKA IKANPNAASYHGHLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  6367 287 1934 SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKMPRRNLSLMRE KLCES KESHHCGESFNQLADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCLQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERLHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADBCKECGNAFSFSEIRRHKRSHTGERPYECKQCGKV FISFSSLQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGEKPYECKVCGKAFTCSSSL YHERTHTGEKPYECKCKGKAFISNYIRYHERTHTGEKPH ECKQCGKAFRYFSSLHHTRTNR AGAGE GAFIRASSCREHERTHTINR 6368 1 327 RPVPAKLNFRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTYYFYCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC FRESEMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFFFLNLCL HER IHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSSTTGEKPYECKQCKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSSOLQHIERTHSG	[	1	}	
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IKANPNAASYHGNLAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMOKKAV  SIGFPVMLVISILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCES KESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHOKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKP CGKAFYFLNLCLIHERIHTGVKPYKCKQCGXAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISSSIQVIKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGEKPYCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVFAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCGGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHMFCRSAACTVTRTHGSPFEDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHICG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG			1	GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
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1934   SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS   QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKHPRRNLSLMRE   KLCESKESHNCHESFNQIADDMLNRKTLPGITPCESSVCGEVGT   GHSSLNTHIRADTGHKSSEYQEYGENPYNNKECKKAFSYLDSFQ   SHDKACTKEKPYDGKECTEFFISHSCIQRHRVMHSGDGPYKCKF   CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER   THTGVNADECKEGNAFSPPSEIRRHKRSHTGEKPYECKQCGKV   FISPSSIQYHKMTHTGEKPYECKQCGKAFTRSTTLPVHER   THTGVNADECKEGNAFSPPSEIRHKRSHTGEKPYECKQCGKV   FISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG   EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA   SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH   ECKQCGKAFTKSSSLHHERTHTGKPYECKVCGKAFTCSSSIR   YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC   GKAFIRASSCREHERTHTINR   PPVPAKLNPRSMPTAGALPLRPPPLTMAVFHDEVEIEDFQVDE   DSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVTYDK   DQFVCGETVPAPSANKELVKC   DQFVCGETVPAPSANKELVKC   AGCRDTRFPTPRGPGSLCHNFCRSACTVTRTHGSPREDTGT   PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET   FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHCG   ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD   TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY   DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL   HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE   CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM   THTGEKPYECKQCGKAFTRSTTLPVHERTHTGVNADECKE   CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM   THTGEKPYECKQCGKAFTRSTTLPVHERTHTGVNADECKE   CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM   THTGEKPYECKQCGKAFTRSTTLPVHERTHTGVNADECKE   CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKFFCASQLQIHERTHSG	1	t	1	IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFFSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTTYPYPCGENNFSITKEBLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGGPSLCHNFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFTGSSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGERPYECRQCKAF	1	1		
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SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADBCKECGNAFSFPSEIRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTETEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALDLRPPPLTMAVFHDEVEIEDFQYDE DSETTYPYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	ł	1	1	KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQYDE DSTTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGTTPCESSVCGEVGTGHSSLMTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQGGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1	1	1	GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ
THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGERPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DS=TYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1	1		SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
FISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFFTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRWMHSGDGPYKCKFCGKAFFLNLCL IHER IHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFISFSSIQYHKM THTGERPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1	1		
EKPYECRQCGKAFRCTSDLQRHEKTETEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVBIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCROTTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETPISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFISFSSIQYHKM THTGERPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				-
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AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNI EDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6369	1	1745	
ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETPISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHER IHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGBKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	[			PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET
TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYELNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYELNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1	I	1	1
CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	Į.			
THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1		1	
FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
RKDHECKECGKUFKYFSSLRTHERTHTGEKPHECKOCGKAPRYF	1			
	1		,	EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

<del></del>	15		<u> </u>
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ļ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
f	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
1			ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
			HERTHTINR
6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
1	1		ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPOEAIMDGTE
ı			IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
i			SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHOD
			RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAORVRRPIPGSDOT
	· ·		TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
ł			SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
	·		PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
	ļ		LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
	1		DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
6371	3	288	KFWKVSRPLELCYAPTKDPK
i	_	200	GVÄNMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG
İ			KSEAKK
6372	2141	625	RVSATASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
			LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
			VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
1			EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE
] .			QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
			DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLOEORMACEVGLY
] ]			YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
i l			APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
6373	67	711	QAAETPALELPLPSVPAPAPL
""	ű,	/11	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
			DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
[ ]	j		WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
1			VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	\$35	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
	[		CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
1			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
1 1	Į.		CPABLOTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
			DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
l .			SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
] ]	Į.		IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR
1 1	· ·	•	VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
1			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL
1			QKNNLNLLRCLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
j <b>i</b>			ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
6375	1	1826	EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
,	+	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
j (	ł		CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
			PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY
[ .			FLEGOIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
ļ j			SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLNVVAGVAAEAVASWIGLGPVAP
	İ		FVANI PLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
! !	1		RVLLLGTIQALFESVIPIFVFLWTPVLDPHGAPLGIIFSSFMAA
			SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP
		I	GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN
			TO STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE ST

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<del>                                     </del>	<del></del>	WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
ŀ	i .		VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
f			QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
ļ			NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
ļ			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
ł	1		VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
	1		ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKPIESAKIMD
1	í		PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
ì			ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKORRTFE
1		1045	
i			QRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHV NMSELIKIIRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
]	1	1	KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
	1	1	DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
İ	İ		WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
ļ			YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	BRAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFQGSQGRAY
		3/0	LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA
1	ì		FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPIGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
	1	702	GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
{	<b>!</b>		LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
		•	CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS
1			PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
1		•	MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
Į.			REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
1	1		LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
i			YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
1			AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
	1		TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
1	[	•	RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD
}	ł .		TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
1	]		SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG
ł	]		LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
l			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA
L	]		VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
l			KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY
l			TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
l	1		LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
l			AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
	[ ]		HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
l	ļ i		KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
l	ļ l		IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
Ł			E
6383	3159	1061	SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK
!			GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
	]		AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
			SSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
			GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA
			TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI
	<u> </u>		T THE STATE OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE

SEQ Predicted beginning nucleotide nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Acid F=Phenylalanine, G=Glyci H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion,                                                                                                                                                                                                                                                             \q	Stop  NIAIF EIQTS READD SARQT STVRSL
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  NO: nucleotide location corresponding to first amino acid, sequence N=Methionine, N=Asparagine, P=Proline, Q=Glutamine, N=Arginine, S=Serine, T=Threonine, V=Valine, N=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, N=possible nucleotide insertion)  LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSING TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVK AKSREWDMEALRSTLQTMESDIYTEVRELUSLKQEQQAF TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDGGFRHSEAFFALQQKSQGLDSRLQHVEDGVLSMQVA GESLESLLSKSQEHEQRLAALQGRLEGIGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	Stop  NIAIF EIGTS FREAD EDSHGP SARQT STVRSL
location corresponding to first amino acid residue of amino acid sequence  L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\text{\t	Stop  NIAIF EIQTS PKEAAD EDSHGP SARQT STVRSL
corresponding to first amino acid residue of amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first the first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence to first amino acid sequence	ONIAIF CEIQTS PKEAAD SDSHGP LSARQT STVRSL
to first amino acid residue of amino acid residue of amino acid sequence  Tequence  amino acid sequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  Tequence  T	ONIAIF CEIQTS PKEAAD SDSHGP LSARQT STVRSL
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion, \ =possible nucleotide insertion)  LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINE TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVK AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAF TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	ONIAIF CEIQTS PKEAAD SDSHGP LSARQT STVRSL
residue of amino acid sequence	ONIAIF CEIQTS PKEAAD SDSHGP LSARQT STVRSL
amino acid sequence Codon, /=possible nucleotide deletion,    -possible nucleotide insertion	ONIAIF CEIQTS PKEAAD SDSHGP LSARQT STVRSL
sequence   =possible nucleotide insertion	EIQTS KEAAD BDSHGP ASARQT STVRSL
LKDLSDGIHVVKDARERDFTSLENTVEERLTKSIND TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVK AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAF TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDDERFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	EIQTS KEAAD BDSHGP ASARQT STVRSL
TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVK AKSREWDMEALRSTLQTMESDI YTEVRELVSLKQEQQAF TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	EIQTS KEAAD BDSHGP ASARQT STVRSL
AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAF TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDGGFRISEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	KEAAD DSHGP SARQT STVRSL
TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKS KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	DSHGP SARQT STVRSL
KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVA ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	SARQT STVRSL
ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLAS GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	TVRSL
GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLL	
QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVD	
SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV	PLVAI
6384 738 1904 IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRA	
AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQA	
NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEY	
AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLN	TOTICO
HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTI	TETPO
SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQ	OOOOO
QQQMQQMQQQQLQQHQMHQQ1QQQMQQQHFQHHMQQHLQ	22222
LQQQINQQQLQQRLQLQQLQHMQHQSQPSPRQHSP	TOSAV
TSPIPAIGSPQPASQQHQSQTQTQTQVLSQVSIP	AUDOT
6385 2 1584 PRVRANDVAAGAQAVVSAGMAKSNGENGPRAPAAGESLS	GTDEC
LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGS	OGARG
ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRC	OKILTE
PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLD	VIEDD
LHROFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYC	
IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQL	
FSLLQKVSPVAHKHLSRQKIDPLLYMTEWPMCAFSRTLP	
RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQY	
LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRW	
ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDA	
KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAA	GDACP
PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESE	DTYL
6386 819 195 TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKD	OMDDL.
RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTP.	
IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSE	
PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEE	MLDNL
PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV	1
6387 1 662 PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAI	ELVKR
KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYI	LTNQK
NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQ	QLIEK
REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQ	QKAAS
STSSGSHHSSHKKRNKNRHSPSGMFDYDFEIDLKLNKK	
6388 1 662 PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAR	
KQELAETLANLERQIYAFEGSYLBDTQMYGNIIRGWDRYI	
NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQD(	
REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQ	}KAAS
STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKE	
6389 1074 497 AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGF	
LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKV	
QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHK	
EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVI	YVYQ
LIGDDVKVERIEYKKP	i
6390 158 535 GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGS	
LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYF	DNLQ
SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP	- 1
6391 5386 2897 VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQR	
MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERI1AYLR	
DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGL	LYRI.

SEQ Predicted Predicted end Amino acid segment	
The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	containing signal peptide eine, D=Aspartic Acid, E=
	enylalanine, G=Glycine,
location corresponding H=Histidine, I=Isol	engine V-I raine
corresponding to first L=Leucine, M=Methio	onine, N=Asparagine,
to first amino acid P=Proline, Q=Glutam	
amino acid residue of S=Serine, T=Threoni	
	cosine, X=Unknown, *=Stop
	nucleotide deletion,
sequence   \=possible nucleoti	
	QNRVLVCAPSNAAVDELMKKIILEF
	VRLGPEKSINSEVLKFSLDSQVNHR
	DYQLDELSRQRALCRGGREIOROEL
	EVQGRPQKTQSIIILESHIICCTLS
	SCVIVDEAGQSCEIETLTPLIHRCN
	AQEYGYDQSMMARFCRLLEENVEHN
	DICLFPSNYVYNRNLKTNRQTEAIRC
	ERRDNDSYINVQEIKLVMEIIKLIKD
	KTMIQKDLDKEFDRKGPAEVDTVDA
	QGSIGFLASLQRLNVTITRAKYSLF
	DAQKRGAIIKTCDKNYRHDAVKILK
	SRPQGGLPSSKLDSGFAKTSVAASL
	PERPPVHDQLQDPRLLKRMGIEVKGG
1 1	PTGEPGFPVVHQDLSHVQQPAAVVAA
	STCQSKCDDPEEELCHRREARAFSE
GEQEKCGSETHHTRRNSRN	
6392 972 186 GRTGVDLASSMAHRLQIRI	LTWDVKDTLLRLRHPLGEAYATKAR
AHGLEVEPSALEQGFRQAY	RAQSHSFPNYGLSHGLTSRQWWLDV
VLQTFHLAGVQDAQAVAPI	AEQLYKDFSHPCTWQVLDGAEDTLR
	egilgglglrehfdfvltseaagwp
KPDPRIFQEALRLAHMEPV	VAAHVGDNYLCDYQGPRAVGMHSFL
	IILPSLAHLLPALDCLEGSTPGL
	GSAVATASKSNVTSFQRRGPRASVT
	GQLLVSTGLPALDQLLGGGLAVGTV
	PLAEGIVNGHTLLVASAKEDPANILQ
	YNHKTPESNIKMKIAWRYQLLPKME
	PQELIEASNWHGFFLPEKISSTLKV
	IYEEGFDGSNPQKKQRNILRIGIQN
1 1	SHSLTKFLYVLRGLLRTSLSACIITM
	DVVVGLESFIGSERETNPLYKDYHGL
	KDLAFKLKRKLFTIERLHLPPDLSD
TVSRSSKMDLAESAKRLGP	
or an order of the contract which is	MAATAAERAVLEEEFRWLLHDEVHA
	PGSGTEGPAKQENFILGSCGTDQVKG
	PRNNQLLHFAFREDKQWKLQQIQDAR
	KTGAEVLKLMDAVMLQLTRARNRLT FAPALPSDLLVNVYINLNKLCLTVYQ
1 1	LHSPGAMFEWGSQRLEVSHVHKVEC
	CQLKDKISVFSSYWSYRPF
	HGGSVSGWPAGRTPTETSNPGSSVM
I JOOKI IKI BELIAMMANA	DSARRSLCKYRMLDQCRTLASRGTP
	ERGILRATGVAWESQLKPEELPSMO
	RMQLVPSIEERETPLTREDRPALOE
	VIPVPTLGHRNPWVARDSGE
	SPEGTPLYNFMGDAFQHSSQSIPRF
	FLCLNLLFTFVELFYGVLTNSLGLI
	ALMSRWKATRIFSYGYGRIEILSGF
1 1	RLIDPPELDTHMLTPVSVGGLIVNL
i i i	SCHSSDHSHSHHMHGHSDHGHGHSH
, , , , , , , , , , , , , , , , , , ,	ADTLGSIGVIVSTVLIEOFGWFIAD
1 1	KDACQVLLLRLPPEYEKELHIALEK
1 1	ASIVAGTIHIQVTSDVLEQRIVQQV
	AYFOHMSGLSTGFHDVLAMTKOMES
MKYCKDGTYIM	
6397 391 122 GAGGVGRFEAIRAPARMIE	VVCNDRLGKKVRVKCNTDDTIGDLK
KLIAAOTGTPWNKTVI.KKW	YTIFKDHVSLGDYEIHDGMNLELYY

·			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid F-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine G=Glycine
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
1	corresponding to first	to first	L-Leucine, M-Methionine, N-Asparagine
İ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
ı	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
1	sequence	Sequence	Codon, /=possible nucleotide deletion
1	acquence	ļ	\=possible nucleotide insertion)
6398	353	1306	Q
, 335	333	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
j	1		RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
1			DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
1	ł	į	SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
1			SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
1			QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
İ			PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS VIIFSKSRV
6399	75	1245	
İ		1	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
ļ			RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN
1	1	İ	EDLLKKLELYKEACEGOHKLECDLQQREEEIAELQKALSDMQVC LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
į			YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
			ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
			RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
			SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
L			SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCDEVVYEVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL
			DNISVTFLSLTDLQKNETLDIILISLSGAVQLRHLSNNLETLLKR
1			DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKOWNKVISACTEVW
1			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKOLEDHEAFETS
1			SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGOCVYGIOT
į			HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTOHFRGHTGAVF
1			SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV
1			VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL
			SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK
1			TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESLISRWPLPEY
1 1			RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW KEHG
6401	109	766	
1	•	7.5	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
! [	1		VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
1 1	1		EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
			RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP
6402	1196	279	TTSQCGGIRQSSAIPVASMEFAAICLRNALLLLPEEQQDPKQEN
[ ]			GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKOE
	ſ		LENLKCSILACSAYVALALGDNLMALNHADKLLOOPKLSGSLKF
1 1	1		LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEODOGS
l í		ľ	DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
} .		ļ	DKARKCLHQAASMIHPKEVPPEAILLAVYLELONGNTOLALOIT
6403	2	1665	KRNQLLPAVKTHSEVRKKPVFQPVHPIOPIOMPAFTTVORK
	-	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ
1			RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
i i			AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK
]			DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
1	i	ļ	LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
	[	I	MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP
1	į	İ	PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG
1	, I	, [	PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
l		1	GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
j	1	j	KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHNKNFTDKCYY
l l		1	FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
1			WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
6404	1012	222	AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
			AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA

C 6TO	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i I	sequence	sequence	\=possible nucleotide insertion)
<b>├──</b>	bequence		RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
<b>,</b>			PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
1			KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
1 1			VAPISDSPKPPPORVTLTLPVLNAARTVIFVATGEGKAAVLKRI
1 1			LEDOEENPLPAALVOPHTGKLCWFLDEAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
6405	1	1456	TAORAAAOVLGSSGLFNNHGLOVOOOOORNLSLHEYMSMELLQE
1 1		1	AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
1 1		ł	
1			FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ
1		ŀ	VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
1 1		1	TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
]		[	LYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQK
1			KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
		İ	TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
1 1			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
i i			LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
<del></del>		167	HPROMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
6406	1036	167	DDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
1 1		1	
1 1		(	VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
1 1		j	KNGMEMTR PTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
1 1		1	SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
1 1		1	YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
		<del> </del>	CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
1 1		i	SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
		l	VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
1 1		i	NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
1 1		1	SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
1 1			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE DVDMEDAP
<b></b>			
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
1 1		:	GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
<b> </b>		<del> </del>	HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
( )			AISGLENCITIHPLNIAAGVWMIMNAFILLLCEAPECCQFIEFA
1 1		1	NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
-		ļ	TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
1 1			GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
			WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
			CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
1 1		1	LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ
1		1	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKQN
			PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
			AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
			LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
1 1	l	1	PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
1	1		TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
	ı	1	RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
]	i		
			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- [	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
I	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ı	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Deguence	Codon, /=possible nucleotide deletion,
6413	2	885	\=possible nucleotide insertion)
1	_	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
	ł		NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
1			NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
I	i		GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
ł	ĺ		LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
ŀ	I	ļ	GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
6414	1	538	MEQSEELYDALMDCHWQPLDTVSSEIPAMM
	1 *	238	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
1	1		SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
į.	1		LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGPDRYKMVVQV
	l		VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
6415	2	10.50	FYY
1 3123	} ~	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
l	1		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
i			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
· F	i		LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
	1		NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
1			TVQSELEEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD
1			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
6416	410	1519	ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
	110	1319	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
-	1 1		GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
	1		VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
			ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
1			AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
1 1	ļ <u></u>	•	TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
	!		ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV
6417	1	845	KGDCQSALLALCRAEDM
	- 1	042	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
	1		LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
1	ł		EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
1 1	ı		KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
1 1			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
] '			AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
6418	2	662	AHTNRKEYTLMKAYRVA
] }	-	002	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
1 1		İ	TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
1 1			YFDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
	-		TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ
6419		973	NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
j l	- 1	213	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
i l	i i		MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
1 1		,	PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
	. [		FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY
1	1	ł	VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
1 1	· 1		NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
1 1	1	l	LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
6420	207	1105	STGVMECRKTFGEPYL
	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
1		1	YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
		Ĭ	NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
		1	GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
	1	.	ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
<u>'</u>			GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
)	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		1	FAPMYGGFPVKLRTYLGDPIPYDPQITAEELAEKTKNAVQALID
6421	1044		KHQRIPGNIMSALLERFH
6421	1844	362	WALSLRROPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
l			YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
1	1		DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE
1		j	LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT
1			LFLPPEPGPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY
			NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG
	1		ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR
ļ			NRIKVTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
1	1	)	QDDHNWKSEFYANEACKRLQAHGRRKPQIICYPETGHYIEPPYF
Ì			PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
L			GREGTIPSKV
6422	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
1	j	1	WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY
{			HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
	1		IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
1	1	İ	KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
ł		1	KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
l		Ì	YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD
ŀ	ļ.		IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
			VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
1	1		FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
ł		i	RFETTYFKKPPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
l			LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
1		Ì	FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
į.	ļ	•	LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ
6423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS
İ		İ	KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
1	1	ł	RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
1			FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQN
			QEDARRHLEYLKSLPSRQKKADEPDDISTVV
6424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
İ	1		GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA
ĺ	1		LKGSKGKDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGGL
]	j		GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH
İ			MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
			LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
		ļ	KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL
1		1	DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
}		1	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
			CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA
1	1	1	WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
1	1	}	RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
<u> </u>			KRPCTSMHFQLPIQA
6426	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
1			LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
}	1	İ	PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
l			NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
6437			ST
6427	145	959	AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
L	L		NIREYVRWMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL

SEQ	Predicted	Predicted end	Amino acid comert
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
<b> </b>	sequence		\=possible nucleotide insertion}
	İ		WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
1			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMODLRSISDA
ľ	1		PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
		ļ	VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
6428	1982	444	VPSDVDS
	1 2502	777	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
			EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
	]		KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYEI
1			PSLKKQIAKCQQLQQEYSRKEEECQAGAAEMREQFYHSCKQYGI TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
1	ľ		VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
	1		PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
1		·	KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
1	1		TETRNQPLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
ļ			QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
1			EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLRK
6429			TKELQKLIEADISKRYSGRPVNLMGTSL
0423	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
	)		VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
1	l i		NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
	1		GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
	· ·		VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
1			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
1 1			TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
	į		ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
l			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
1			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
1	i		ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
1			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
6430	1046		TYIHVF
"-30	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTG1PGSGEGGAGPGGGEG
ļ 1	ĺ		AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA
1 [	1	,	YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
i 1	1		QTFVKKAKSSKRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
] [		,	KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
!!!	ŀ	i	KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEMA
			TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
]			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
			GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
	1	1	LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
<u> </u>	1		RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEOLEAAKPEPV
•	1		IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
-6432			LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVOROFPE
1	j	-1	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKOR
i	1		FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKROENO
j			WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
l		ļ	LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
ŀ	'	1	AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
	<del></del>		MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
•	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR
1	Ì	1	SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
	1	t .	GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
	i.	į	AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGOVR
	[	1	PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
	Ì	1	THFAAKFPTRGNTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
	1	1	PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
			LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
		1	HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
ł		1	PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
	i	i	SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
	t		SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
		1	AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
~	1	2002	
			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
		j	TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
İ			DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKENLRDS
İ		l .	KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHFPDFSY
	!	1	SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
	Į.		KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
[	1	]	IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
}		}	SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
!	ł	1	LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
		1	LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSQSGTSGSKKFKK
•	1	1	TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK
]			KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
		1	MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
			DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
	ì	1	VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE
	Ì	ļ	QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
	1	1	VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
	ŧ	ł	PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMEAM
		1	HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI
	1	1	GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
	l .	1	GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
	1	1	AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
	1		VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
	1		LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
		L	LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
	1		YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
			NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
	1	1	VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
		1	AFYRSYTTQLTMNVPFQAIHFMTYEFLQBHFNPQRRYNPSSHVL
	1	1	SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
	1		AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
	1		KRQEEWRAGK
6437	1828	360 .	PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
	1	300	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
	Į.	1	
	1	1	SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
	1	1	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
	I	i	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLESEKAH
	1	1	DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
	L	<u> </u>	ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

Desiming nucleotide location corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid asquence   Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Personnel Pers	SEQ	Predicted	Predicted end	
No:		•		Amino acid segment containing signal peptide
Cocation   Corresponding   Coffee   Corresponding   Coffee   Corresponding   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffe	NO:		I .	Glutamic Acid Enhanced lands & C.
Leucine, Me-Methionine, Na-Asparagine, provides and acid and acid and acid and acid and acid and acid sequence   S-Ferline, O-Golutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, and acid and acid sequence   S-Ferline, O-Golutamine, K-Unknown, *-Stop Codon, /-possible nucleotide deletion, /-possible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   Proposible nucleotide insertion)   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY   THE NUCLEAR SENDING NEW PROPERTY				Halistidine Targeleugian V. Lucian
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residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1	to first	amino acid	P=Proline O=Glutamine P-Arginine
amino acid sequence sequence (adon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide disertion)  **TRENIERICH/POHRYVITCE/APAPILLATISH/POHROM, *-stop    **TRENIERICH/POHRYVITCE/APAPILLATISH/POKYVININOFD    LETLCOARSTEHQLKOFTEDMSEEDUSTWICAQDLKDLVGIPKM    **NIEGKELININ/RESIADULKISIGLISK/PUERIKELEHTKYKS    LESGIPDEFICPITREIM/DPVIASDGSYSEKEAMEMDPAKEN    RTSPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/POHLAGYMAQFGGLPVFLDOTILPINV    **NEALPISPTGLAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVE/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVI/PLOTILPINV    **RESPP    **POPTICAGSLINIAL/ROMAD/FEGULVI/PLOTILPINV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTICAGSLINIAL/ROMAD/FEGULV    **POPTIC		amino acid	residue of	S=Serine, T=Threonine, V=V=line
Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide dissertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-st
Apossible nucleotide insertion	j	amino acid	sequence	Codon, /=possible nucleotide deletion
THTENLIHILTQUIRTEVUTCEAPAPHILLATISMINKTVAINOPD LETLCQARSTEDQLKOFTEDWSEDVSTWLCAQUICALUQUIKW NN 11 GOKGLLMLTKESLADDLKIESIGLESKUJRKIEELBTKVKS LSG1PDEFICCITTERLKMOPUTASIGGSVEKEAMENDPAKRIN RTSPP  6438 109 901 EVQILRARMFOTGGLIVFYGLLAQTMAQFGGLPVPLDOTIPINV NPALPLSPTGLAGSLIVALSIGGLIGGLIENLPLLDILKPG GGTSGGLIGGLIGKVTSVIFGLISALDILILGLIGUNGSP DCHRLIVYTIPLGIKLQVNTPLVGASLIKLAVKLDITAEILAVRD KQERIHLULGGUCTHSPGSLIGJGLISLDGLEDPIJDRILGLIGVSS DCHRLIVYTIPLGIKLQVNTPLVGASLIKLAVKLDITAEILAVRD KQERIHLULGGUCTHSPGSLIGJGLIGLGEKTAVKLDITAEILAVRD KQLPELVQGNVCPLVMEVLRGLDITLVMDLVMMLHHLOFPIKV KVLPELVQGNVCPLVMEVLRGLDITLVMDLVMMLHHLOFPIKV KVLPELVQGNVCPLVMEVLRGLDITLVMDLVMMLHHLOFPIKV KVLPELVQGNVCPLVMEVLRGLDITLVMDLVMMLHHLOFPIKV KVLPELVQGNVCPLVMEVLRGLDITLVMDLVMMLHHLOFPIKV KVLPELVQGNVCPLVMSULGGLOKARKEAPELOS KQAKESAQMEVEQYRRERHEFOSKOQAAMSGOGNLSAEVGGAT RRQVGMMSSQORNEREVLAQLIGMVCUNPEVLYMYTGA KQAKESAQMEVEQYRRERHEFOSKOQAAMSGOGNISAEVGGAT RRQVGMMSSQORNEREVLAQLIGMVCUNPEVLYMYTGAT KLLTGSSFVKVKKLSTSTLOVENTSIGGCUPHVTNISTGGRUPWTRIST IKLLTGSSFVKVKKLSTSTLOVENTSIGGCUPHVTNISTGGRUPWTRSTE KULTGSSFVKVKKLSTSTLOVENTSIGGCUPHVTNISTGGRUPWTRSTE ARARNSDMSDLFGLVRLSIALARIONDSFFFVKDTTHHT ATARALTTDVMCLDDLVREWWRCYVETVEKLPERRPDATTEGC AQUKEMNTLLAMHTYPPIKKSGGGGAATKTANGTLGSVCDALGY RNCKENSTVANGSFPSVLTEVTQEHRYFFRAMFULGSVCDALGY RNCKENSTVANGTSFFFKKSFTLTVGERRFYFYRKBSERGGRGRGHDAPHATYDA LLAAGNSMSTLCHRAMFHOSGGAATCTIAGCIGRTWWREPULGT AGAGLARAFDLDRINTSTELCRAMGGARGGGATGGATGATGGRAPGACHAGGATG GGTGGUPMDLCHARAGTATATATATATATATATATATATATATATATATATA		sequence		\=possible nucleotide insertion)
LETTLCOARSTENQLKOFTEMSEEDVSTHLCAQDLKDLGIFKM   NINIGKELLINITKESLADDLKEISLGIFKNIKENELTKYKK   LSSGIPDEFICPITREIMKDPVIASDCYSTEKEMENWDPAKRN   RTSPP	1			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWOED
NNI DOKKELINITKESLADDIKIESIGIRSKVIRKIEELEKTYKKS LSSGI PIC PITTERIMKDYVIASDGYSTEKEMENWOPAKEN RTSPP	1			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAODLKDLVG1FKM
LSSGIPDEPICPITRELMKDPVIASDCYSTEKEAMENWDPAKRN RTSPP	į		}	NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEFLRTKVKS
6438 109 901 EVGILBARMFOTGGLIVFYGLLAGTMAOFGGLEVFLDOTLPINN NPALPLSPTGLAGSLTNALSNGLLSGGLIGHLENLEVLDIUKPG GGTSGGLIGGLIGKVTSV PGGNNT ID INFOPLIALEGUNGS DGHRILVUT PLGIKLOWTPLVGASLIRLAWKLDITAETLAVRD KQERIHLVIGDCTHSPOSLOT SLIDLGGLIGGLIGGLIGGLIGGLIGG KQERIHLVIGDCTHSPOSLOT SLIDLGGLIGGLIGGLIGGLIGGLIGGLIGGLIGGLIGGLI	1			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
PRAPILES PTOLAGEST TAN LENGTLES GELEV PLOTTLE INVESTIGATION OF THE TANK OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE				RTSPP
NPALPLSPYGLAGSLTNALSNGLESGLIGILENLPLLDILLYGE GGTSGGLIGGLIGKYSY TECHNI 11KUTPOLLEIGINGS DCHALYVTI PLGIKLQUNTELVGASLLKIANKLDTAGILAVRO KQREI HINLIGCTHS POSLQISLIGLIGLIGHDE J GGLIDSLITGILM KULPELVQGNVCPLVNEVLRGLDITLVIDUYNMLHGLOFVI KV KULPELVQGNVCPLVNEVLRGLDITLVIDUYNMLHGLOFVI KV SULPELVQGNVCPLVNEVLRGLDITLVIDUYNMLHGLOFVI KV CAMERAQMEVEQYRREREHEFQSKQOAMGSGGNISAEVSQAT RRQVQGMQSSQQRRERVLAQLIGMVCDVRQVHNYRISA  6440 3 517 RAWMINSDEDJEGULVRIS LALRIQVEDDFVYFXDGQFRGCNRT IKLLTGSSYKVEVKI KPSTLQVENS LGGVLVPLPHYDIGTFETVMQVK KVYYTTYTTECVTPTKSGROPLOJGTNPFTDIGTFETVMQVKK KVYYTTYTTECVTPTKSGROPLOJGTNPFTDIGTFETVMQVKK KYNYHKRDHCQMGSPFSVI EVECKPMETESIMWNNKESEL KSGGLRRRGPFGRSANGEEGLPFGKRAMLIGSGVGDALGY RNVCKENSTVGMKLQEELORSGGLDHLVLSFGEWPYSDNTIMH ATRALITTYDWCLDLLVREWRCYVLEHPARDPATIEC AQUKPNNYLLAWHTPFREKSGGGLGAATKAMCIGLXWKPBELLET LIEVSUGCRAFMHHPTGFLGSLCTALWFPRRAMCIGLXWKPBELLET LIEVSUGCRAFMHHPTGFLGSLCTALWFPRRAMCIGLXWKPBELLET LIEVSUGCRAFMHHPTGFLGSLCTALWFPRRAMCIGLXWKPBELLET LIEVSUGCRAFMHHPTGFLGSLCTALFYFRAKOFTLEERKISK DSENKAL FPDNYDAEEREKTYRKMSSEGRGGRGDAPMTAYDA LLAAGNSWTELCHAMPHGGESAATGT IACCLFGGLIVGLUVER GLYDDLENKERLEDJGAAIYRLSTEEK  6442 34 796 AEDPAGGLAGODTHFRAGKKRCVGHEEDDVBEKLIFK GRINDENTALAFEY CHAPTEN GENERALFYFRAKOFTLIERKRISK DSENKAL FPDNYDAEEREKTYRKMSSEGRGGRGDAFKKSVS LORGSLLDMSLVKLQLCHHLVEPRILCSSVLLANTVTGOLGEMTO DETWRTVAPQAAERAPLDELDSTTIACCLFGGLIVGLUVET GHTTLTRYNSCMELELFBOUDSPYTUTLTOMMGGARAPGC GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCGAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCGAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCGAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCGAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCGAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARQGCAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARGGCAHPASGLGAHPAT AVPIPERMS SPRPPRKYRFTTANTSARGGCAHPASGLGD GHTTGFTLTRYNSCMELFFEDDVBSYLVARGGAAGGGAFFTUTRYNLRRR EVGRODYNDAMAKGNULDEFFOLHERFENGUKKERGNARGGC KLEKKLLLAKMKLEQKKQGGAGAASSVRANGALTRANSLIGGMSSKVANNALTHARGTUN PSEVACAGAASSVRANGALTBAGGGAHPASGPGCAMBERLAGSF SEGGFWARAGAASSPRPRANGKGGAHTAGAGGAATARRKGNQ KLEKKLLLAKWALEQKVATATA	6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
GGTSGGLIGGLIGKVTSVTSCIANTITICKVTDPDLLEIGLIQGSP DGHRIVTTPICHKLQVMTPLIVGASILAVKDLTTREILAVRD KQBRIHLULGDCTHSPGSLQISLLDGLGPLPIGGLIDGLTGILM KQBRIHLULGDCTHSPGSLQISLLDGLGPLPIGGLIDGLTGILM KQBRIHLULGDCTHSPGSLQISLLDGLGPLPIGGLIDGLTGILM KVLPELLVQGNVCPLUNDVLGLDTIVLDVINMLHGLOFVIKV SIQTASATTTEMAGSQGIQQLLQAEKRAAEKVADARKKARRI KQAKEBAQMEVEQYTREREHEFQSKQAAMSAGSMISAEVEQAT RRQVQGMQSSQQRIRERVLAQLLGWUCVNRQVHYNTISA RARWNSDMGDLPGLVRLSIALRIQPNDGPVYVNDQRFGQNRT IKLLTGSSYKEVEVIK KPSTLQVENIS LGVUPDLELKSKEPDGD RVVYTGTYDTEGVYPTKSGERQPIQITMPFDIGTFTVMQVK NYHKRHONGWSSPSVIBVECKPHETMWYNKEST.  6441 234 1373 KSGGLRRGRPGRSAAVGEELDPGMEFFKAMLLGSVGDALGS RVVYTGTYDTEGVYPTKSGERQPIQITMPFDIGTFTVMQVK NYHKRHONGWSSPSVIBVECKPHETMWYNKEST.  6441 234 1373 KSGGLRRGRPGRSAAVGEELDPGMEFFKAMLLGSVGDALGS RNVCKENSTVGMKT GEBLORSGGLDHLSFGBNYDNTIMH ATABALTTDYWCLDLVREWNCYVEIVERLPSRRPDPATIEGC AOKENNYLLAWHTPPRIKSGFGRAATCANCIGLRYWGSVE MLEAVPLAEEVCRTIHHTAEVQEHWFYFFEKWOYFLEERKISK DSENKAITPDRYDAERERETYYRKWSSERGGGRGBIDAPMTAYDA LLAAGNSWTELCHBAMHGGESAATGTIAGCLGLLYWIGDGEMTQ DGTWRTVADQAAERAPLDBLUSTEILCRAAMGGEGAHPASGLGD GHTQGFVSDLCFVTTSAGALYRISTEEL GROGLDKSKKLIEDLGAALYRISTEEL GROGLDKSKKLIEDLGAALYRISTEEL GROGLDKSKKLIEDLGAALYRISTEEL GROGLDKSKKLIEDLGAALYRISTEEL GROGLDKSKKLIEDLGAALYRISTEEL GROGLDKSKKLIEDLGAALAGERGPGC GEGLEGLAPATFGSSSCKSDLGELDHTVEILUTT GROGLDKSTALDLAWER GROGNERMYNDAAGAALYRISTEEL GROGLWAARGAGAASVASALTAARGENGAKRAGPGC GEGLEGLAPATFGSSSCKSDLGELDHTVEILUTT ANSPAASSVRPFRFKERFTTVIFWASSAGGASGGFHYVRILIRR FYROGDYDHAMAEKOLDAEFCKRIEREDGKIKLERLMKNPDK AVPIEKKSEMAPRPPFEVERDTVIFWALABEGNKLUERLMKNPDK AVPIEKKSEMAPRPPFEVERDTVIFWALABEGNKLUERLMKNPDK AVPIEKKSEMAPRPPFEVERDTVIFWALABEGNKLUERLMKNPGVA RSDQVDRVI IAASVAGMGLAAMSLIGWMSRNKRQKQ  GSTPRGKRRAPSPPPFFYGSKALAGERGSPGCRREAAGSP PSEVAGAAASVANSALATKAEGCTAKRYRQ KLKKKLLAKKMLLEQKKQEGGPQVKEGGSSSSAEASGTEEKEE TVYWEVKYPFMSNDTVYLRGRRDLDMEGRKHAVILARSTSM PSEGGRBAARGEDLAAGABANGAASVAGNELAAMSLIGWMSRNKRQKQ  FKVFGVLSVSTLUAVAKYAGSLAIEBGDGWYKELYEGGCGGE TVYWEVKYPFMSNDTVYLRGRRDLDMEGRKHAVILARSTSM PGLGERSCVLTRVOKYAGSLAIEBGDGWYKELYEGGCGGE TVYWEVKYPFMSNDTVYLRGRRDLDMEGRKHAVILARSTS				NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
DCHRLYVTIPLGIKLQUNTPLUCASILLEIAPKILDTTAEILAVER   KQERIHLVLGCCHNSPELGISLIDLGIPEPIGGLIDSLITTIN     KVLPELUQCINVCPLVINEVLRGLDFTLFUGGLIDSLITTIN     KVLPELUQCINVCPLVINEVLRGLDFTLVUDIVUMILHGLGFTIKW     KVLPELUQCINVCPLVINEVLRGLDFTLVUDIVUMILHGLGFTIKW     KVLPELUQCINVCPLVINEVLRGLDFTLVUDIVUMILHGLGFTIKW     KULPELUQCINVCPLVINEVLRGERAFEKVADAEKRKARRE     KOAMEBAQMEVEQVFREREHEFOSKQAAMGSOGNESAEVEQAT     RRAVOGMOSSOGNEREVLAOLLGWUCDVREYVHYMETS     RRAWINSDMGDLPGLURISTALRIQVINDFVVYKDGGGPEGONRT     IKLLTGSSYKVEVKIKPSTLQVENTSIGGVUPHTYBTEVTPTTAEVTPTTKSGVPTFLGTMPTWGVKF     VANYHKRDHCQMGSSPSVIEVECKPMETTSIMWINKESFL     KSGGLERRGRFGFSSAAVGEELPFEMETMANILGSUGGDALGY     RINVCKENSTVGMKIQEELQRSGGLDHLVLSFGEMPVSINTIMH     ATABALITTYNCLDLLVKENVERVYLKJEPRRPDATTIEC     AQUKPNNYLLAWHTPFNEKGSGGLGAATKANCIGLRYMKPERLET     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDERLIEF     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDERLIEF     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDERLIEF     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDERLIEF     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDGRIEH     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDERLIEF     LIEVSVECGRYMHNHPTGFLGSLCTALFYMRDGRENTATATOA     LLAAGNSWFELCHRAMFHGGESAATGTTAGCLFGLUTYLDDWGK     LLAAGNSWFELCHRAMFHGGESAATGTTAGCLFGLUTYLDDWGK     LLAAGNSWFELCHRAMFHGGESAATGTTAGCLFGLUTYLDLVBK     GALVODLUBDEKKLEDLGAATYSTEE     LORGULDMSLVKLQLCHMLWFRILCSSVLLIANTVRQLOEMTA     LAGRISLDMSLVKLQLCHMLWFRILCSSVLLIANTVRQLOEMTA     LAGRISLDMSLVKLQLCHMLWFRILCSSVLLIANTVRQLOEMTA     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAHASGEALD     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAHASGEALD     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAHASGEALD     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAMGGRAHASGEALD     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAMGGRAHASGEALD     GHTQGFVSDLCPVTSAQAPRHLQSSAMEMGGRAMGGRAMFGREALD     GHTQGFVSDLCPVTSAQAPRH     GHTAN     GHTAN     ARSPANSSANSALTTANSCALSAGNGGGAFFVVRILIRR     GHTAN     ASPANSSANSPRFKKKFKTFTIV FUNKAGGAKGKA     GHTAN     ASPANSSANSPRFKKKFKTFTIV FUNKAGGAKKKKO     KLEKKKLLAKKKLEQKKQFGQDYKKKFKQFQDYVKELTAGGGC     KLEKKKLLAKKKLEQKKKGGGAMASSFFPOGRMELIANTS     SEQGWARAGARSFFPOGRMELIANTS     SEGGRAMBEDELD		ļ		GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVOSP
412 SIQTASAITTEMASOGGIQGILGAERAREKVARREKARRE, KQAKEBAOMEVEQYRREBEHEFQSKQQAMSGGRIASAEVEQAT RRQVQGMQSSQQRIRRERULAQLLGMVCDVPROVHPNYRISA  6440 3 517 RARWINSDMGDLEGLURLSIALRIQPINGGPFYKVUSGGREGORIST IKLLTSSYKVEVKIKPSTLQVENISIGGGULDYLELKSKEPDGD RVVYTGTYDTECYTPTSGEGREDJTIMPFDIGTFTVWQVKF YNYHKRDHCQWGSPPSVIEVEKPNSTSSHWVNKESFL  6441 234 1373 KSGGLKRRQRFGRSAAVGEBELPGSWFAMALLGSUGDALGY RNVCKENSTVGMKIQBELQRSGGLDHLVLSPGEMPSVSDNTIMH ATRALITTDYWCLDDLYREWVRCYVEIVEKPRRPDDATIBGC AOLKPNYLLAWHTPFNEKGSGGOLDHVLSPGEMPSVSDNTIMH ATRALITTDYWCLDDLYREWVRCYVEIVERPREPPDATIBCC AOLKPNYLLAWHTPFNEKGSGGCAATKAMCIGLRYWREPRLET LIEVSVECGRMTHINHPTGFIGSLCTALFVSFAAGKELUQWGRD MLRAVVELAEEYCRKTIRHTASYGGRGRGHDAPMTAVDA LLAAGNSWTELCHRAWFGGESAATGTIAGCLFGLLVGLDLVPK GLYQDLEDKEKLEDLGAALTVESSGGGRHDAPMTAVDA LLAAGNSWTELCHRAWFGGGSGAATGTAMGCGGRHDAPMTAVDA LLAAGNSWTELCHRAWFGGGSGAATGTAMGCGGRHDAPMTAVDA GLYQDLEDKEKLEDLGAALTVESSGGGGRGHDAPMTAVDA GLAQDLEDKEKLEDLGAALTVESSGRGGRGHDAPMTAVDA GLYQDLEDKEKLEDLGAALTVESSGRGGGGGHDAPMTAVDA GLYQDLEDKEKLEDLGAALTVESSGKBEDVEGALAGLKTVSSYS LORGSLLDMSLVKLOLCHMLVEPNLCRSVLLANTVRQIGEBMTQ GTTRTTAPQAARRAPLGRLXVSTEILCRAAMGOGGAHPASGLGD GTTQTPAAQAARRAPLGRLXVSTEILCRAAMGOGGAHPASGLGD GTTQTPAAQAARRAPLGRLXVSTEILCRAAMGOGGAHPASGLGD QTFETLETKNIPSCMEELFSDVDSPYYDLDTVLTCMMGGARFGGC GGGGLAPATGGGSSCKSDLGEBLOWELLARGKFYKSGG GHTQGPVSDLCPVTSAQARHLQSSAWEMDGFRENNSGFKKSL QUESTAGLAPATGGGSSCKSDLGEBLOKALERLMKNPDK AVPIEKKENSEMARPPFEFVROWVELVEILVET EGGGDLAPATGGGSSCKSDLGEBLOKALERLMKNPDK AVPIEKKENSEMARPPFEFVROWVELIVET EGGGDLAPATGGGSSCKSDLGEBLOKALERLMKNPDK AVPIEKKENSEMARPPFEFVROWVELIVET EGGGDAAMAEROKLAMSLIGHTVATSERGGGGSGGGGFTWYHTHLARR EYGRODYMDAMAEROKLDARSTGWRGKVENKHALARGVYANHA DKYSPLPCSKI IQRAEELVGORVLYKLISPENCHYNA RSOQVBOWITAASVARMGLAMSLIGVFSNIKGRO VPSFTMGR 6444 390 899 GSTPRKWRAPIPEPPKPDWGRAGGAGGGGGRFWENERBLDG KKEKKLLAKMKLEQKVAGGGFQGVKEGGSSSAEASGTEEBEB VPSFTMGR 6545 2 753 AGAGGAGAASVASALTDKAIVKELLIYDVASSBKYQVNINHD DKYSPLPCSKI IQRAEELVGORVLYKLISPENCHYNA SEGOPWACAGAASVANGLAMSLIGHTVSSRNIKGRO FVVWGKKEPPPPMSRRDYVYLRQRERDLDMSRRIKHVILARSTSM POLGERSOVINKONGVKGRAFTFORGRAVFSNIKRGUS SEGOPWA	1			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
5197ASAITTEMASOSOGIQLQAEGRABEKVADARKRKARRI. KQAKEBAQMEVEGYIRREBEHEFOSQAMASGOGIASAEVEDAT RQVOGMOSSOGNRERVIJAGLLGMVCDVEROVHENYRISA FARBINSDMGDIPELVULSILAIRIGDEVYFYKVDGQRFGQNRT IKLLTGSSYKVEVKIKPSTLQVENISIGSVLVPLELKSKEPDGD RVVYTGTYDTGCVTPTKSGERQPIQTIMPFTDIGTFETVMQVKF NYHKRDHCQMGS PFSVLEYEKCHNETRSIMMVNKESFIL  6441 234 1373 KSGGLRRRQRFGGRSAAVGEBELPPGMEKFKAAMLLGSVGDALGY RNVCKENSTVGMKIGEELQRSGGLHULSGEGERYSDNITMHI ATARALTTDYWCLDDLYREWMYCCYVEIVEKLPERPDDATIEC AQKEPNYLLAWHTPSNEKGSGFGRAMACHGLGYWEDRITMH ATARALTTDYWCLDDLYREWMYCCYVEIVEKLPERPDDATIEC AQKEPNYLLAWHTPSNEKGSGFGRGRRGHDAPMAYDA LLAAGNSNTELCHRAMFHGGESAATGTIAGCLFGLLYGMGD MLRAVPLAEEYCGRYTRHTASYQEHMFYPEAKGGFLCHDUMGRD MLRAVPLAEEYCGRYTRHTASYQEHMFYPEAKGGFLCHGLLYGMDLWFK DSENKALFPDNYDAEEREKTYRKMSSGGRGRRGHGAPMIAYDA LLAAGNSNTELCHRAMFHGGESAATGTIAGCLFGLLYGGLDWFK GLODLEDKEKLEDLGAALVKLETEKK GLODLEDKEKLEDLGAALVKLETEKK GLODLEDKEKLEDLGAALVKLETEKK GLODLEDKEKLEDLGAALVKLETEKK GLODLEDKEKLEDLGAALVKLETEKK GLODLEDKEKLEDLGAALVKLETGE GHOGPVSLCPVTSAQAPHLGSCRVLIANTVRGJGEMTO DGTWRTVAPQAAERAPLDRLVSTELLCRAMGGGAALPASGLOD GHYGFVSLCPVTSAQAPHLGSSCKSDLGSLGAAGKKVUSSYS LORGSLLDMSLVKLJCLCHMLVERDLVSTLUTUTGMMGGRPGPC GELGLLDAATGPGSSCKSDLGSLGAWENDGGFENGSFHKSLD QIFETLETKNIPSCMEELFSDVDSPYYDLDTVLTOMMGGRPGPC GELGLLDAATGPGSSCKSDLGSLGAWENDGGFENGSFHKSLD QIFETLETKNIPSCMEELFSDVDSPYYDLDTVLTOMMGGRPGPC GELGLLDAATGPGSSCKSDLGSLGKMDGFFRKNERFKKC KKEKKLLAKKMKLEQKKQGGPCQPKECGSSSSAEASGTEEBEB VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKFGDLIEIFRFFYHWATYVGDGVVVILA PSEVAGAGAASVARALTDKATVKKELLYDVASGDKYQVONNHD DKYSPLPCSKTIQBAEBLVGGEVLYKLTSBKCSHFVNBLRYGVA KKEKKLLAKMKLEQKKQGGPCQPKECGSSSSAEASGTEEBEB VPSFTMGR 6445 2 753 AGAAGAAGARRSPFPQAHTKGVRGLFSERRSPDCGRMELAAGSP SEEGFWBACABLQQPALAGAGMQLLVETSGISTYRLLDKKTGLY BYKVFGVUEDCSPTLLADITMDSDYRKOMDYVKELTSGECNGB TVVYMEVKYPPPMSNRRYVYLRQRRDLDMSGRGTHVLLARSTSM PQLGERSCVTRVKGYKGSLAISGAGGAVENEEDLPELS SELVENDAAGAGAAWGLDLFFTGSTGGRGAVENEEDLPELS DGGDBAAWEDDDADLPHCKQCTPCLPCNRLFTSAEPTFSICKS BRQNNIDSMYHKGLEPYGSTKLINFTRLKNRSINNPV WEKKETLIADITADDTFFLOORYFSSYGFTAMCSLASGROPOVPHTDVTT CSSTSTVIJALDCEDEDGVYFSSYGFTGGGRAVENEEDL			l	KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
6440 3 SITMASHITEMASUSQIIQULQAERRAEWADARRIKARRIL KQAKEEAQMEVEQYNEREHHEIGUSKQAMMSQGAISAEVEDAT RRQVQGMQSSQQRNERVLAQLLGMVCDVRPQVHRVNYRISA RARMSDMGDIPEJUKUSIALRIQDEDFYPYKVDEQDFEGNRT IKLLITGSSYKVEWKIKPSTLQVENISIGSGULDPLELKSKEEDGD RVVYTGTYDTEGUTPTKGEGERQIYTMPTDIGTFSTVWQVKF WYNHKRDHCQMGSPPSVIEYECKPNETRSLMWNKESFL  6441 234 1373 KSGGLRRRGRFGRSAAVGEBELPFGMEKFKAAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAINFAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGSVGDALGY RNVCKENSTVGMKIQGELQRSGCAATKAMLIGRIYMEPRLET LIEVSVECGRMTHINHPTOFIJCSLCTALFVSFAAQGKPLUQMGD MIRAVPLAEEYCRKTIRITASVQGAATKAMCIGIRAVKPERLET LIEVSVECGRMTHINHPTOFIJCSLCTALFVSFAAQGKPLUQMGD MIRAVPLAEEYCRKTIRITASVQGAATKAMCIGGRAVKPERLET LIEVSVECGRMTHINHPTOFIJCSLCTALFVSFAAQGKPLUQMGD MIRAVPLAEEYCRKTIRITASVQGAATKAMCIGGRAVGEDALFAGGIAG GLYQDLEDKEKLEDLGAALTRITEEK DSENKAIFPDINDABERRKTYRKWSSEGGGRGHDADAMIAYDA LLAAGISWTELCHRAMPFGGESAATCTIACLFGLLLYGIDLIVFK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLEDKEKLEDLGAALTRITEEK GLYQDLYBDAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERAPLDRIJVSTEILCRAAMGGCAHPASGIJO GHTQGFVSLCPVTTAAQAAERACHAMATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	6439			KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6440 3 517 RARWISDMGLIE-GLUNES LALRI OPNDGEVEN VENGGREGORET IKLLTGSSYKUEWKI KUSTLQUENIS IGGVIVPLELKSKEPDGD RVWYTGTYDTEGVTPTKSGEROP IQTITMPTDIGTFETWQWKF KWYTGTYDTEGVTPTKSGEROP IQTITMPTDIGTFETWQWKF WYTGTYDTEGVTPTKSGEROP IQTITMPTDIGTFETWQWKF YNTHKKDHCQWGSFFSVIEYECKPMETRSIMWWKRSFL RVWYKGNENTYGMKIQEELORSGELDHULLSGEWBYSDNTIMH ATABALTTTYWCLDDLYREMVRCYVEIVEK,PERRYDDATIGC AOLK PNYLLAWHIPPNEKGSGAATKAMCIGLWKPERLET LIEVSVECGRMTHNHPTGFIGSLCTALFVSFAAGKRPLQWGRD MLRAVPLAEEYCRKTIRHTAEVQEHWFYFERKWGYTLERKISK DERNKAIFPDNTYDAEEREKTYKWSEGRGGRRGHDAPMIAVDA LLAAGNSWTELCHRAMFHGGESAATGTLAGCIFGLLWGCDLVPK GLYQDLEDKEKLEBLGAAAIVRISTEEK AEDPAGGLAGODTMPARGIKRKCVGHEEDVEGALAGLKTVSSYS LORGSKAAFDELLSTEEK AEDPAGGLAGODTMPARGIKRKCVGHEEDVEGALAGLKTVSSYS LORGSKAAFDELLSTEILCRAAMGGGAHPASGIGD GHYQGFVSDLCPVTSAQAPRHLQSSAMEMDOPRENNGSFHKSLD GIFTLETETNDSCHEEPSDVSGALAGLKTVSSYS LORGSKAAFDELLSTEILCRAAMGGGAHPASGIGD GHYGGFVSDLCPVTSAQAPRHLQSSAMEMDOPRENNGSFHKSLD GIFTLETETNDSCHEEPSDVSGALAGLKEVLEREMFOK AVPIPEKMSEMAPRPPEPSKEPDTJVIPKNMGGARPGPC EGLEGLAPAASGVRPPRPREKEPDTJVIPKNMAAEGKLLAKRNPDK AVPIPEKMSEMAPRPPPEPKKEPDTJVIPKNMAAEGKLKLERLMKNPDK AVPIPEKMSEMAPRPPPEPKKEPDTJVIPKNMAEGSALGGEFBEE VSFTMGR SGRPGAASSVRPPRPRPKKEPDTJVIPKNMAEGSALGGEFBEE VSFTMGR GGRPGAASSVRPPRPRPKKEPDTJVIPKNMAEGSALGGEFBEE VSFTMGR GGRPGAASSVRPPRPRPKKEPDTJVIPKNMAEGSALGGEFBEE VSFTMGR GGRPGAASSVRPPRPRPFFKKEPDTJVIPKNMAEGSALGGEFBEE VSFTMGR GGRPGAASGVRPPRPRPRPRPRHATYVQDGSVVYHLA PPSEVAGAAASVMSALTDKAIVKKELLYDVAGSSDKYQVNNKHD DKYSPLPCSKI IQRAEELVGGEVLYKLTSACCHIVVBLIRGVG SEGGFWACAGELQOPALAGADWULVSTGGISTYRLDKKTGLY EKKVGGVLEGGSPTLADIVBTGGISTYLLDKKTGLY EKKVGGVLEGGSPTLADIVBTGGISTYLLDKKTGLY EKKVGGVLEGGSPTLADIVBTGGISTYLLDKKTGLY EKKVGGVLEGGSPTLADIVBTGGISTYLLDKKTGLY EKKVGGVLEGGSPTLADIVBTGGISTYLLDKKTGLY EKKVGGVLEGGDETAKKGVGGVPCLECRELTTSAETFSHCKS DGGDEAAWEDEDDDADLHGGQQTPCLECRELTSAETFSHCKS EIGDBAAGSPROCHTUNKT VVVEKLKHMERRALSAEAALARREDLQKKKRPAQDFVMHIDVRT VVEKLKHMERRALSAEAALARREDLQKKKRPAQDFVMHIDVRT VVEKLKHMERRALSAEAALARREDLQKKKRPAQDFVMLTDVRT VVEKLKHMERRALSAEAALARREDLQKKKRPAQDFVMLTDVRT VVEKKHMERRALSAEAALARREDLKKKRPAGDFSPROLSENTS VVEK	0433	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
RARMINSMGLPGLVRLIS LALRIQPIDEDFYKVUGGRFGONRT IKLLIGSSYKVEVKIKDSTLQVENTS IGGVLVPLELKSKEPDGD RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFFTWQVKF RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFFTWQVKF RVYTKRCHCQWSFFSVIEYECKPMETRSIMWYNKESFI  6441  234  1373  KSGGLRRRQRFGERSAAVGEEELPFGMEKFKAMLIGSUGDALGY RNVCKENSTYGMKIQEELQRSGGLDHLULSGEMPVSDNTIMHI ATARALITDYWCLDDLYRRWYRCYVEIVEKLPBERPDATIEGC AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRWKDERLET LIEVSVECKERTIRHTBETQEWFYFFERMOFYLLOWGRD MLRRAVPLAEFYCRKTIRHTBETQEWFYFFERMOFYLLOWGRD MLRRAVPLAEFYCRKTIRHTBETQEWFYFFERMOFYLLOWGRD MLRRAVPLAEFYCRKTIRHTBETQEWFYFFERMOFYLLOWGRD GENKAIFPDNYDAEEREKTYNKWSSEGRGGRGHDAPMTAYDA LLAAGNSWTELCHRAMFHGGESAATGTLAGCLFGLLYGLDLVPK GLYQDLEDKEKLEDLGAALYRLSTEEK AEDPAGGLAGOPTMFARGLKKKCVGHBEDVEGALAGLKTVSSYS LORGSLLDMSLVKLQLCIMLLUFPNLCRSVLIAMTVXRQIGEBMTQ DGTWRTVAPQAAERAPLDDRVSTEILCRAAMGGGGAHPASGLGD GHTQGPVSDLCPVTSAQAPRHLOXPNLCRSVLIAMTVXRQIGEBMTQ DGTWRTVAPQAAERAPLDDRVSTEILCRAAMGGGARHPAGG GHTQGPVSDLCPVTSAQAPRHLOXPNLGSVLIAMTVXRQIGEBMTQ OIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC GLEGLAPATPGPSSCKSDLGELDHVVELIVET ANPIEKMSEMAPRPPSPEVRDVMSSSAGGSGEFHVYHLIRRR EYQRQDYMDAMABKOKLDAEFRJKLENKTAAEGTAKRRKKRQ KLKEKKLLAKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEB VPSFTMGR GSTPRGKMRAPIPEPKFQDLTEIFRPFYRHMAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLIYDVAGSDKYQVNNKHD DXYSFJPCSKII GRAEELVGGQUKLISTENSTEPVCTMSVAGA RSDOVEDVI IAASVAGMGLAMMSLIGVMFSRNKRQKQ AGAGGAAGAARSPRPPAGAHTKGVRGLESRRSPDCCRMELAAGSF SEEQFWEACABLQQPALAGADWQLUVETSGISTYRLDKKTGLY BYKVFGVLEDCSPTILADIYMDSDYRKQMDYVKELYEQCENGE TVVWGVKYPPPMRNDVVVLIGGROUDMEGRKIIVLIARSTSM POLGERSGVIRVKQYKQSLAIESDGKKGSKVMYYFDNPGGOIP SMLINMAAKNOVPNFLICMMRACQNTLKKT PROGUEDGESGEAAMEDEDDDADLPHGKQQTPCLPCTRGTSAGETFSEICKS ERQPMEACABLQOPALAGAARACQNTLKTATVNPV PWEKEEYLKPVLEDDLLLGFGVYSUFFSYPROLSENTS VVEKLKIMERARALSAEAALARAREDLGWKKRPAQDFVMHIDVRT VVEKLKIMERARALSAEAALARAREDLGWKKRPAQDFVMHIDVRT VVEKLKIMERARALSAEAALARAREDLGWKKRPAQDFVMHIDVRT	1	•		KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
I KLUTGSSYKEVENKIRPSTLOVENTSIGGULVPULEKSKEPDED RVYYTGTYDTEGYTPTKSGEROPIGITHDTD IGTFETWIQVKF YNYHKRHCHQWS PFSVISYECKPNETRSIAWVNKESFL  6441 234 1373 KSGGLRRQRPGRSAAVGEEELPFGMEKFKAAMLIGSVGDALGY RNVCKENSTVGMKIQEELQRSGGLDHLULSGEWPVSDNTIMHI ATARALTTDYWCLDDLYREWKCYVEIVLEKIPERRPDPATIEGC AQLKPNNYLLAWHITPFNEKGSGFGAATKAMCIGLRYWKDPRLET LIEVSVECGMETHINHPTOFIGLSCTALPVSPAAQGKPLVQWGRD MLRAVPLAEEYCRKTIRHTAEYQEBWFYFEAKWGPYLEERKISK DSENKAIFPDNYDAEEREKTYHKWSSEGGGRGRRGHDAPMIAYDA LLAAGNSWTELCHRAMFHGGESAATGTLAGCLPGLLYGLDLVPK GLYQDLEDKEKLEDLGAALYRLSTEEK  6442 34 796 AEDPAGGLAGODTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS LORQSLLDMSLVKLQLCIMILVEPRILCRSVLIAMTVKQIQEEMTQ DGTWRTVAPQAAERAPLDERLVSTEILCRAAMGQGGAHPASGLGD GHTQGFVSDLCPVTSAQAPRHLQSAMEMDOPERBUGSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTCMMGGARPGPC GGLEGLAPATPGPSSSCKSDLGELDHVVEILVET AVPIFEKMEN AVPIFEKMENAPRPFPEFVRDVMGSSAGGSGEFFVYHHLRRR EYQRQDYMDAMAEKQKLDAEFFQKSLIEKIKKLERLMKNPDK AVPIFEKMEKQKKLDAFFQKSLIEKIKKLAREGTAKKRKRQ KLKEKKLLAKKMKLEQKKGEGFGQPKEQGSSSSAEASGTEEKEB VSPFTMGR  6444 390 899 GSTFRGKMRAPIPEPFKPGDLIEIFRPFYRHMAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKEGLLYVLTISENCEHVVEILYGVA RSDOVRDVI IAASVAGMGLAMMSLIGWMFSRNKRQKQ KLKEKKLLAKKMKLEQKKGEGFGQPKEQGSSSSAEASGTEEKEB  6444 390 899 GSTFRGKMRAPIPEPKFGDLIEIFRPFYRHMAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKEGLLYVLTISENCEHVVEILYGVA RSDOVRDVI IAASVAGMGLAMMSLIGWMFSRNKRQKQ  GSTPGKMRAPIPEPKPQALTKGVRGLFSRRFSPDCGRMELAAGSF SEEQFWEACABLQQPALAGADWQLVLETSGISIYRLLDKKTGLY EKVNFGVLEDCSPTILADIYMGSDYRKQMQVVELLYEQCENGE TVVWEXYPPPBMSNPVVVILGRRCDLDMEGKRIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDKKKSKVFMYYFDNPGGQIP SWLINMAAKNGVPNFLICMARACQNTLKKRT SWLINMAAKNGVPNFLICMARACQNTLKKT UNDEKKERSTVANDLGBERGNTS VVEKLKIMERARALSAEAALARAREDLQMVKRFADPFVSPSINGLSENTS VVEKLKIMERARALSAEAALARAREDLQMVKRFADPFVSPROLSENTS VVEKLKIMERARALSAEAALARAREDLQMVKRFADPFVSPROLSENTS VVEKLKIMERARALSAEAALARAREDLQMVKRFADPFVSPROLSENTS VVEKLKIMERARALSAEAALARAREDLQMVKRFADPFVSPROLSENTS	6440	<del></del>	612	RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
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AEDPAGGLAGODTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS LOROSLLDMSLVKLQLCHMLVEPNICRSVLIANTVRQIQEEMTQ DGFWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSPHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC EGLEGLAPATPGPSSSCKSDLGELDHVVEILUET  ANASPAASSVPPRFKKEPQTLVIPKNAAEQKLKLERLMKNPDK AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGGEFHYVRHLRRR EYQRODYMDAMAEKQKLDAFFQKRLEKNKIAAEQTAKRRKKRQ KLKKKLLAKKMKLEQKKQEGPGQPKEQGSSSAEASGTEEEEE VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKFGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIJAASVAGMGLAAMSLIGVMFSRNKRQKQ  6445 2 753 AGAAGAAGARSPRPQAHTKGVRGLPSRRSPDCGRMELAAGSP SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYPDNPGGQIP SWLINNAAKNGVPNFLKDMARACONYLKKT CPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSICKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYJKPVLEDDLLLQFDVERUYFEVSVPFGSVPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQCDEDGYVFSSYGHYGIHEEMLKDKIRTESYRD	ļ			GLYQDLEDKEKLEDLGAALYRLSTEEK
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GHTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC EGLEGLAPATFGPSSSCKSDLGELDHVVEILVET  6443  2 555  MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK AVPIPEKMSEWAPPRPPEFVRDVMGSSAGAGSGEFHVYRHLRRR EYQRODYNDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKRQ KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSAAEASGTEEEEE VPSFTMGR  6444  390  899  GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ  6445  2  753  AGAAGAAGAAFPRPQAHTKGVRGLPSRRSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGISIYLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYPDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  1  1651  RCPTRSPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS EHQFNIDSMVHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLDLLQCDVEDLYSPVSVFFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	1 . [			LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVROIOEEMTO
GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDEPRENRGSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC EGLEGLAPATPGPSSCKSDLGELDHVVEILVET  MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGGGFHVYRHLRRR EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKRQ KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSAEASGTEEEEB VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKPGDLIEIFRPPYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ  6445 2 753 AGAAGAAGAARSPRPQAHTKGVRGLPSRRSPDCGRMELAAGSF SEEQFWEACAELQPALAGADWQLLVETSGISIYRLDDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQVVKELYEQECNGE TVVYWEVKYPPPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT BCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETTSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEEDDLLLQFDVDFYFSYPNGLSENTS VVEKLKHMEARALSAEAALARARREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	] ]		j	DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGOEGAHPASGIGD
6443 2 555 MASPAASSVRPPRPKKEPQTLV1PKNAAEQKIKLERLMKNPDK AVPIPEKMSEWAPRPPPFYRDVMGSSAGAGSGEFHVYRHIRRR EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE VPSFTMGR 6444 390 899 GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ 6445 2 753 AGAAGAAGARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQVVKELYEQECNGE TVVYWEVKYPMSNRDYVYLRQRRDLDMEGRKHHVILARSTSM PQLGERSGYIRVKQYKQSLAIESDGKKGSKVFMYYPDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKKEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKNKIRTESYRD	1 1			GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK AVPIPEKMSEWAPRPPPEFVRDVMGSSAGGSGEFHVYRHLRRR EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ KLKEKKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEB VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALITDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ  6445 2 753 AGAAGAAGARSPRPQAHTKGVRGLPERRSSPDCGRMELAAGSP SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPPPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYPDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  1 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMYHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	1 1			QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
AVPI PEKMSEWAPRPPREVDYMGSSAGAGSGEFHVYRHLRRR EYQROQYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKRQ KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSAEASGTEEEEE VPSFTMGR  6444 390 899 GSTPRGKMRAPI PEPKPGDLI EI FREFYRHWAI YVGDGYVVHLA PPSEVAGAGAASVMSALTDKAI VKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKI I QRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVI IAASVAGMGLAAMSLIGYMFSRNKRQKQ RSDQVRDVI IAASVAGMGLAAMSLIGYMFSRNKRQKQ SEEQFWEACAELQQPALAGADWQLLVETSGISI YRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPPPMSNRDYVYLRQRRDLDMEGRKIHVI LARSTSM PQLGERSGVIRVKQY KQSLAI ESDGKKGSKVFMYYPDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNI DSMVHKHGLEFYGYI KLINFIRLKNPTVEYMNS I YNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	6443	<del></del>		EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ KLKKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALITDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ AGAGAGAGAARSPRPQAHTKGVRGLPSRRSSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQVVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT ACPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	"	-	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK
KI,KEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEB VPSFTMGR  6444 390 899 GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ AGAGAAGAARSPRPQAHTKGVRGLPSRRSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPPPMSNRDYVYLRQRRDLDMEGRKIHVLIARSTSM PQLGERSGVIRVKQYKQSLAIESDCKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	1	1		AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
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DKYSPLPCSKI I QRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVI I DASVAGMGLAAMSLIGVMFSRNKRQKQ  AGAGAAGAAGAARSPRPQAHTKGVRGLPSRRSSPDCGRMELAAGSF SEEQFWEACAELQQPALAGADWQLLVETSGI SI YRLLDKKTGLY EYKVFGVLEDCSPTLLAD I YMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLA I ESDGKKGSKVFMYYPDNPGGQI P SWLINWAAKNGVPNFLKDMARACQNYLKKT  RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNI DSMVKHGLEFYGYI KLINFIRLKNPTVEYMNS I YNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD		-		PPSEVAGAGAGSUMGAL TOWN TUNNER TOWN CONTROL
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SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	6445	2	753	
EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  1 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMYHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	j 1		·	SEEOFWEACAFI.OODAI.AGADWOI I UPPOCTOTUDI I NUMBER
TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  1 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAERTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	[	1	İ	EYKVFGVLEDCSPTLLADIVMDSDVDVDVDVDVDVDVDVDVDV
PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT  RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAERTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	1	1	. 1	TVVYWEVKYPFPMSNRDYVYIRORPDI.DMEGPKIRITI ADGMON
SWLINWAAKNGVPNFLKDMARACQNYLKKT  1 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD			!	PQLGERSGVIRVKOYKOSLAIESDGKKGSKVFMVVFDMPGGOTD
1 1651 RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEBTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKKIMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	<u></u>		ĺ	SWLINWAAKNGVPNFLKDMARACONVILKET
DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEBTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINPIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFFQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD	6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATCCPGAUPAIDEDT DOTC
EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD		ŀ	i	DSGDEAAWEDEDDADI.PHCKOOTDCI.PCNDI.PTCAPDIBATIONA
PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS  VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT  CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD			ļ.	EHOFNIDSMYHKHGI EFYGYIKI TNETDI KNOTTEVMAG TURBU
VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD		1		PWEKEEYLKPVLEDDLLLOFDVEDI.VEPVSVPFSVPNGI.CENTRO
CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD				VVEKLKHMEARALSAEAALARAREDLOKMKOFAODFVMHTDVDT
FIYONPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDOSEI		.		CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESVRD
				FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDOSET

- CEO-	1 2 1 1		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid R-
140.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	Dequence		\=possible nucleotide insertion)
1			LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY
			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
1	İ	Į	DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
	1		IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
i	ľ		RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
6447	1554	1068	KDPRSLTVTLTLNNSTQTYGLQ
	1	1000	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMMP
(			SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA
ļ	l		LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
6448	74	559	PGFYHLRIAYYASKGYRGYSYDDIPDFDD
		333	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK
1			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
6449	597	1876	QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
1	1	2070	EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG
1			GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
1			ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE
			FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
			DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV
1			RQEQQEGGHEAGEGRGCGPRESQPSPAQPRAEAPSKGPDGTPG
			EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1			CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
			SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
1			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPPMQSFQGNQFQGEWF
1			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC
			DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
			RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDABEWTYPMRREMQE
1			ILPGLFLGPYSSAMKSKLPVLOKHGITHIICIRONIEANFIKDM
1 1			FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLOMGGKVLVH
l i	Ì		GNAGISRSAAFVIAYIMETFGMKYRDAFAYVOERRFCINDNAGF
l i	l		VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
6452			EEDDFGTMQVATAQNG
0452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
[ [	1		LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCO
	ł		LTDRNYLGLKELHKEFGPSHFSVLAFPCNOFGESEPRPSKEVES
]	1		FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
6453	827		YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
	uz,	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
l I	i	i	RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
1			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
<b> </b>	}	j	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALGET
6454	827		PADSSGTAEGGSGVASPAQADKAEL
	02,	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
i f			RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
ŀ			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
6455	1042	173	PADSSGTAEGGSGVASPAQADKAEL
	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
[	i	į	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
. 1		İ	SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
l			RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
	<del></del>	L	VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

SEO	Predicted	I Day 22 - 6 - 2 2 -	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
].	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
· f	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	sequence		\=possible nucleotide insertion)
	1		LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
6456	2	555	VFDPEKERESGVLKSNKKSLRSRQH
0430		555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
1			TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
}	1	į	RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
1			KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
6457			DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
	l	ļ	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1	1	1	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
	1		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
ł	ł		DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
L-6459			SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
ì			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
i			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
•			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
5450			SFLTLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
1			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVPAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
	į		DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
	<u>{</u>		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6460	23	892	SFLTLSSQLKPKPVGEENICLDLKS
0 200	23	692	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
1	}		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
	l	•	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
i			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6461	1653	360	SFLTLSSQLKPKPVGEENICLDLKS
	1033	300	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
			LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
1			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
1	İ		YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
			GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
1 .			APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQODSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
	]		QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
	="		PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
1			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
i l			KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
1	,		PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
1			GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	<u>2</u>	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
	_	330	LHOAEEDADEWOESEENVEHIPFSHNHYPEKEMVKRSOEFYELL
1 .			
6464	12	7754	NKRRSVRFISNEQVPMEVIDNVIRTAGL
		1154	GILRQKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG

WO 01/53312 PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Sequence	\=possible nucleotide insertion)
<del></del>	- July		
1			LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
	İ		YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
1		}	GISRDTQTLKRLAEETGVHIISGAGFYVDATHSSETRAMSVEQL
Ì			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
I	1		AQAQLGCPVIIHPGRSSRAPFQIIRILQEAGADISKTVMSHLDR
1	Ì		TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
1	ł		IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
L CACE			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
ı			QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI
ì			LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLQEV
i	1		VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI
1	1		TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
1	1		KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
1	1		EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
1	i		LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSR
			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV
			EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
1			PFCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
			YSDWIDACEAANQ
6467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
1			IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
İ			YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
1			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1	1		ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
1	1		VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
i			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
1	1.		FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
l	ľ		SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
1	1		SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
1 .	i		LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
1	ł		LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
· ·	[		FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
1	ł		FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
1	1		VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
1			CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
1	1		EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
-	<u> </u>		SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
	l		LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
1			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
Ī			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1	1		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
	f		GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
	l		PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
1	1	1	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
1	1		TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
L	<u></u>		GKGKFSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
1	· ·		LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
1	1		KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
l .	·		SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1			QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
L			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
	<u> </u>		

SEO	Predicted	I becall to	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
-	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWIMAAI.
-			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLE
ŀ	İ		ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
ļ			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
6470	2726	1437	GKGKFSRAHFVLLSLL
	1	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS
ł			GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
			QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
			ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG SLQKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
			YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
1			SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV
	1		PYTSWREMFLERPRVRFDGVYISKTTYIROGEOSLDGFYRAWHO
6471	1250		VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
64/1	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
1		•	GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLSEAPN
1			EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
1			VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR
1			LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGODEFFLE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS
1	·		AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
1	İ		ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQORRREKA
1 [			VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
1			RQARREAEADKPRRLGRLKYQAPDIDVOLSSELTDSLRTLKPEG
6472			NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIOL
04/2	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDOHLRPPARRPGTTTP
1	1		ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY
			ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
1 1	1		DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF
1	į.		LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPWPLN
<u> </u>	i		RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
6473	22	912	SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK
1 1		ĺ	NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
[			LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAOMYREKIRO
j i			LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTOPPAW
1 1			DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL
} }			KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE
6474	3	462	KLREQQAADAKKQAEESMVASMRLAYQELQIDR
[ . [	-	402	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
[	ŀ	j	KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
	1	ļ	PSTLSVKGQIETVRVKGTEN
6475	3	462	LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS
		i j	KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
	ŀ	ì	KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP
			PSTLSVKGQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
1	j		KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKAROEALVRERE
		· ·	RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD
			QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELROEW
Į.			EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
ł	1	1	QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
		ļ	SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF PASRWEAYDPEKKWDKYTIR
			FINDRIGHTDPERKWURITIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l .	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6477	227	915	LQGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
l .		•	SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR
1			AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTLAKSFTA
	ļ	]	SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPY
		ļ	IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM
			TFKVEKPEY
6478	2	1495	FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNIRKTF
1		}	IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN
l		!	EIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE
	1		RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
l			ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA
		]	VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW
Ī		l	DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI
			YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
1			EVENRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPC
1		ĺ	QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
	1		SSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVMVPVKASGSS
(430			HCRAGQTGVCLIM
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLFPVFDLS
1		ł	YFIVSILYLKYEPGAVELSRRIIPIASWLCAMLHCFGSYILADLL
		]	LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
	1		IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA
l	}	1	LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW
1		į	LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL
			FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
6480	192	514	KKAKKAD
0400	132	314	DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY
ŀ		ĺ	QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL
6481	110	1131	VQEDEQDNCEETAKENKEQ
0.02	1	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
I			WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD
l			MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH
1		1	QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC
i	1	1	SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ
} .		ļ	NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG
1	1		HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA
1	1		ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE
1	1		RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV
l	1	}	NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
			LWSEREEISTAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE
J	1		EKLTEQERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL
}			KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI
l	1		FGQTGKISATEDTPEAEGEVPELYHORKGEIARCWIKYCLTLMO
1	1		NAQLSMQDNIGELDLDKQSELRALRKKELDEEESIRKKAVOFGT
İ	1		GELCDAISAVEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ
	ļ		IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
			PLTVDLNPQYYLLVNROIOFEIAHAYYDMMDLKVAIADRLRDPD
			SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA
	!		MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
			EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARAMEORLAEFRAARKRAGLAAOP
			PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP
,	1		GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
1			LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPEEKKEGEKSAYS
	·	<u> </u>	1 Table Call I Valle 1 Will volice upictoble Alo

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	The second segment containing signal nential
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
			VFNPGCEAIQGTLTAEQLERELQLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF
,	1		MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT
*			DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK
1		1	NTQKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
			RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
	1		RYLHNAYAREEFTHTCPEDKEIENTYANVAKOKS
6485	6	1091	FVDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILEEDEE
j		1	DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
ı	ľ		KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
	1		NQDIGWCVSLITDYRVRLGCGSFAGSFLEYYAADISYPVRKSIQ
· J			QDVLGTKLPQLSKGSPEEPVVGCPLGOROPCRKMI, PDPSPAARD
1			RANQKLVEYEGKAKGAESHLRAILKSRKPSRWLOTFLSSSOVUT
			CVETYLEDEGQLDLVVKYLOGVYOEVGAKVLORTNGDRIBETLD
	i		VLLPEAIICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL
6486	<u> </u>		LEERNRRRR
0400	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA
			GGTGRFSGPLHRAWRMMNFRQRMGWIGVGLYLLASAAAFYYVEE
1			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAOLLSLPFW/WPTV
			IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHOAFV
6487	352		KASNQISRLQLIDT
1	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
1 1			YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL
1 1			KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
6488	878	241	GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
			TALQEFGTSGPPLSLRFALPSGTGRFKPLFGARGPSWPPSPRVP
1 1	Ì		MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL
1			SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
L 1			SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
6489	1457	375	KVAKMATALSEELDNEDYYSLLNVRREASSEELKAAYRRLCML
1 1			YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR
1 1	. 1		GLEMEGWEVVERRTPAEIREEFERLQREREERRLQQRTNPKGT
1	1		ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
1	1		TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
1 1			DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
1 1	į		NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFI.HVP
1 1			TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHOLLLLTPR
6490			SKRRTGGG
".,"	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1		i	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
]		i	HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG
i			QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
1 1			APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
	. 1		DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
] }	· .		GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
į l	į	ŀ	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
6491	3	1183	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
]		7103	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1		ŀ	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
			HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
'		i	QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
1		ľ	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
	1	ļ	DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
		ľ	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
			Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z

SEQ	Predicted	Predicted end	Daning and government and desired
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
6492	74		KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKKS
0432	34	2573	IPFLKSCCCCCLFDFPPPPLDQVQEEECEVERVTEHGTPKPFRK
i	ļ.		FDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
ļ		[	KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
•	!		IFSNLEDILQLHIGLNEOMKAVRKRNETSVIDQIGEDLLTWFSG PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRFQTFVODAESN
1	Ì	1	PLCRRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEREKVKK
1			AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
1		•	VEELRNLDLTKKKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
	1		QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVROVATDN
1		1	KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
			TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG
1			LESTLISSKPOSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
1			EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
j	]	1	EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
1		1	FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH
1			MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
1	}		EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
1			AVESTHQQQHSPQNTHSDGAISPFTPEFLVQQRWGAMEYSCFEI QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCQRLAGS
[	1		ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
1			KEQNTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT
1		,	VGHTTTNHLI PALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN
1			VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH
5404			EPERLGLNGIAETTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
1	į		VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
1			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIBSVNLLVSAN
1			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
İ			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRINTHVK
			PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
1			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
6495			PWVRYITQNGDYQLRTQ
0495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
1			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL ETGAPRPPATVTNAVSWRSEGIKYRKNEVPLDVIESVNLLVSAN
			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
1			PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
]			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIBKSGYQAL
			PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFY
]			HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
6007			SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
			GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
			DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
<u> </u>			ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ	Predicted	1 5	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
į.	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
ı	sequence	Dequence	\=possible nucleotide insertion)
		<u> </u>	EPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
		. ~ . *	LDVCHTCCCCCDDCCCPAVCCDCCDCATCCCATA
			LRVSWIGGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
I			VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
Ì			AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
ŀ			SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
ŀ	1		LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE
ſ			KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
	i		QAQIRNLTVLTPEGEAGLSWPVGLPAPFTEHSRFEVLGWDYFTE
	I		OHTESCANCIA DECIDIO CA CHADICO A LETAL DOLADA CONTRACTOR
-			QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL
1	į į		LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
1			NVLEPREHALLTLLLVYGPREGGRGAPDFFLGVKAAAAELERRY
1			PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
1	1 1		PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP
-			DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
į	Į		ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
1	i		CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
6499	3	2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
			GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
	·	•	ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG
j			GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPOPGVFDC
	1		LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
			PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
1	1		KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
1	i		LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
•			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
			LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
1			EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF
			LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
1	1		VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF
İ			RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR
	}		MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRNRACYYSLA
6500	1703		SKVEGPPGSTQKAEAACA
] 5500	1773	726	TGPTHASADAWGLVRSVTBWCANVRGNPCAAALSCPQAVLDAGK
	1		MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
]			QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
	i		TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
	. [		YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSG
			DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
,	ľ		KQLAVCLKYAGVFAENAEDADGKDVPNTKSVGLSIKEAMTYHPN
6501		570	QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
	-	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
}	1		THERLIDHREVIQUETRYFVKEFEEKRGLREMRVLENLKNMIHE
	•		TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI
j l			HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF
6502	213	1650	
ļ ļ		1030	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
Į			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
1 1			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
1 1			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
j			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ.
] ]			EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
1 1		٠	AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLBEQGLAVDVGETGPSPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		i	IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
1	l .		KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
ļ	ì		EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLOOSYOAVKE
ł	1		KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
1			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
1			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSOFCLEEK
	1		KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHOLEO
(		ļ	EQARRDALKQRAEQSISEEPGWEEEEELLMGISPISPKEAKVPV
i		l	AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
1			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
l	1		IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
1	1		KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG
}		]	EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	
0304	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
1			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
J	}		DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
ł	<u> </u>		PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
	1		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
j	]	j	SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
	i		WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
ł	1	ł	PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1	ļ	i	REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
į.	1		DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
í		l	ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
ļ	1		STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYOOAY
i	1		RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
			LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFOASPSV
1			PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
1			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
	i		EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAKVET
İ			REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
i		i	PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
	•		OAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWONKPHGA
	1 -3/-	1	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
1		1	IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMORNASVPNLR
1		1	GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
			101
]		į.	ASETPOPESPGSSNVSSPEPCFGSSFHSTTSFVISDITEETEVE
1	1		VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
I			DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
6500	l		EDISRKGN
6508	862	342	WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
1		1	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
I	i	I .	DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
		1	ILQLVGDAVHPOFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
İ		1	KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
]		1	APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDQKV
1	1	1	RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
	·	<del></del>	

SEO	Predicted	I beads et al.	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Doguemee	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
			CCVVNTTCULICICITY VO
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
[	ļ	i	LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
6510	37	1156	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
		1130	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
1			SCTECTLFTDQATVERFGKBHAVIILNHNFEIDFLCGWTMCERF
			GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
1	į į	,	EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
1			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
	<b>i</b>		YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
1	1		NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
6511	2541	1425	GSPLLILTFLGFVGAGNGHCR
1		1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
1	{ i		TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
1	[		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
1	1		SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
1	] ]		QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
ı			LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQEGEQI
			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYPCTPTT MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
1			LLKPKPSQGDSSEAKTPSO
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
ŀ			EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
			TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
1	}		EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
			LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLINQLTDTKQLVHSFAEGQDQGSAYANRTA
1			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
i l			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
1			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
1 1	ĺ		SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
	i		PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
l i			PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
1 1			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
1 1			QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
			EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
	j		QAENHLNGKNSSLTLTGETSSAKLPRCROGGWAGDSVKASKFRR
	į.		KASERIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA
İ	.1.		APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP
ĺ	i		EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP
			AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
	1		VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
	1		AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
	ļ		VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
			LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
1	.		ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
1			KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
ا جیزی			TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGODATAAARDLRTRGLOGYCPSATAROOVLVSALOOL
. 1	İ	. 1	KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
[		į	KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
į		1	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
		I	ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

SEQ	Predicted	Dwodi at ad	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
1		1	EXFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
			INRAPMNGHCHLWYAVLCGYVSEFEGLONKINYGHLFKEHLDIA
1			IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
- [			QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENONALKFCNL
6517	<del></del>		ALLLPTVTKEDKEAQKEMQKIMTSLKR
1 5517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPYFR
1 .	1		KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATODAGYD
		ļ	LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
ı			EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
j			SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
1	1		ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
1	1		SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
		,	GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE
			ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
L	1		PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA EKAADIIKGQPALWDKDVPVYKPRTLATQR
6518	242	1098	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
•	]		RHRCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN
1			LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT
ŀ			TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
1	1		GTDSQSENEASPVKRPRLLENTERSEETSRSKQKSRRRCFQCQT
1	[		KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
			KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
i	ł l		AKKVRTEEKKAPRRVNGEGGSGGNSROLOPPAAPSPOSYGSPAS
i			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSOPGPRKLI.
1			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGI.
1			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKHK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
1	. ,		KNLDTKNYDSKI PENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
6520	3	1113	HIEHQPNGGASVIHCLQ
	İ		ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS AKKVRTEEKKAPPPUNGEGGGGGGGGGGASPOLODDAARGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	l		AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
	1		VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGL
j i	j		GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
]	j		VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK
1 1	Ĭ	İ	ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
1			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
J - 65.77			HIEHQPNGGASVIHCLQ
6521	. 184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
{		Ì	IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEOENE
1			TPPATSSEAEQPKGEPENEEKEENKSSEETKKDEKDOSKEKEKK
1 1	1	1	VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEATKAC
[ ]			FQKSGASVVAIRKYIIHKYPSLELERRGYLLKOALKRELNRGVI
[ [		ļ	KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPOVKLE
[		i	DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPOLLKNA
į l			LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS
] ]	ļ	1	AIAAMNEPKTCSTTALKKYVLENHPGTNSNYOMHLLKKTLOKCK
, ,	ļ	İ	KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
1	1	i	DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA
]	ł	[	PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
6522	1042	391	KKPATSARKE
			NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

SEQ	Predicted	Dradiated and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	L	\=possible nucleotide insertion)
l			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
1	1	Ī	SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
ļ	ļ.	]	RKRRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSOOGSP
6523			PTKRQRRSRGRPSGGARRRRRGPQPHPSSSOSPPDLPLKAK
6523	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
1			RSRKLGIFRRCWLVFKKASSKGPRRLEKPPDEKAAYFRNFHKVT
			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
	1		KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1	1		WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
· .	İ		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
	1		IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
			RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
Ì			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1	1		WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEOHER
İ	1		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRONSVGR
1	1		IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
6525	<del> </del>		MDTSTCKVVHDLE
6525	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
İ	j 1		PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
	ļ .		KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
}	1		NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
1	i I		SYAPSSPSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
	i		EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
i	i		KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
1			PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
}	' (		LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
1			MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
			LMRELDFAACVEERLDGVIPLARGGVVROYWSSSFLVDLLAVAA
	•		PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
6526			IKT
6326	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
			GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
]	j		NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
			KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
1			LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
j l			KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
1 · 1	1		FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
į !			GGVS1AGHSLGSL1LFD1LTNQKDSLGD1DSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFD1FEKEKVDKEALALCTDRDLQEIG1P
1 1			LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
1 1			KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
			PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
1 1	1	ļ	PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
ļ [			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
<u> </u>			LKEIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
1 1	l		FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMS
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amino acid residue of amino acid sequence  S=Sexime, T=Threonine, V=Valine, S=top Codon, /=possible nucleotide deletion, \				P=Proline, O=Glutamine R-Arginine
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6529  363  2215  THIRYNKIGUVETMSCOREFUFTLKKIGUPKADNILDEGA ALDEALKTCKTSDLKTERLOKSGKPILBGA ALDEALKTCKTSDLKTERLOKSGKPILBGA ALDEALKTCKTSDLKTERLOKSGKPILBGA ALDEALKTCKTSDLKTERLOKSGKPILBGA ALDEALKTCKTSDLKTERLOKSGCILMAMTTKIS NELQALIDEVTOLMAMFERBALLOGGTPILVTLSGFSEKYLSGG EQSTAALTLYTKKOFFGOIHEVVESSNESGFPILKKOTFSICD NOEILBERRLEMBRUGLAYICAQHOLHIHKASNSSMKSSIKNAB ESLHSLTSKAVDKENLDAKISSITSEIMKLEKETTQIKDESJEA VVEENAGLLAMPUVKGFDLOLATKOYTARGEIVLNOLIKQKA SFELLQLSYEIELRKHRDIYRQLBHLVQELSGSMMLYKQLEML TDPSVSQQINPRNTIDTKOYSTHRIYQVLEGENKKKLEILTHEN LEEVARKKQNISLVQDLAVSAGGEISFFLSKRIKKDVDLCDTL YQGGNQLLLISDQELTEQPHKVESQLNKLNHLLITDILADVKTKRK TLANNIKLHOMEREFYVYFLKDEDFLYDEVILKOVBLCDTL YQGGNQLLLISDQELTEQPHKVESQLNKLNHLLITDILADVKTKRK TLANNIKLHOMEREFYVYFLKDEDFLYDEVILKOVBLCDTL YQGGNQLLLISDQELTEQPHKVESQLNKLNHLLITDILADVKTKRK TLANNIKLHOMEREFYVYFLKDEDFLYDEVILKOVBLCDTL YQGGNQLLLISDQELTGGKRKKAUSLE DE LYIRVVDKVEIGKTVKAVVRVLDLHKKPFLAKVYPFDMLKLRA ASPIITLVALDEALDNTITTFLIRGVAIGGTSTLASVTNKAGGR INSAPQQIEVFPPRIMPRVTLLIGATMQVTSSGGPQOSNIL FSISNESVALVSAAGLVQGLAIGNGTVSGLVOAVDABETGKVVII SQDLVQVELLILAWRIRAP IMMRRIGTQMPIYVTGITHHQDFF SPENAAVPGITFHWSVTRADVLDLRGRHHEASIRDPSQYSFANNV LGRVKGRTGLRAVAVAVALARELSDBLOVQVPEKLQ LINPBIEADGILMSPNSYIKLQTNRDGAASISVRVLDGPEKVPV VHDEKGFLASGSMIGTSTIEVJAQEPFSQNYFANNV LGRVKGRTGLRAVAVAVALGREISDBLOVQVPEKLQ LINPBIEADGILMSPNSYIKLQTNRDGAASISVRVLDGPEKVPV VHDEKGFLASGSMIGTSTIEVJAQEPFSQNYTIVAVKSPVS YLRVSMSVLJATUGKEALVAVPLGATVTTFVHFIDNSGDVFIAH SSVLMFANNAGRGCTPT QREVJQALHPBTLISCQSQFKAVVSDJUTTVFFVHFIDNSGDVFIAH SSVLMFANNAGRGCTPT QREVJQALHPBTLISCQSGFKAPATFSPEQUA EVPFSPGLFADQAEILSNHYTSSEIRVFGAPEVLENLEVKGGS PAVLAFAKEKSFGWPSFITTTVGVLDPAAGSGGFLSTTLTFSSP VNQALHPFRAKSFGGFSPSTTTTVGVLDPAAGSGGFLSTTLTFSSP VNQALHPFYAALTPVTAVVVDRRGCGFTPTGASFGKFTBSP SYLMFAAESFGFBPFYFAAS STISPNAALPPARKASFGFSFSHTYTVGVLDPAAGSGGFLSTTLTFSSP VNQALAPTAKESFGGFSPSTTTTYGVLDPAAGSGGFLSTTLTFSSP VNQALAPTAKESFGFBPFFTAALFANNAGGCTTPT ALLACTAVMITATYTVTVVVDRRGCGFTPGAASLFGGRSFHTYFFAAS STISPNAADAPARKASFGGGSFGFTTLTTTSSP VNQALAPTARAESFGFBPHYFFAAS STISPNAADAPARKASFTVYFACGCKRNYTYFASTYVAQA QCCQUTYCNSMSSPQLQSSLP	1			
EGVEDES FILMEN CGNINE ON UNSERBLEARS ILQKSGRP ILBEA ALDEALKTCKTS DLKTPRLDDKELEKLEDEN VILLKLIKI KI QG RINCOLMAS VITSHKSIRINANE BERVIKKLKSOG LINAMITKI S NELQALIDEV TOLMMEF FRISILG GGT WILVE LINKLIK I QG EOSTALITIYTK KOFFOG HE VYFLSOF SLEXY LSOG EOSTALITIYTK KOFFOG HE VYFLSOF SLEXY LSOG WOE ILBERRIEMAR LOLAY I CAOHOLIHLKASNS MKSS I KWAE ESLHSLITSKAVDKENLDAKIS SLITSE IMKLEREV TOT KORS LAP VVRENAQLIMME VVKROPTOLI JAKOPY THROELVINDLIK (KOKA SFELLQLS VEIELRIKHER) I YRQLENLVQELS GSNMML YRQLENL TDPSVSQQ IN PRINT I DIT KDYSTHILY GVY LESOR KKELELTHEN LEEVARKLKON I SLVOD LAVS AG SHEFFISKEN KONDONLOTL WOGGOLLIS DOGLTOP HIKVES OLD KLINHLIT DILAD WITKEK TLANNKLHOMEREFYVYFLKDED YLKDI VENLETGSKI KAVSLE D ASPITIVALDES ALD NYTITEL HIGVAI GOTSITAS VITSKAGG ELYIR VVDKVE I GKTVKAY VEVLDLIKK KPJLANY FFFMDLKLRA ASPITIVALDES ALD NYTITEL HIGVAI GGTSITAS VITSKAGG INSAPQO I SUFFPFRIMP KYTLIGAT MOYTE GGOPOPOS NIL FSISNES VALVSA AGLVOG LA I GROTT VSGLU VAD VADETGKVVI SQDLVQVEVLLLRAVRIRAP I MRMRTGTOMP I YVTGI TINHOMP F SPRANA PGLITHWS VTKROVILDLERG SIT LOVOFERLO LIN PETERA GILMS PINSY I KLOTNEGARAL SISVLUDGER KYPK VHUDER GFLASS GRITSTI I SUT LOVE PGRANOVIL VALVE SPS VLRVENS SVLHTON KRAD PLOT GROTT PHYTHEHD MSGDV PHAH SSVLINFA THROED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED POL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED PROL I GROTT PHYTHEHD MSGDV PHAH SSVLINFA TRANED PHYTH I GTS GRATA SKVI VAVGDRSSIN GRECT PT ORREVIOLAL PHYTHA PLOT PROL AVAR ANS SSISSIFSTEQUA EVPES GLEDADAE I LLENHTIS EIL FRAD FOR THE PARS PANAL PARK KSF GWPSPITTY VY VAUD PAGS GORD TITLES SP VINQA I ALBACTAVM I AYHTVCTPROLAVPALITER PASPOR PHYF	6529	363	2215	) <del>-</del>
ALDBALKTCKTSDLKTPRLDDKELEKLEDBYQTILKLKUKLKIG RNKCQLMASVTSHKSURLMAKEEATKKLKQSQGILNAMITKIS NELQALTDEVTQLMMFFRHSHLGGTRPLVFLSQFSLEKYLSGE EQSTAALITYTKKQFFQGIHEVVESSBESQFFFFLKIQTPSICO NQSILEERRLEMARLQLAYICQHQLIHLKASNSSMKSIKNAE ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA VVRENAQLLMPVVKGPFDQLAVYTANGELVLNQLIKQKA SFELLQLSYEIELRKHRDIYRQLENLVQELQSSMMMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQVLESEMKKELELTHGN LEEVABKLKQNISLVQDQLAVSAQEHSFFLSKRNPDVMLCDTL YQGGNQLLISDQELTEOPHKVESQLNKLNHLITDILADWKTKRK TLANNKLHOMEREFYVYFIKDEDYLKDIVENLETQSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDTQ ELYIRVVDKVEIGKTVKAYVEVLDLHKKPPLAKYFFPMDIKKRA ASPITITLVALDEALDNYTITFLIRGVAIGGTSLTASVTNKAGGR INSAPQQIEVFPPFKIMPRKYTLIATMOVTSEGGPOPQSNIL FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVI SQDLVQVSVLLLRAVTRAP_MRRRTSTOMFIVVTGITHQNPF SFSNAVPGLTHMWSVTKRDVLDLERGHHEASIRLPSQYSFANNV LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ LIMPBIEABQILMSNNSYIKLDTBCASLSSVLDGEEKVDV VHVDERGFLASGSMIGTSTIBVIAQEPFGANQTIIVAVKVSPVS YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVPHAH SSVLMFATNRDDFVQIGKGPTINTCVVRTVSVGLITLRRWDAKH PGLSDFMPLPVLQAISPELSGAMVGDVLCLATVLTSLEGLSGT MSSSANSILHIDPKTGVAVARAVDFPSQDVFTVLEPQFDTALG QVFCSITMHRLIDKGRKHLSKTALVVSASISSSHFSTEQVGA EVPFSGLFADQAETLLSCQSGFKPAVFDFPSQDVFTVLEPQFDTALG QVFCSITMHRLIDKGRKHLSKTRALVVSASISSSHFSTEQVGA EVPFSGLFADQAETLLSCHPTASCVTYPEVGHERTYKEVV SVPQRIMARHLHPIOTSFORATASKVIVAVGDRSSNLRGCCTPT QREVIQALHPETLISCQSGFKPAVFDFPSQDVFTVLEPGFDTALG QVFCSITMHRLIDKGRKHLSNKTRALVVSASISSSHFSTEQVGA EVPFSGLFADQAETLLSCHPTASSPCHSPHYFAAS SPTSNALPPARKASFPSGLMSPAYSH  6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SPTSNALPPARKASFPSGLMSPAYSH 65511	1		2217	
RNKCQLMASVTSHKSLRIANKEERATKLKOSGGILMAMITITIS NELQALIDEVIOLMMFFRIBILLOGCTMPLYNTLSQFSLEKYLSOE EQSTAALTLYTKKOFFOGIHEVVESSNESOFFFFLKIOTPSICD NOEILEERRLEMARLQLAYICAQHQLIHLKASNISSMKSSIKMAE ESLHSLTSKAVDKENLDAKISSIKTSEIMKLEKYTOIKORSLPA VVERNAQLLMMPVVKGOFDLQIAKOPYYTARGELVLNQLIKORSLPA VVERNAQLLMMPVVKGOFDLQIAKOPYYTARGELVLNQLIKORS SFELLQLSYSIELRKHRDIYOLDENLVQELGSONMALKAQLIBML TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN LEEVAEKLKQNISLVQQDLAVSAQEHSFFLSKRNKKDVDMLCDTL YQGGNQLLLSDQELTBOPHKVESQLINKLHHLIDTLADVKTRKK TLANNKLHGMERFFYVYFLKDEDYLKDIVENLETOSKIKAVSLS D 6530 128 2986 GAAHHGAIVQVHPLLPGSSTIMHDLCLVPPAPAKAVVVVSDIQ ELYIRVVDKVSIGKTVKASVAVVLDLIHKKPFLAKYFFFMDLKLRA ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPOPQSNIL FSISNESVALVSAAGLVQCIAGTMYSGLQVOADABTSKVVII SQDLVQVEVLLLRAVRIRAPINMRTGTOMPITVYTGITNHOMPF SFSNAVPGLTFFHNSVYKRULDRGHHEASIRPSQVMPANNV LGRVKGGTGLRAVVKADPPSGQLYGLARELSDEIQVQVFEKLQ LLNPBEIBAEQILMSPNSYIKLQTNRBGAASISYRULDGPEKVPV VHVDEKGFLASGSMIGTSTIEVIAGEPGGANGTIIVAVKVSPVS YLRVSMSSPVLHTONKSALVAVPLGMTVTTVUFHDNSGDVPHAH SSVLNFATNRDDFVQIGKGFNTCVATTVSVGILTLLRWUNDAKH PGLSDPMPLLPVLQAISPELSGAMVVGDVLCLATVLTSLEGGLSGT WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTISFGBATASKVIVAVGDRSSNLKBECTPT QREVIQALHPETLISCQSGFKDAVETPSQDVFTVEPQFDTDLG GVFCSTTMRELTDKORKHLENKILVVSASLSSSHFSTEGVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSPTTYTYTVULDPAAGSGQFLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGGPTGASLFQHFLDSYQWMFFTLF ALLAGTAVMILAPHTVCTFROLAVPRAALTPRASPCHSPHYFAAS STISNALPPARKSPSPGLUMSVARSPAVASH 6531 845 1425 PSSSIPPSASPDDVPDIRTCHFCLVEDEDSVGCISGSEKCTISSS SCHWITTYYYDVVRRFGCGYTSYRGCGRNTYFFABYNYAA QCCQYDYCNSWSSPQLGSSLPEPHDRPLALPLSDSQQUWFQAL NILSLEIPNPHAGTEPDGLDPMVTLSLNILGLSFAELRRMYLFINS SCLLUPPAGALTTPHS	ŀ			
NELQALIDEYTQLMMFFRIENLGGCTNPLVFLSQFSLEKYLSGB EQSTAALITLYTKQFFGGIHVVESSNESQFNPLKIQTFSICD NQSILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSI KWAE ESLHSLTSKAVDKENLDAKISSITSEIMKLEKEVTQIKDRSLPA VVEENAQLLMPWVKGFDFLJKKQYTYTAGELVLNQLIKQKA SFELLQLSYBIELRKKRDIYRQLENLVQELGSNMMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL YQGGNQLLLSDQELTEQPHKVESQLIKKHLLIDTLADVKTKRK TLANNKLHQMERFYYYFLKDEDYLKDIVENLETGSKIKAVSLE D GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVDKVEIGKTVKAVVRVLDLHKKPFLAKYFFFMLKURA ASPIITLVALDEALDNYTITFLIRGVAIGGTSLTASVYNKAGQR INSAPQQIEVFPFFRLMPKYLLIGATMQVISEGGQPQFOSNIL FSISNESVALVSAAGLVQGLAIGNTVSGLVQAVDAETGKVVII SQDLVQVEVLLLRAVRIRAP-MMRTGTQMPIYVTGITNHQNPF SFSNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQNIFAMNV LGRVKGRTGLRAVVKAVDPTSQLVGLARELSDEIQVQVFEKLQ LLMPBIEARGILMSPNSYIKLQTNRDGAASISYRVLDGFEKVPV VHVDEKGFLASGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS YLRVSMSPVLHTONKSALVAVPLGMTVTFTVHFHDNSGDVPHAH SSVLNFATRRDFVQIGKGFTNNTCVVRTVSVGLITLLRWDAKH PGLSDFMPLFVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTYYFWGHCHLTKVEVV SVPQRIMARHLHFIGTSFQBATASKVIVAVGDRSSNLGGCTPT QREVIQALHPETLISCQSFKPAVFDFPSQDVFTVEPQFDTALG QVFCSITMRRIDDKKGRANARVAGSVTYYFWGHGHLTYKEVVV SVPQRIMARHLHFIGTSFQBATASKVIVAVGDRSSNLGGCTPT QREVIQALHPETLISCQSFKPAVFDFPSQDVFTVEPQFDTALG QVFCSITMRRIDDKGRKHLSKKTALVVSASLSSSHFSTEQUGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSPITTYTVGVLDPAAGSGPLSTTLIFSSP VTNQATAIPVTAFVVURRGGGPTGSLFQHFLDSYQMFFTLF ALLAGTAVMIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS STISNNALPPARKASPPSGLUMSPAVASH  6531 845 1425 PSASIPPBASPDPVPDIRTCHFCLVEDEVGCISGSEKCTISSS PSASIPPARAGSPPSASHVVVARGRSSNLGGCTSTSSS SCHWITTYYDVKVRFVKRGGQYISYRQGERNTYFAEWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQMFYQAL NLSLELPRHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SCLLVLPQAGLITPPHS		1		
EGSTAALTLYTKOFFGGIHEVVESSNESOFNPILKIOTPSICO  MQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKNAE ESLHSITSKAVDKENLDAKISSITSEIMKLEKEVTQIKORSLPA  VVRENAQLLKMPVVKGOFDLQIKKQDYYTARGELVLNQLIKQKA SFELLQLSYEIELRKHRDIYGLENLVQELGSSNMLYKQLEML TDPSVSQQINPRNTIDTKDYSTHRLYQVLGGENKKKELFLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFILSKRNKDVDMLCDTL YQGGNQLLISDQELTROPHKVESQLNKLMHLIDTILADVKTRKK TLANNKLHQMEREFYVYFLKDEDYLKDIVENLETQSKIKAVSLE D  6530  128  2986  GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ ELYIRVVDKVEIGKTVKAVVRVLDLHKKPFLAKYFPFMLKURA ASPIITLVALDBALDNYTITHIGWAIGQTSLTASVTNKAGQR INSAPQQIEVFPPFRLMPRKYTLLIGATMQVISGGPQPQSMIL FSISNESVALVSAAGLVQGLAIGNTSVSLVVADATGKTVKYI SQDLVQVEVLLRAVVRIRDYLLIGGHHEASIRLPSQYNFAMNV LGRVKGRTGLRAVVKAVDFYLNGTVSGLVQAVDAETGKVVI SCOLVQVEVLLRAVVRNDPLOLRGRHHEASIRLPSQYNFAMNV LGRVKGRTGLRAVVKAVDFYSCLYGLARLESEIQVQFEKLQ LLMPRIEAPQILMSPNSYIKLQTNRGAASLSYRVLDGPEKVPV VHVDEKGFLAGSMIGTSTIEVIAQEPFGANGTIIVAVKVSPVS YLKVSMSPVLHTQNKSALVAVDLGPFKTVPTVHFHNSGDVPHAH SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRWDAKH PGLSSPMPLPVLQAISPELGSWVCDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVRAVGSVTVYYEVAGHLRTYKEVVV SVPQRIMARHLHPIQTSFQEATASKUJAVGDRSSNLRGECTPT QREVJQAIHPETLISGQSGFKAVFTFPSQDVFTVEPQFTDLG QVFCSITMRHLTDKQRKHLSNKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPSVLENLEVKSGS PAVLAFAKEKSFGWPSFTTYTTVGVLDPAAGSGGPLSTTLTTSSP VTNQAIAIPVTAFVVDRRGGPGFYGASLFQHFLDSYQMFFTLF ALLACTAVMILAYHTVCTEDAJVPAATPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH  6531  845  1425  PSASIPPSASPDPVPDIRTCHFCLVEDDFVGCTISGSEKCTISSS SLCMVITTYYDVKVRFIVRGCQYISYRCQEKNTYFFAEVMYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQQQMFYQAL NLSLPLPNFHAGTEPDGLDPWVTLSINLGLSFAELRRMYLFINS SCLLVLPQAGLLTPHPS	į.	į		
NORILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKMAB ESLHSLTSKAVDKENLDAKISLTSEIMKLEKEVTQIKDRSLPA VVRENAQLILKMPVVKGPFDLQIAKQDYYTARQELVLNQLIKQKA SFELLQLSYBIELKKHRDIYRQLENLVQELSQSMMMLXKQLEML TPDSVSQQINDFRYTTDTRYSTHRLYQVLEGENKKKELFLTHGN LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL YQGGNQLLLSDQELTEQPHKVESQINKLMHLITDILADVKYKRK TLANNKLHGMEREFYVYFLKDEDVIKDIVENLETOSKIKAVSLS D GAAHHGAIVQVHPLLPGSSTIMHDLCLVPPAFAKAVVYVSDIQ ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKVFPFMDLKURA ASPIITLVALDEALDNTTITLIRGVAIGOTSLTASVTNKAGQR INSAPQQIEVFPPPRMPRKVTLLIGATMQVTSEGGPQPQSNIL FSISNESVALVSAAGLVQELAIGMCTVSGLVQAVDAETGKVVII SQDLVQVEVLLLRAVRIRAPLMRNKTGTQMPIYVTGITNHQNPF SFSNAVPGLTFHWSVTKRDLDLARGRHHEASIRLPSGYNFAMNV LGRVKGRTGLRAVVKAVDPTSQLYGLARELSDEIQVQVFBKLQ LLNPBIEABQLLMSPNSYIKLQTNBGAASISVRVLDGPEKVPV VEVUDERGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS VLRVSMSSVLHTQNKEALVAVPLGMTYPFTVHFHDNSGDVPHAH SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH PGLSDFMPLPVLQAISFELSGAMVVGDVLCLATVLTSLEGLSGT WSSSANSILHIDPKTGVAVARAVGSVTYYYEVAGHLRTYKEVVV SVPQRTMARRHLHPTQTSFGATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFRPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKTTALVVSASLSSSHFSTEQUGA EVPFSFGLFADQABILLSHYSSEIRVFGAPEVLEMLEVKGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VINQALAIPVTVAFVVDRRGGGPYGSALFGHFLDSYQVMFFTLF ALLGTAVMITATHTUCTPRDLAVPAALTPRASFGHSPHYFAAS SPTSPNALPPARKASPPSGLWSDAYASH  6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKNRSSPQLQSSLPEPHDRPLALPLSDSQIQMFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSINLIGLSFAELRRMYLFLINS SCLLVLPQAGGLTFPHS				
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SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT QREVIQALHPETLISCQSQFKPAVFGFPSQDVFTVEPQFDTALG QYFCSITMHRITDKQRKHLSNKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFCHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH FSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFLVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS				
QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGFGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASFDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQVDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS	1			
QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA EVPFSPGLFADQAEILLSNHYTGSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITTYTGVLDPAAGSGGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH  6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGGGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	l			SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT
EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITTTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFASYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS				
EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS PAVLAFAKEKSFGWPSFITTYTVGVLDPAAGSQGPLSTTLTFSSP VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMILAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH  6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFASEWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS	]			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS SPTSPNALPPARKASPPSGLWSPAYASH 6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS				EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
ALLAGTAVMI LAYHTVCTPRDLAVPAALTPRASPGHS PHYFAAS  SPTSPNALPPARKAS PPSGLWS PAYASH  6531 845 1425 PSAS I PPSAS PDP VPD ITCH F CLVED PS V G CLISS S SLCMVITIYY DV KVR F LV R G CG Q Y I S Y R C Q K K R T Y F A E Y W Q C Q Y D Y C N S S P Q L Q S S L P E P H D R P L A L P L S D S Q L Q W F Y Q A L NLS L P L P N F H A G T E P D G L D P M V T L S L N L G L S F A E L R R W L F L N S G L L V L P Q A G L L T P H P S	1			
SPTSPNALPPARKASPPSGLWSPAYASH  6531 845 1425 PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA QCCQVDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	1 1			
PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQNFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	]			ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA QCCQYDYCNSWSSPQLQSSLDEPHDRPLALPLSDSQIQWFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS				
QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQNFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	6531	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQNFYQAL NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS SGLLVLPQAGLLTPHPS	j i			
SGLLVLPQAGLLTPHPS	1		•	
				NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
6532 2 954 AAGPPSEVVNQDSLFPEPEFGPAPQVLLGPQGPGL1KGVAPPTL				SGLLVLPQAGLLTPHPS
	6532	2	954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid .	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\≈possible nucleotide insertion)
	1		ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
ł	j.		QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
1	1		QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAO
			PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
	1		EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
1			DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
6533	120		LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
1			ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
1	i		GAKLCSKLKAELKFLQKVEAGKVAIKESHLOSTNLTHLRAIVES
-			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
1			KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
ŀ	-		FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
1	ĺ		ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
1			KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNO GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
1 1			EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
i í	ſ		LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
1 1	- 1		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
1 1	l.		TIDHTPERKDEKERIKKCGGFVAWNSLGOPHVNGRLAMTRSIGD
1 1	Į.		LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSOFTW
1 1			DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
6536	242		SEINFSFSRSFASSGRWA
0550	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
! !			LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
1 1	i		LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
	1		GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
1	ľ		INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1	1		IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
1 1		1	DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
1	I		FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
1 1	-	ł	DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
] ]		1	LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY
	1	1	STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEOLRRLTKOVOE
1		Į	ARHNRDDEAIKKAVNEYDETMEKYIPVLMAOAKIYWNI.ENYDMV
]		i i	EKIFRKSVEFCNDHDVWKLNVAHVLFMOENKYKEAIGFYRDTUK
i i			KHYDNILNVSAIVLANLCVSYIMTSONEKAEELMRKIEKEEFOL
Ī		1	SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN
1	. 1	i	KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIOECVOFLGHC
			ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
6539	210		NK
6540	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
0.540	3	391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
1	!	Į.	KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTOIGPSLLP
			IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
l	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
l	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
l	ļ		RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
			RSSSLQGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
1	•		KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
1	(		SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
1	}	1	KRGFLSKKTAEASRWHEKWFALYONVLFYFEGEOSCRPAGMYLL
	ì	Į	EGCSCERTPAPPRAGAGOGGVRDALDKOYYFTVLFGHEGOKPLE
	1	i	LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
1		†	
1			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
i	1	1	DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
1	1	1	NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
		1	VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
1	<b>§</b>	1	LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
	i	1	LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
i	1		SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
í	į.	i	SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
1		1	KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
1	<u> </u>		TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
į.		l	YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
i	į	1	IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
	Ţ		PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
ł	1	ł	LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
1	l .		YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
<b>!</b>	1		DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
}	]		MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGOGWMKLDK
			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
į.	1		
ł		1	ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
1	1	1	KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
ļ	1	İ	PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
6543	1857		LDKDLIIDEDTLYELSLKIEPRLPA
0343	182/	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
1	1	{	LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
I	1		YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
Į.	1	1	TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
1		] .	SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
	1	ĺ	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
1		l	EPSDTDPEPRTLNPSPAGWFVQQHPELELMSSFRERFGRNWLOY
1	1		RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
ł			GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMAPLPEAHLG
I	ĺ	1	EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAOALDCHVCAYNGDN
1	[	ا	CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
1	]	}	SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	
5545	103/	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
1	1		SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
1			IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
			HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
I			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
	j		EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAFTVAVSIIA
		·	KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP
			**************************************

oro.			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid r-
	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	ooquoc	Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
	<del> </del>		TPILOKKESTEODI VECCI MEDITERRALIA
i		<b>{</b>	TPILQKKPSTEOPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA
			EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLLPLVLL
İ		,	PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
1			PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
			RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
L	}		IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
1			ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC
į.			SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM
1			DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
i			VLRHLEKMGCRLMNRPQAILNCVNKFWTFOELAGHGVPLPDTFS
1			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
1			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
1	}		DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
[			MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG
1			RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
6550	2293	922	PESTERELLTKLPGGLFNMNQLLANEIKLLVD
	2255	922	FRVSRDGAPDCGTEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
i			LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ
1 1			LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR
1 1			QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML
1			NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS
			LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD
į l			IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ
i l			AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
1 1			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
LI			LESQRPPAGIPVAPSSG
6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1			ADTVDLNWCVISDMEVIELNKCTSGOSFEVILKPPSFDGVPFFN
( )	ł		ASLPRRRDPSLEEIQKKLEAAEERRKYOEAELLKHLAEKREHER
j			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
6552	157		EKDKHAEEVRKNKELKERASR
5552	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
[	1		ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
[ [			ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
[		ľ	EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
6553	2	1007	EKDKHAEEVRKNKELKEEASR
[	- ,	1807	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
	1	Í	EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
! <b>!</b>	1		RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
			LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
	i		LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
	1	1	SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
	· 1	. [	YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAETRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA
		1	PGSLANHTSTAFLTEDIMTERDIMENT TOTAL
	1	ì	RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
}	[	1	YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
j		İ	QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
			EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSQL
		ŀ	EDGGTEYVIATTKLMNGTSWIEALMEKPF
			THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PA

	T		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G≈Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1 -	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
			KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
1		[	LKNOMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
Ī			AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH
1		İ	SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
1	1		EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
1	l .		SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
1			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
1	}		LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
]			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVOGDIOELYDTTLA
1	<b>}</b>		LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG
1			ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
1			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
6556	241	1449	QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
		4447	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
1			PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
ŀ			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
j			EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
			WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
ì			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
			STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
1			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
i l			SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWORC
			QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
1 1			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
			EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
i i			PECLAPVOLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
)			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP YSO
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS
1 .		-200	VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
i i			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
] [	ĺ		GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
1	i		NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
1	1		VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
i i			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
	ì		TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
- <u></u> -			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS
	[		DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPOPCVPTCF
- <u></u> -			LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLOVRDTSSRIAKG
}	ļ		GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESOLTPC
		l	IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
ļ		İ	SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
		·	NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAE
!		İ	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
			TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
L	L		ECHIVVLTDDDVVDWDEEYPPQMGEEYSQ11YSTKLYRFFKY1E

ē			
SEQ	Predicted	Predicted end	Imino ocid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	N Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Company of the Comp	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
Į		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=pcssible nucleotide insertion)
i		•	NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
Ì	1		YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
		<u>'</u>	QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
	į.		PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
ł	1		A KOLUDDOWOLF A CHIEF CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE
f	1		AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
1	İ		IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
1	į		INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
			VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAFPRVRDVI
I	j		NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
6562	<del> </del>		LPRPADSV
0302	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
	1		LYEWFLGKRSEGVPVSGPMLIEKAKDFYEOMOLTEPCVFSGGWI
ŀ			WRFKARHGIKKLDASSEKQSADHOAAEOFCAFFRSLAAEHGI.SA
į.	i		EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
	1 1		DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
1	]		SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
			YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEBE
1	[		LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
	j i		REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR
1	ĺ		GALGAVIKUENI OFGROGOGATI OSET PROGET COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA COLORIA C
6563	1319	2694	GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
· .	] [	2001	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
1	! f		HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
į.	l i		GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
1	i i		LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWPVDFSVPGG
1 1			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
1			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
1			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
1 1			YPSQPAGDCWYHIPSPPRQRLKOVSAGOTSVYALDENGNLWVPO
		1	GITPSYPQGSSWEHVSNNVCRVSVGPLDOVWVIANKVGGSHSLS
1 1		[	RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
6564			SQEQEPSAPPEAHGPVCC
6364	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
1 1	· i		KRAAETHFGFETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGT
1 1			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR
) )			KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDTNKEMLK
1 . [	1	i	VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
1 1	[	1	THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
1	į	ļ	IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
<u></u>		i	YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
			AVEKGESDCT.T.KI.GDGMANVDOOT DOWNSTANDERS OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF TH
]		j	AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
1 1	1	1	VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
6566	3	1385	LLPAFPVLLVSLSAALATWLSF
j [			KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
1	i		HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
			ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
	İ	i	STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVTF
l İ		l l	TVALLLTLVEVIINTEWLIITLVRGSGEGGPOGNSSAGWAVASP
ĺ		i i	CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
	1	ŀ	LLTTATSVAIWVVWIVMYTYGNKOHNSPTWDDPTLAIALAANAW
ļ j		1	AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
<u> </u>			QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL
			The Italian

No.   Degining   nucleotide   location   corresponding   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation   coation	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Moleschide   Cocation   Corresponding to first amino acid residue of samino acid residue of samino acid sequence   Secrine, M=Methionine, N=Asparagine,				(A=Alanine, C=Cvsteine, D=Aspartic Acid E=
corresponding to first anino acid residue of section (http://www.news.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/html.com/h	NO:	nucleotide	I B	Glutamic Acid. F=Phenylalanine G=Glycipe
Leucine, M-Methionine, N-Asparagine,   Deleucine, delivatine, N-Asparagine,   amino acid   residue of   amino acid   residue of   amino acid   sequence   S-Serine, T-Threonine, V-Waline, N-Trytophan, Y-Tyrosine, X-Duknown, *-Stop   Codon, /-possible nuclectide insertion)   NHKWYSEGATUHLERATANSGOWGSANSTHRAEMYSAGSHOA   ATPROXINGNSYMPPTYMO   NHKWYSEGATUHLERATANSGOWGSANSTHRAEMYSAGSHOA   ATPROXINGNSYMPPTYMO   TREASHLAWARGSHIMINENTSYMPHOSSGOTHYLLGRIDGDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVENDEN   SERVE		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Totatet amino acid residue of securine, Threenine, V=Valine, amino acid amino acid amino acid sequence   Secrime, T=Threenine, V=Valine, white of  Secrime, T=Threenine, V=Valine, Sequence   Secrime, T=Threenine, V=Valine, Sequence   Secrime, T=Threenine, V=Valine, Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequ			to first	L=Leucine, M=Methionine, N=Asparagine.
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amino acid sequence  Cadon, /-possible nucleotide insertion, coposible de, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible nucleotide, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, coposible, copos	ı			S=Serine, T=Threonine, V=Valine,
Sequence   Nepossible mucleotide insertion	1	1		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
### ### ##############################			sequence	Codon, /=possible nucleotide deletion,
6567 125 863 TRENNIKAYAGSIHHIRTISVVEVNDSSQTNUPLLQACIDGER YSKELLESGEPDNIRDSRGTTGHILAAARGNUDICQLLIKEPAD LLATDYQOTHALHICCHUDTIQUSNIKISIILIGHQATELVI ARRRGVNKOVIRLIESLEEQEVKGEPRRGTHSKLETMQTAESESA MESISLIRPINQGGEVLISSFERTTMQGFVEUGRYKLLIFUY ALLADTYQOTHALHICCHUDTIQUVSNIKIILIGINGQATELVI ARRRGVNKOVIRLIESLEEQEVKGEPRRGTHSKLETMQTAESESA MESISLIRPINQGGEVLISSFERTTMQGFVEUGRYKLLIFUY ALLADIGATYVSGVLEPVENQPELVH ALLSIGIAYYVSGVLEPVENQPELVH LEGGABLYFNVOHGYLEGIJVRGCKASLIJQQDTINLAVQCETLEDL KIHLQTTYVGRYLDKIJNTSHGOASSANLOGFSKTTELFPHTLASISSPM LEGGABLYFNVOHGYLEGIJVRGCKASLIJQQDTINLAVQCETLEDL KIHLQTTYVGRYLDKILITETPLAPPGOERSTALDEIN LEPLISTFLTYWTCSYMIDNYLLIMBGALQKKSVKELIGKCHPLG RPTEMBAVNILABETSGLINRALLETPLAPPGOERSTALDEIN LEPLISTFLTYTGKYMIDNYLLIMBGALQKKSVKELIGKCHPLG RPTEMBAVNILABETSGLINRALLETPLAPPGOERSTALDEIN NAWADHYGYKPLFEAWGGSGGKTLEDDYTEREVQMAVLAGDEPDOMK NVADHYGYKPLFEAWGGSGGKTLEDDYTEREVQMAVLAGDEPDOMK NVADHYGYKPLFEAWGGSGGKTLEDDYTEREVQMAVLAGDEPDOMK NVADHYGYKPLFEAWGGSGGKTLEDDYTEREVQMAVLAGDEPDOMK NVADHYGYKPLFEAWGGSGGKTLEDDYTEREVQMAVLAGEDEPDOR PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF PROPERTION OF P		sequence		\=possible nucleotide insertion)
Section   125	1		1	MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
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NVADHYGYYKPLERAVGGGGKTLEDVFYEREVQMNULAFNRQP HYGYYAYVKLKEQETRIN TUMECLSQRHRIK INSYIP JI. 6569 205 1532 RREGPQRLGHGRPTPILCRWRTAGPSHWEKQARAFQGLRPVDPR RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLESLRWSHSSI AEIQKDVEYKLPPTINNLTINILLIPPQFPQEWATSVTPPIR HHLMDKQGVYVTSPLVNNFTMISDLGKIIQSLLDEFMKNPVLA PTSTAFPYLVSNSPGMPYASQFDFPLPYPPPQBARNSITSLSV ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG FGYMMPDVPDAFPELSELSVSQLTDMNEDEEVLLEGFLTLPQLK KSTFEKKMQRHELSESCASALQARLKVAAHEAEEESDNIAED FLEGKMEIDDPLSSFMEKRTICHCRAKEEKLQQAIAMHSQPHA PL ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDWKKGLVPSAP PASRKMGSKALPAPIPLHESLQLTMYSFLQAVNTFPATVDHLQG LYGLSAVQTMHMHMYLGYPNVHEITRSTITEMAAQGIVDARF PFPALPFTTHLEHPKQGAIAHHAPLHKORPRFPANLAVAATQ EDPPKMGBLSKLSPGIGSPISGLSKLTPDRKPSRGRLDSKTKKE FICKFCGRHPFKSYNLLIHERTHTDEPFANLAVAATQ EDPPKMGBLSKLSPGIGSPISGLSKLTPDRKPSRGRLDSKTKKE FICKFCGRHPFKSYNLLIHERTHTDEPFANLAVAATQ EDPPKMGBLSKLSPGIGSPISGLSKLTPDRKPSRGRLDSKTKKE FICKFCGRHPFKSYNLLIHERTHTDEPFANLAVAATQ EDPPKMGBLSKLSPGIGSPISGLSKLTPDRKPSRGRLDSKTKKE FICKFCGRHPFKSYNLLIHERTHTDEFFANLAVAATQ EDPPKMGBLSKLSPGIGSPISGLSKLTPDRKPSRGRLDSKTKKE FICKFCGRHPKKLYDATTTKNCKHLPRGFFDNDDGCVNVLEMIHGL SLEFIRGSLEEKMKYCZBVPDLNGDGPISKEMERTENTLE SAAAKCSGETVIGGGT APPOMRKKLQKUTATTTTNCKHLPRGFFDNDDGCVNVLEMIHGL SLEFIRGSLEEKMKYCZBVPDLNGDGPISKEMERTETLLE EARGPCLPDBGIKDLVEITILKNCHHDEDIGLSFADVYELAVREETLLL EARGPCLPDBGKSQMEFEAQVKKDENDSGNROWONSDRNV ORKOFLRILQNEQFELDMEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQCVRGNSIELEKKLKAAYMNKERAA VIAEKDAILKHESLKDEKMRQCVRGNSIELEKKLKAAYMNKERAA VIAEKDAILKGEBERKLEGERGKEREMERNIT EFAAMQQQREEDRMARVQENBEKRLICQUERGGFINNITEE FAAMQQQREEDRMARVQENBEKRLQLONALTQKLEEMLRQRED LEQVYGELYGEQAEITYSKLKEEBEERNRIT EFAAMQQQREEDRMARVQENBEKRLQLONALTQKLEEMLRQRED LEQVYGELYGEQAEITYSKLKEEBEERCHENRINGLE ERKLULGKERHARDLGREPKITMLAKFAEDDRIELMAAGQGRMKQGLE HRRAVEKLIERRRQOFLADKQREEMGLORGGGFINAIIERE RIKLLKKHATNLLGYIPKSGYFKKEDDIDLIGEEFRKVYQQGSEI LKELLKKHATNLLGYIPKSGYFKKEDDIDLIGEEFRKYYQGGSED CEEK  GGGGGESQSFRAQDGTRTFATDCLMYLGGFPKLMTQGGYBKWOK	ļ	·		IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAOAEDFDOMK
6569 205 1532 RRRGPORLIGHERPFULCRWATAGESMEKGARAFGGLERPVDER RMSMLFPLTKSASSSAAGS PGGLTSLQQQKQRLIESLRNSHSSI AEIQKDVEYRLPFITINSLITINSLILIPPGPFORKPUTSVYPPIR RMSMLFPLTKSASSSAAGS PGGLTSLQQQKQRLIESLRNSHSSI AEIQKDVEYRLPFITINSLITINSLILIPPGPFORKPUTSVYPPIR HHLMDKQCVVYTSELVNNPHMEDLGKIIQSLLDEFWKHPPVLA PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEAMRSITSLSV ADTVSSTTSEITTAKPAAPSGVLSNILPLIPTYDASITPSOMG FGYKNPDVPDAFPELSELSVSQLIDMMEQEEVILEGPLTLPQLK QLITOKDDLVKSIELARKROTVLDKYRLLTQM KSTFEKKMQRQHELSSESSALQARLKVAAHEAEEESDNIAED FLECKMGIDPLSSFMEKRTICHCRRAKEEKLQQATAMHSQFHAPL PLECKMGIDPLSSFMEKRTICHCRRAKEEKLQQATAMHSQFHAPL PLECKMGIDPLSGLGSLGSALQARLKVAAHEAEEESDNIAED PLECKMGIDPLSGLGSLGSLTPDRKSGGLDSAMKGIVPSAP PASRKMGSKADAPIPLHPSLQLTNYSFLQAVMTFPATVDHLQG LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGIVDARF PFPALPFTTHLFHEKQGATAHVLAVHATHAMAAQGIVDARF PFPALPFTTHLFHEKQGATAHVLAVHATHAMAAQGIVDARF PFPALPFTTHLFHEKGASALGKUTPDRKPSGRGLDSKTKKE FICKFCGRHFTKSYNLLHERTHTDERPYTCOICHKAFRQDHL RDHRYHISKERPFKCQBCGGCSCRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APDMNRKKLQKLTGTTKKSVNLLHERTHTDERPYTCOICHKAFRQDHL RDHRYHISKERPFKCQBCGCCCGGTREFTGRATAHVHKTLHMQTSSPTAA SSAAKCSGETVICGGT SEEDFDBGIRDLUEITLKNCKHLFRGFDKDNDGCVNVLEWHIGL SLEFLGFCLLAVRGFTLLL EAFGPCLPDPSKGMEFFACYBCGGATAGAGCCVCGGRRWPRSHERGYFSSAKMGSKRRN LSCSERPIGKLVDHRYCKKLHVDALRVNNSQIRNQMVQNENDRNV QRKQFLRLLQNBCFFELDMREATICKAEENKKLKAALYNNKCERAA QIAEKDALKHESLKDEKMRQQVEENSIELERLEKKLKAANYMKERAA QIAEKDALKHESLKDEKMRQQVEENSIELERLEKKLKAANYMKERAA QIAEKDALKHESLKOBKMRAMARRYIEREKERLEKKKKKAANYMKERAA QIAEKDALKKURGAKGACCCCCGGRRWPRSHERGYFSSAKMGSKRRN LELAKLKHESLKOBKMRAMARRYIEGEBGREKKKQRAVEQLLKKLKHURDBIVRKIYRED QLEKQOKLBERMAMARRYIEGEBGRAKKAKKRCKEMKOPEECQMA LKULVQAAKEEBENFRKINAMARGRYIEGEMAMARGACCCCCCGRRWPRSHERGTLERLEKKKKAANYMKERAA LELAKLKHESLKOBKMRAMARRYIEGEBGRAKKARKAKCKEMKOPEECQMA LKULVQAAKEEBENFRKINAAACGRAKAA PALDALTIKLEEHLIRQGCG LKULKGARGACCCCCGGRRWPRSHERGCGCCCCGRRWPRSHERGGCGGACCCCCGRRWPRSHERGGACCCCCGGRRWPRSHERGGACCCCCGGRRWPRSHERGGACCCCCGGRRWPRSHERGGACCCCCCGGRRWPRSHERGGACCCCCGGRRWPRSHERGGACCCCCCGGRRWPRSHERGACCCCCCGGRRWPRSHERGACCCCCCGGRRWPRSHERGACCCCCCGGRRWPRSHERG				NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNROF
RRRGFORLGHROFPTELLCRNITAGESHINEKQARRFGGLRPUPER RMSMLFPLITKSASSASAGSPGGLTSLQQQKQRLIESLRNSHSSI AEIQKDVEYRLPPTINNLTININILLPPQFPGERKPUISVYPPIR HHLMDKQGVVYTSELVNNPTMHSDLGKIGSLLDEFWKNPPVLA ADTVSSTTSHTAKPAAPSGGFPFLPPVPPQEARMSTISLSV ADTVSSSTTSHTAKAPAAPSGGFPFLPPVPPQEARMSTISLSV ADTVSSSTTSHTAKAPAAPSGGFPFLPPVPPQEARMSTISLSV ADTVSSSTTSHTAKAPAAPSGGFPFLPPVPPQEARMSTISLSV QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTFEKKMQRQHELSESGSASALQARLKVAAHEAEESSDNIAED PLECKMEIDDPLSSFMEKRTICKGRAKEEKLQQAIAMHSQFHA PL  6570 330 1304 ARLEPLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLITNYSFLQAVNTFPATVDHLQG LYGLSAVQTHHMNHWTLGYPNVHEITRSTITEMAAAQGIVDARF PFPALPFTTHLIFHEKQGALAUPALHKURPREPPANLAVATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSGRGLDSKTKKE FICKFCGRHPTKSYNLLIHERTDERPYTOLICHKAFRRQDHL RDHRYIHSKEKPFKCQBCGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APDWRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFSVFDLINGGGFISKEEMHHMKNSLLKQP SEEDPDBGIKDLWEITLKKNDHDHDGKLSFADYELAVREETLLL EAFGPCLPDPKSQMEFEAQVFXDPNEFNDM  6572 49 1646 TPERAQPGALLGAAGCCVCGGRWPRSHERGYFSSAKWGSKRRN LSCSERHQKLUDENTYCKKUHDALKVNINGSIROMWONSNDNRV QRKGFLBILLQNEQFELDMERAIQKABENKRLKSLQLKQEEKLAM CEGERHQKLUDRNYCKKLHDALKKSLGLUKQEEKLAM CRAQYYLDLEKQLEEQBKKKQRAYEQLLKEKLMIDBIVRKIYEED QLEKGALKWEGLKEDGEKKKQRAYEQLLKEKLMIDBIVRKIYEED QLEKGQKLEKMNAMRRYIEFFOKQALKWRKKEEMEEERRRIIT EFAAMQQQREEDRMAKVQENBEERLOLQNALTOKLEEMLRQRED LEQVYRQELYQEEQAEIYKSKLKEEAEKKLRKGKEMKPEPERMRIT EFAAMQQQREEDRMAKVQENBEERLOLQNALTOKLEEMLRQRED LEQVYRQELYQEGQAEIYKSKLKEEAEKKLRKKREMEPERMRIT EFAAMQQQREEDRMAKVQENBEERLOLQNALTOKLEEMLRQRED LEQVYRQELYQEGQAEIYKSKLKEEMEEKKROFTEERMA LKELVUQAAKEBEENPRKTMLAKFAEDDRIELEMNAQKORMKQLE HRRAVERLIEERRQOFIADKGRELEEWOLQORROGFINAIIEEE RLKLLKHERATNLLGYLPKGVKKKEEDDIDLLGEEFRKVYQQRSEI CEEK GGGGGGGGSGGFGGGFGADGGTTRTPATTOLLKYLGGFRLMTTQGGFDMVOK LFLDFFRRRLSQRPTAEELEGNNILKPRNEQGEGEEKERIKRRL				HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
AEIQKDEYRIPPTINNTITINNILLDPGPEQBERUISVYPPIR HHHMDKQQVVYDSPLVNMPTMISDLGKIIQSLIDEFWRMPPVLA PTSTAPPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV ADTVSSSTTSHTTARAPS3GVLSNLPLPFIPTVDASIPTSONG FGYKNPDVDAFPELSELSVSQLTDNNEQBEVILLEGPLTLPQUK QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTOM KSTPEKKMQRQHELSEGSAALQARLKVAAHEAEEESDNIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQALAMHSQFHA PL  ARLERLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHIPSLQLTMYSFLQAVNTPPATVDHJQG LYGLSAVQTMMNNHTLGYPNVHEITRSTITEMAAAQGIAVDAR? PFPALPFTTHLFHHKQGALAHVLBAHKORPRFPPANLAVAATQ EDPPKMGDLSKLSPGLGSFISGLSKLTPDRKPSRGRLPSKTKKE FICKFCGRHFYKSYNLLHERTHTDERPYTCDICHKAFRQOHL RDHRYIHSKERPFKCQEGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKSGETVICGGT  APDMNRKKLQKLTDTLTKNCKHLFRGFDXDNDGCVNVLEWIHGL SLFLRGSLEEEMKXCFEVFDLNGDGFISREMFHHIKNSLLKQP SEEDPDESIKDLVSITLKAMHDHDHGKLSFADYELAVRETLLL EAFGGCLPDPKSQMEFEAQVEKDPMEFNDM  GFRGFLRILQNEQFELDMERIGKREMKRIKELQLKQEEKLAM LSCSERHQKLVDRNYCKKLHVQALKNUNSQIRNQWONENDNRV QRKQFLRILQNEQFELDMERIGKREMKRIKELQLKQEEKLAM ELAKLKHESLKDEKMRQOVRENSIELREKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEHHRIIKKENAARDKKNKA KAQYYLDLEKQLEEDEKKKQBAYEQLLKEKLMIDEIVRKIYEED QLEKQALEKUMNAMRRYIEPGKREAMEKKREEMEENRRII EFAMMQQQREEDRNAKVQENEEKRLQLQNAITQKEEDMA LKEUVQAAKEBEENFRKTMLAKFAEDDRIELMNAQKQRMCDLE HRRAVEKLIERRRQQFLADKQRELEEWGLQORGCFINAIIEEE LLEQVRQELYQEEQABIYKSKLKEEAEKKLRCKEMRQDFEEQMA LKELVLQAAKEBEENFRKTMLAKFAEDDRIELMNAQKQRMCQLE HRRAVEKLIERRRQQFLADKQRELEEWGLQORGCFINAIIEEE RLKLLKHAATNLLGYLPEQARKLKEEAEKKLRCKEMRQDFEEQMA LKELVLQAAKEBEENFRKTMLAKFAEDDRIELMNAQKQRMCQLE HRRAVEKLIERRRQQFLADKQRELEEWGLQORGCFINAIIEEE RLKLLKHAATNLLGYLPEGGEKKLCAGASYCOLDIGLEEFKKYQQRSEI CEEK GGGGGSSQSFRAQDGTRTPATDTCLMYLQGFRKLMTQGGYDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGGSERERERIKRI LFLDFFRRRLSQRTRAEELECGNILLKERNTGGGYDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK LFLDFFRRRLSQRTRAEELECGNILLKERNTGGSTDWOK	6569	205	1532	RRRGPQRLGHGRPTPLLCRWRTAGPSHWEKOARAFOGLRPVDPR
HHLMDKQJVYTSPLANNFTMISDIGKIIQSILIDEFWRNPPULA PTSTAFPYLISNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIFTSONG FGYKNPDVPDAFPELSELSVSQLITDMREGEVILEQFTITLPQLK QIITOKDDLVKSIEELARKNLLLEPSLEAKGRTVLDKYFLLTOP KSTFKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAHHSQFHA PL  6570 330 1304 ARLPRITFLREGFLYVLLSHWVFVGAPRFPASDSWKKGLVPSAP PASKKMGSKALPAPIPLHPSLQLTMYSFLQAVNTFPATVDHLQG LYGLSAVQTMEMNHWTLGYPRVHEITRSTITEMAAAQGI.VDARF PFPALPFTTHLFHFKQGAIAHVLPALHKORPRFPPANLAVAATQ LYGLSAVQTMEMNHWTLGYPRVHEITRSTITEMAAAQGI.VDARF PFPALPFTTHLFHFKQGAIAHVLPALHKORPRFPPANLAVAATQ EDPPKMGDLSKLSPGLGSSIGLSKLTPDRFSCRGLPSKTKKE FICKFCGRHFTKSYNLLHERPHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT SSAAKCSGETVICGGT SLERGSLEEMKYCGFEVDLINGDGP ISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMHDHDIGKLSFADYELAVREETILL EARGPCLPDFKSQMEFFEAQVFKDDMFFDAM LSCSERHQKLUDENFSCMEFFEAQVFKCDMFFDAM LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN LSCSERHQKLUDENFCKMHPRGFBCANGAGSKREN QIAEKDAIKYEOMKRDABIATIMBEHKRIIKEENAADDKRIKA AQAYYLDLEKQLEBCDEKKQBAYEQLLKEKKIMIDBIVRKYIYEED QLEKQRLEKMANARRYIEEFOKBQAMRKKKREEMEEENRKIT EFFAMMQQREEDRMAVQENEEKRLQLONALTOKLEEMIRQRED LEQVRGELYQDEQABITKEKKEPAKKINGKEMKQDFEQMA LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMAQKQRMKQLE HRRAVEKLIEERRGQFLADKGRELEEWQLOORRGGFINAIIEEE RLKLLKEHATNLGYJEPGGGTADKGRELEEWQLOORRGGFINAIIEEE RLKLLKEHATNLGYJEPGGGTADKGRELEEWQLOORRGGFINAIIEEE RLKLLKEHATNLGYJEPGGGTADKGRELEEWQLOORRGGFINAIIEEE RLKLLKEHATNLLGYJEPGGGTADKGRELEEWGLOORRGGFINAIIEEE CEEK GGGGGESQSFRAQDGTRTPATDTCLMYLQGFRKLMTGGYDMVQK LFFDFFFRRLSQRFTABELECRNILGFGGYDMVQK LFFDFFFRRLSQRFTABELECRNILGFGGYDMVQK LFFDFFFRRLSQRFTABELECRNILLKFRETRIGGFERKYQ				RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV ADTYSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG FGYKMPDVPDAFPELSELSVSQLTDNMEQGEVLLEQFITLPQLK QIITDKDDLVKSIEELARKNLLLEPSLFARRQTVLDKYELLTQM KSTFKKMQRGHELSESCASALQARIKVAAHEAEESDNIAED FLEGKMEIDDFLSSPMEKRTICHCRAKEEKLQQAIAMHSQFHA PL  ARLPPLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG LYGLSAVQTMHNMHVTLGYPNYHEITRSTITEMAAAQGIADARF PFPALPFTTHLEPHRGGAIAHVLPALHKDRPRFPFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRRYSGRGLPSKTKKE FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKFFKCQECKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APDMRKKLQKLTDTLJKNCKHLFRGFDKDNDGCVNVLEWHGL SLFLRGSLEEKMKYCTEVFDLNGDGFISKEEMHMLKNSLLKQP SEEDPDEGIKDLVEITLKKNMEHDHDGKLSFADYELAVREETLLL EAFGCPLPDPKSQMBFEAQVFKDPNEFNDM  6572 49 1646 TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDBRYCKKLHVQALKNUNSQIRNQMVQNENDNRV QRRGFLRILQNEOFFELDMEATQKKENKLKEELGLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEGMKRDAEIAKTMEEHKRII KEENAAEDKRNKA KAQYYLDLEKQLEEQBKKKQRAYEGLLKEKIMLDIVRKYEED QLEKQQKLBKNNAMRRYIEFGKKAGRAYEGLLKEKKIMLORGED LEQVRGELYQEEQBALTYKSKLKEEAEKKLEKGLORGEKNNAA KAQYYLDLEKQLEEQBKKKQRAYEGLLKEKLIMIDETURKIYEED QLEKQQKLBKNNAMRRYIEFGKKRQFTEDINGRUFURKYEED ALKGUNGCEDRMAKVQENEEKRLCLQNALITQKLEEMLRQRED LEQVRGELYQEEQBALTYKSKLKEEAEKKLKKQFGFENGMA LKELVLQAAKEEEMFRKTMLAKFAEDDRIELMMAQKQRMKQLE HRRAVEKLIEERRQOFLADKGRELEEWQLOORRGGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGFRKLMTQGGYDMVQK LFLDFFRRRLSQRFTAEELEQRNILKPRNEGEEGGEEKREIKRRE	1			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
ADTVSSTTSHTTAKPAAPS-GULSNLPLPIPTUDASIPTSONG FGYKMPDVPDAPPELSELSVQUIDMNEQEEVLLEQFITIPQLK QIITDKDDLVKSIEELARKNILLEPSLFAKRQTVLDKYELLTQM KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEESSDNIAED FLEGKMEIDDPISSPMEKRTICHCRRAKEEKLQQAIAMHSQFHA PL  6570 330 1304 ARLPRITFLREGFLYVILSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPHPSLQLTNYSFLQAVNTFPATVDHLQG LYGLSAVQTMINNHWILGYPNVHEITRSTITEMAAQGIVDARF PFPALPFTTHLFHPKGGAIAHVLPALHKDRPRFDFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGELPSKTKKE FICKFCGRHFTKSYNLLHERTHTDERPYTCDICHKAFRRQDHL RDHRYHSSKEKFFKCQECCKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT SSAAKCSGETVICGGT SSARCSGETVICGGT SSARCSGETVICGGT SEEPPDEGIKDLVEITLKKMDHDHDGKLSFADVELAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM  6572 49 1646 TPERAQPGALLGAAGCCVCGGRWPRSHERSYFSSAKMGSKREN LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNSNDNRV QRKQFLRLLQNEQPELDMEBAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDBEWNRQQVRENSIELRELEKKLKAAYMNKERAA QIASEGAAIKYEQMKRDAEIJAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBCEKKKQRAYEQLLKEKLMIDEIVRKIYEED QLEKQQKLEKNNAMRRYIEEFQKRQALWRKKKREMEEENRKII EFAAMQQREEDRMAKVQENEEKRLQLLQALURKKKREMEEENRKII EFAAMQQREEDRMAKVQENEEKRLQLLONALTQKLEEMLRQRED LEQVRQELYGERQALYKSKKREEMEEFENRKII EFAAMQQREEDRMAKVQENEEKRLQLOORRQFINAIIEEE LAKLLKEHSTHLIGETPRKYTKMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLAKKREEEMKRCKEMKQDFEEQMA LKELVLQAAKESEEMFRKTMLAKFAEDDRIELMNAQKQRMKQLE RLKLLKEHATNLLGYLPKSVFKKEDDIDLLGEEFRKVYQQRSEI CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPITAEELEQRNILKPRNEGEEGEEKREIKRRL	1			HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
FGYKMPDVPDAFPELSELSVSQLTDMNEGGEVLLLEGFLTLPQLK QIITOKDDLVKSIELLARKNILLEPSLEAKRQTVLDKYELLTOM KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED PLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA PL  6570 330 1304 ARLPRLTFLREGFLYVILSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTMYSFLQAVMTFPATVOHLOG LYGLSAVQTMHNMHUTGYPRVHEITRSTITEMAAQGLVDAR? PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRDFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSGRRLPSKYKKE FICKRCGRHFTKSYNLHERTHTDERPTYCOLCHKAFRRQHL RDHRYIHSKEKPPKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APDMKRKKLQKLTDTLTKNCKHLPRGFDKDNDGCVNVLEWHGL SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP SEEDPEGSIKDLVEITLKKNDHDHDGKLSFADVELAVREETLLL EARGGPCLPDPKSGMEFAQVKKODPMEFNDM LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQNENDNRV QRKOFLERLQNRDGFELDMEEAIQKAEENKELKELGUKGEEKLAM ELAKLKHESLKOEKMRQQVRRNSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQEAYEQLLKEKLMDEIVRKIYEED QLEKQALBKNNAMRRYIEEFGKEQALMEKKKREEMEEENRKII EFANMQQQREEDMAKVCENEEKRLQLADALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEREKKLRKQKEMKQDFEEQMA LKELVLQAAKEESENFRKTMLAKFAEDDRIELMNAGKORMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQORRCGFINAIIEEE RLKLLKEHATNLLGYLYPKGYFKKEDDIDLLGEEFRKVYQQRSEI CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFILDFFRRRLSQRPTAEELEQRNILKPRNEGEEGEEKKRRL	ŀ		•	PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
CIITOKDOLVKSIEELARKNILLEEPSLEARRQTVLDKYELLTOM KSTFEKKMQRQHELSESCASAALQARLKVAAHEAEESDNIAED FLEGKMEIDDFISSFMEKRIICHCRRAKEEKLQQAIAMHSQFHA PI  ARLPRITFLREGFLYVILSHWVFVGAPRPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTMYSFLQAVMTFPATVOHLOG LYGLSAVQTMHMHWHTLGYPMVHEITRSTIITEMAAQGLVDARF PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ EDPPKMGDLSKLSPGIGSPISGLSKLTPDRKPSEGRLPSKYKKE FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTIHMQTSSPTAA SSAAKCSGETVICGGT APDMKRKLQKLTDTLTKNCHLFRGFDKDNDGCVNVLEWHHGL SLFLRGSLEEKNKYCFEVFDLINGDGFISREMHMIKINSLLKQP SEEDPDEGIKDLVGITILKKMHDHDHOSKLSFADVELAVREETLLL EAFGPCLPDPKSQMEFEAQVEKDPNEFNDM  FPERAQPGALICARAGCCVCCGGRWBPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDENYCKLHVQALKNVNSQIRNQMVQNSHDNRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVERSIELERLEKKLKAAYMNKERAA QIASKDALKYEGMKRDAEIAKTMMEHKRIL KEBNAAEDKRNKA KAQYYLDLEKQLEEQEKKKQBAYEQLLKEKLMIDEIVRKIYEED QLEKQGKLEKNMAMARRYIEEFQKEQALWRKKREEMEEERRKII EFAAMWQQREEDRMAKVQEMEKRLQLONALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEBAEKKLRXQKEMKQDFECMA LKELVLQAAKEEEENFRKIMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRROGFINAIIEEE RLKLLKEHATNLLGYJPKGYFKKEDDIDLLGEFFRKVYQQRSEI CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEGEEQEEKREIKRRL LFLDFFRRRLSQRPTAEELEQRNILKPRNEGEEGEEKREIKRRL	l			ADIVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG
KSTFKKMOROHELSESCSASALQARLKVAAHEAEEESDNIAED FLEGKMEIDDPLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA FLEGKMEIDDPLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA PL  ARLPRITFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVUHLQG LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGINDAR? PFPALPFTTHLFHPKQGAIAHVLPALHKORPRFDFANLAVAATQ EDPPKMGDLSKLSFULSEPISGLSKLTPDRKFSRGRLPSKYKKE FICKRCGRHFTKSVLLSHFUTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQBCGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT  APPMRKKLQKLTDTITKNCKHLFRGFDXDNDGCVNVLEWHGL SLFLRGSLEEKMKYCFEVFDLMODGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM  TPERAQPGALLGAAGCCVVGGRWWPRSHERGYFSSAKMGSKREN LSCSERHQKLVDRNYCKKLHVQALKNVNSQIRNQMVQNENDINRV QRKGFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDERMQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYECMKRDAEIAKTMMEEHKRIIKEEDAAEDKRNKA KAQYYLDLEKQLKEQDEKKKQBAYEQLLKEKLMIDBIVRKIYEED QLEKQGKLBKMNAMRYIEFGVEGALWRKKKREEMEEENRKII EFAAMQQQREEDRMAKVQENEERKRLOLQNALTGKLEEMLRQRED LEQVRQELYQEEQABIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQGFLADKORELEEWGLQORROGFINAITEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK GGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEGRNILKPRNEGEEGEEKKRIKRKI				FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA PL  ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPIPLHPSLQLINYSFLQAVNTFPATVDHLQG LYGLSAVQTMHMHNHTYSPNVHEITRSTITEMAAAQGINDARF PFPALPFTTHLIFHPKQGAIAHVLPALHKDRPFDFPALAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSGRLPSKTKKE FICKFCGRHFTKSYNLLHHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT  169 656 APDMRKKLQKLTDTLTRNCKHLFRGFDKDNDGCVNVLEWHGL SLFLARGSLEEKMKYCFEVPDLNGDGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNERNDM  1646 TPERAQPGALLGAAGCCVCGGRNWPRSHERGYFSSAKMGSKRRN LSCSERHQRLVDBNYCKKLHVQALKNUNSQIRNQMYQNSMDNRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMMKERAA QIAEKDALKYEGMKRDAEIAKTMMEEHKRIIKENAAEDKRNKA KAQYYLDLEKQLEEQEKKKQBAYEQLLKEKLMIDBIVRKIYEED QLEKQGKLEKMNAMRRYIEFQKERQLULKEKLMIDBIVRKIYEED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRGYLADKGNELEEWQLQORRQGFINAIIERE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEGRNILKPRNEGEEGEKRREIKRRL	1			WITTOKODLVKSIEELARKNLLEPSLEAKRQTVLDKYELLTQM
6570 330 1304 ARLPRITFLREGFLYVILISHWVFVGAPRPPASDSWKKGLVPSAP PASRKMGSKALPAPI PIHPSIQLTMYS FLQAVNTFPATVDHLQG LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAQGI.VDAR? PFPALPFTTHLFHPKQGAIAHVLPALHKORPRFDFANLAVAATQ EDPPKMGDLSKLSPGIGSPI SGLSKLTPDRKPSRGRLPSKTKKE FICKFCGRHFTKSYNLLIHERTHTDER PYTCDICHKAFFRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APDMRRKKLQKLTDTIJTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFEVFDLINGDGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL EAFGPCLPDPKSQMEFEAQVKDPMEFDMM FPRAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDRNYCKKLHVQALKNVNSQIRNQMVQNSMDNRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEEKQEKKKQBAYEQLLKEKLMIDEIVRRIYEED QLEKQQKLEKUNAMNRRYIEFFQKEQALWRKKKREEMEEENRKIT EFANMQQREEDRMAKVQENBEKRLQLQNALTQKLEEMIRQRED LEQVRQELYQEEQABIYKSKLKEERAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMAQKGOMKQLE HRRAVEKLIEERRQQFLADKQRELBEWQLQORRCGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL LFDFFRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL				RIFERMORQHELSESCSASALQARLKVAAHEAEEESDNIAED
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
L			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
- 1	· ·	1	LARFROAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
ł			KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
ł	}		GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
i	1		PRKTRAELMKA I DEEVYCYI DEDDCYII DE DOCUMENTO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DESCRIPCIO DE DE DESCRIPCIO DE DESCRIP
			PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
1	1		KWKAEREARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG
	1	į.	GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ SEEARRLLGY
6575	117	820	
1	Į.	1	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP
ŀ		Ī	ASPERODGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
1		1	SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1			LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQORIER NKQLALERRQAKLP
6576	1	1060	
1	1	1 1 1	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
	1		RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
1	1	•	GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1	<b>.</b>		YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
1	ł		AGPAGSWSPEHADIERCERGERENCERGERGEREN
ļ	1		AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGOEEALRDR HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1	1		WHHOVHNI, WMCCESCRI SCAEL OFFICE TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED TO BE SEED
	<u>                                     </u>		WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
1			TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
1			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
I	1		REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV
1	1		GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
1	1 1	j	VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
	1		MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
1	! !		EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
1			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAQAAALQLNGAVPLGA
h			LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
1		]	LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
	· ·		VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
			MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
		j	LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
]		į	YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF
j		Į	AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
- <u></u>			KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
	ſ	1	IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
		ļ	EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
. [		1	DVGQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK
	1	1	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
		j	ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
į	. 1	- [	RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
	[		PREALSQLRVLCCEWLRPBIHTKEQILELLVLEQFLTILPQBLQ
ı	i i		AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
ŀ		. 13	KISSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
i i	i	l i	QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
[		1 )	ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI
			Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z

CEO	Dunging 3	1	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
İ			CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
1	ļ	l	HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
ł		1	KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLH
	Ì	ļ	TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
6581	220		SKSNLSKHQRVHTGEGEAP
6361	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
6582	1428	1	AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
0302	1420	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
		į	QHP11FWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
ł		İ	QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
			QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE
1		1	ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
1		1	LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
1	İ	1	RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
L			SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
			WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYG
Ĭ.			IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTO
			CPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH
ł	ļ	ĺ	FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS
1		ļ	SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS
1			DDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
}			DSSEESEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE
ı			ESDIDSEASSAFFMAKKKTPPKRERKPSGCSSRGNSRPGTPSAE
ı			GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST
ľ			PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	. 3	1678	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ
1	_	1070	HWKEQRAAQKADVI.TTGAGNPVGDKLNVITVGPRGPLLVQDVVF
			TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE
			HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL
			VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR
			PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK
j			FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
}			TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
1			PVNYFAEVEQIAFDPSNMPPGTEASPDKMLQGRLFAYPDTHRHR
1 1			LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF
			GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE
			EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
6586	32	804	DKYNAEKPKNAIHTFVQSGSHLAAREKANL
		004	PLPEQPASSTSTMPVSGTPAPNKKKKSSKLIMELTGGGQESSGL
1 1			NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
1			DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE
1			TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
1			YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV
6587	75	1117	RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
1	-		HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
	I		POGYOFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
1 1			LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
]	1		LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
1 1	I		INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
į !	ļ		FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
<u> </u>			RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

3

SEQ	Brodieto	1000000				
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide			
NO:	nucleotide	location	A=Alanine, C=Cvsteine, D=Aspartic Acid R-			
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,			
ı	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,			
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,			
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,			
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,			
ł	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop			
	sequence	sequence	Codon, /=possible nucleotide deletion,			
6588	137		\=possible nucleotide insertion)			
1 7300	1 23/	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLRQKVAYLDKEFSK			
1			AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA			
6589	<del> </del>	!	EFSKLCSQMEQLEQENOOLKEGAAGAGVAOAGP			
0303	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA			
- 1	1		CRLLWRLGLPSYLKHASTVAGGFFSLYHFFOLHMVWVVLLSLLC			
1	j		YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA			
- 1	l I		QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW			
	ļ		ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYI.			
ì	1		FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV			
	į i		GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV			
[			TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSPH			
ı	[		LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR			
ı			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY			
L			TVHKWSELSWASHWVTFGCWIFYRLIG			
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR			
	į į		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY			
ł	1		GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY			
1	1 1		VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR			
1	1	•	PVI.EFVII.EFVI TERIGARDANA DEVENTA DEVENTA DE LA CONTRA  LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA	1		RYLEFYVLESKLTEFHGAPPDAQLPSKRIIGPKNYEFLKSKREE
1	1		FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG			
			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL			
1	1.		SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY			
<b>†</b>	l i		DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL			
İ	1 1		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM			
1	l i		MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI			
6591	2177	656	VIQELFPELNKVQKEVTSVTSWM			
1		036	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR			
	1		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY			
	1 1		GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY			
1	i I		VDFFEDPSSBRKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR			
1	1 1		RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE			
1			FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDK1LPDVNLG			
ł	1	·	KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL			
•			SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY			
1	1 )	i	DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL			
		i	EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM			
1	]		MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI			
6592	3	1961	VIQELFPELNKVQKEVTSVTSWM			
		1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG			
	i	1	DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV			
[		1	LGTDMSDRRAAVIFADTLTLLFEGIARIVETHOPIVETYYGPGR			
	1	1	LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS			
] [	İ	j	TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS			
[	ı l	1	MASEEVKQEHQKCLDKLLNNCLLSCTMOELIGLYVTMERYFMPE			
[	ľ	ļ	TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSTDCI.			
j 1	ļ		CAMINLATTELESDFRDVLCNKLRMGFPATTFODIORGVTSAVN			
] ]	ļ	j	IMHSSLQQGKPDTKGIESTDEAKMSFLVTLWNVEVCSENISTI.K			
į í	F	ĺ	KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLOR			
j !	i	i i	GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVO			
	į	1	QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVI.KS			
1 1		1	TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKPARLSOMATILN			
j í	· 1		LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR			
	<u> </u>		LRL			
6593	3	1837	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR			
]		Ì	RGGEGGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL			
			RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR			
		<del></del>	THE TAX PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u></u>	\=possible nucleotide insertion)
1	1		EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
1			YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI
1			EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
1			IKAKIMAKKRSTIKTOLDDDITALKQRSFVDAEVDVTRDIVSRE
1	}	}	RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
		į	GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
İ			IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
			IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
İ	1		GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVOKW
1			DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
1	1		DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDLL
į		}	NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
1	1	1	ARKMEEFREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE
i	ļ	İ	QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
	1		AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALWL
	1		HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQI
İ	1		PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
6595	<del></del>	501	NYSLVDDYSLLYQ
6555	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRLLPDMLRKD
ł	1	1	GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
l	1		GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
i			QQDPSLPLLHTPIPLVSENPQ
6596	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
l	<b>l</b> .		VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
		j	KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
	1		AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
6597	2	1026	ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
"35"	1 4	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
1			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVML?NEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
1			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
1			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
L	<u> </u>		ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
1			VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
}			LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV
Ī			FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
1			DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
			SKGLQS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
1			MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
1			DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
			LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
i .			VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
1			EAVAAVTEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
L	L	1	RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE

SEO	Predicted	Dungling and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<del> </del>	1 1		\=possible nucleotide insertion)
			VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
6600	2	934	ADDGAHSQNEKLNRYNYIEGTKMLAAYLYBVSQLKD
""	1	334	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
ł			AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
· I	1		LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
ĺ	ì		QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
1	i		LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
ļ			TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR
1			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
6601	529	1450	GC .
1 5551	323	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
	]		KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
	l I		NHQHQQCMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQQKL
			RLQRIQMERERIRMRQEELMRQEAALCRQLPMEAETLAPVQAAV
1			NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
İ			PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
6602	127		NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
""	12,	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
1 .			ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
j			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
6603	79	660	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
	, ,	000	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
			SGMGATGTLRTSLDPSLEIYKKMFRVKRREQLLALKNLAQLNDI
1			HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
1			AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
6604	3	688	NCTGVFNQGPHSPILSLM
	_ 1	900	TSTAQRQGGERMSFRGGGRGGFNRGGGGGFNRGGSSNHFRGGG
1 1			GGGGGGNFRGGGRGGFGGGGGGFNKGQDQGPPERVVLLGEFL
	į		HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDE1FGQLR
1 1			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
1 1			GPPRGGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
6605	7	848	
		040	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
į l			ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
1 1	1		SVTLKDLDVALPI IENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
] [			QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
1 1			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
			LETDSPALGPEKOVRNEPWNISISABYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK
6606	<del></del>	1682	
[	-	7002	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
j			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
[		į	KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
1 1	I		SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLBEYVHKRYPGL
i i			VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
		i	VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
	1	ļ	YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
		į	MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
	İ		GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
			RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
I	Į.		LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
! !	i		DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
6607	137		RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
200,	13/	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
i i		. ]	GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
I	sequence		\=possible nucleotide insertion)
			SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE
1			DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA
I		1	IYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLE
			SCQEDDNIMRSLQLFQNVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
1		}	TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY
1			CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
1			VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
1	ĺ		AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
i		1	KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTFSGQFYC
			SMCNVGAGEEME FRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
ł			PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ
6610	319	0.00	GKFRRFQKRKKDPSS
8870	319	881	GRKSLCNLHIPIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
1			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
1			DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
6611	978	212	CGWDTESADEF
1 3322	1 7,5	212	PGCSGAGSRVWWDPALRHLAMGSTESSEGRRVSFGVDEEERVRV LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNDRAPHKEST
I			LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
1	Ĭ		TKHSKASLPTGEGSISHEEQKSVRLARELESREAELRRRDTFYK
1			EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
1			QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
1			STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
1			SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
1	1		TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
	1		SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
	L		ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
			PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
			FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE
			SPSREVQSSEABALAR'IWKCAFMETSAKLNHNVKELFQELLNLE
6614		22.00	KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
0014	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
1	!		DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELIDKLE
]			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
1	]		GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
}			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN
İ	]		MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
i	j		EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
ĺ			GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
6615	832	35	NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
1			GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
l			QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYEECQKQGVEY
J	j l		VPACLVHRRRRREDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
			TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
			EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS
			G
6616	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
		<del></del>	VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

CBA	Dundi at 3	1 5	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown. *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence		\=possible nucleotide insertion)
1	,		PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
İ			PPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
			KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEA
	,		PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
1			GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
1	1		QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
1			LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
1			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
			IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
			KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
	1		RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
6618	548	136	LGPATFTFL DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
	·	-50	NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA
			WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
		i	YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS
ì			RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
1	1	•	YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
6620	3	1879	ILSDVQEGKHIKYKFEVCEKDD
		1079	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
1			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
1			VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
1			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
1 ' 1			APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS
1 1			QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG
[		1	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVARAO
1 1			HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI
1	1		SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
1 1	-		STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
1 1	Ī		WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
1 1	i		LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV
			SIPHAANMG
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
1 1	ŀ	ľ	AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
	1	l	SVKVIGAQRRRSPSALATEVFEAHLGSHILQSLDGYVFALNQEG
1 1	· 1	ľ	KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
6622	2	319	LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFILL
1 1	- 1	313	GRASGAQEETENGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
1			IFDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
1		j	VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF
	l		AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
ľ	l	ļ	IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
	<b>!</b>	1	MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI
1	1	]	LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN
<u></u>	<del>_</del>		LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Doquesion	\=possible nucleotide insertion)
			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
		l	LEI CHYTEVI DI CYNDIDEI DELCHE COLOURCE ENDEN
i	į.	•	LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
1.		i	DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
6624	218	1786	LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
1	1	1700	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
			RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
1	ĺ		REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
ŀ	1		KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
1			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
	1		YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
1	1		AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1	i	}	ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
1	ļ		HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
	1		PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
İ			QGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
6625	1124		QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
] 0025	1 1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
1	<b>[</b>		GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
1	1		SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI
i			YETPRGPDPALLEATGGAAGAGGAGRGEDEENREHRVRRIHVRR
6626	3	1400	HITHDERPHGQQIVFKD
5525	,	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
	i .		LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV
i			RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
1			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
l	1		GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
			KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDLLRSAL
1			TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
		!	LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
i			RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
1 .	) ]		PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
6627	1	697	PGKNSSIQLKTSFL
-52,	-	091	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
j l			GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
1			KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
j			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
1			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
6628	i	1861	SQKKRSSCCSFM
	•	T00T	QCAEFGGGGGGGGGGGGGGGGGGENKENERPSAGSKAN
1 :			KEPGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
]			KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
[			QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
]			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
1			EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
[	1		GLIAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
i I	, <b>!</b>		GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
}	}		KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
j	ļ		KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
{	1		YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
1 1			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
] [	1		GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
6629			GFRS
1 5023	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
L			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

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Corresponding			3	H=Histidine T-Tsolevoire V-Typine,
to first amino acid araino acid residue of sequence control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the	1			L=Leucine M=Methionine N-Asparagine
amino acid residue of amino acid sequence surveytophan, Y-Tyrosin, X-Unknown, *-stop Codon, /-possible nuclectide idection, \	1		1	P=Proline, O=Glutamine, N=Arginine
### ### ### ### ### ### ### ### ### ##	ì	amino acid	residue of	
sequence    Codon, /-possible nucleotide deletion,    -possible nucleotide dissertion    Nucleotide dissertion    Mucleotide IAPICTUCHERULPTPOPANEPTDECFI     PDESPHCQHEPOSINIALIDESIAVVGGGIERTAPEADSDHERGEFI     PDESPHCQHEPOSINIALIDESIAVVGGGIERTAPEAPEACECIT     TRKTFGFLRPFSMLC     GUOVAVGERERIKIVGSDEAGRIQUEMEVATALLOQANENG     NSTGKACGGTITEPEEKLINDFROEGIGGLOGLEMATEMPROFSI     SESNIKORF     SESNIKORF     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT     GEGIT		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   N-possible nucleotide insertion	1	amino acid	sequence	Codon, /=possible nucleotide deletion.
MIGGGGMIFAQALVCERLIGHDMENTGRREGPDSYFSVURAFTDER KDSYYSHIGLAMONGVEGEKSIGGWTONTTAGKKLAVFOTMS SLAWHLAMDNYTVMERI RILCETSUP-CAGATAFPADSDERNGEF PAGAEVTINE PS PREPULLIL TURKICLETMING QSLGVIGGKPBSAHYR IGYVGERLIYLDPHTYQPAUFPTDECFI PDESFHICGHP PERMISTALDDPSTAVRGGHLSTQAPADSDERNGEF PAGAEVTINE PS PREPULLIL TURKICLETMING QSLGVIGGKPBSAHYR IGYVGERLIYLDPHTYQPAUFPTDECFI PDESFHICGHP PERMISTALDDPSTAVRGGHLSTQAPAGECLGM TRKTFGPLR FFSMLG  6630  2 423 LUQCGGTRRESAMGAMPERINGSWALYKRVLGLIRVLLPPDLKS SENKKPF SENKKPF  6631  2 423 LUQCGGTRRESAMGAMPERINGSWALYKRVLGLIRVLLPPDLKS SENKKPF  6632 LODGYVADEFRIKTVGSDBAQRFLQEMEVYATALLQOANENG NSTGKACFGGTISJEEKLINDFRDEGIGGLGELMQEATKENRQFSI SENKKPF  6632 LODGYVADEFRIKTVGSDBAQRFLQEMEVYATALLQOANENG NSTGKACFGGTISJEEKLINDFRDEGIGGLGLEMQEATKENRQFSI SESNKKPF  6634 LODGYVADEFRIKTVGSDBAQRFLQEMEVYATALLQOANENG NSTGKACFGGTISJEEKLINDFRDEGIGGLGMAGATKENRQFSI SESNKKPF  6635 MIRSGRTQGGAAJLAPAAMRAVOQFVTRASVTVGCEGISATGR GICVLLGISLEDTOKELEHMVRILINLRVFEDESGKIMSKSVMD KOYELL CVSQFTLQCVLKGNKEDPHLAMPTEQABGFVNSFPLGIL RVTRPELIKOKGFGAAJLAPAAMRAVOQFVTRASVTVGCEGISATGR KOYKLEKQQGREEKTRAKOPSESSKERNTFRKEDKSASSAGRE  VXSSREP  6633 L145 617 ATGRHEGOVTLGGILQOLVNGILTPATTIPSLGPAFGTATSDP AGAGAGLBAI TIQLINGFETGPPAANKKIQALPTVFVTESHDY AGAGAGLBAI TIQLINGFETGPPAANKKIQALPTVFVTESHDY AGAGAGLBAI TIQLINGFETGPPAANKKIQALPTVFVTESHDY AGAGAGLBAI TIQLINGFETGPPAANKKIQALPTVFVTESHDY VXSSREP AGAGAGLBAI TIQLINGFGTGPPAARLEDCLFRIMTLTESILLWSLVVCYCG GLASHHLLKUMSIGKGRAPATFFRAARLEDSPELGTHIC GSGLEFFREIDFARRARRDCLFFRANTTINTSKILLWSLVCYCG GLASHHLLKUMSIGKGRAPATFFRAARLEDSPELGTHIC GGAASHLLKUMSIGKGRAPATFFRAARLEDSPELGTHIC VXSSKCHILDRATTYVFSQCGLISGFINGFFRYSKYTQLEFF KSKRVALDLINGKGGTAPAHLALLGRPETLVFBLTGSTLTINTSKILLWSLUVCYCG GGAASHLFRAARLADLURGFTARAPATFATORGSTILGFFINIAK TILAQCTGRVUTVAARHGGTAFRAALLALLGRPETLVFBLTGSTLTINTSKILL MILAQCOGPTUTVAARHGGTAFRAALLALLGRPETLVFBLTGSTLTINTSKILL MILAQCOGPTUTVAARHGGTAFRAALLALLGRPETLYFBLTGSTLTSTRINTSKILL LUGNSKYHFFINIATIALDELPRSTAKTADDLUPTSTRISTA TILAGCTGRVUTVAARHGGTAFRAALLALLGRPETLYFBLTGSTLTSTRISTAL AARROPLU  6635 LUGNGCARFFINIATIAGSTRAGAGRAFATATAFAAGPGG	L	sequence	_	\=possible nucleotide insertion)
KDSYYSTHOTAOWSVEEKSIGOWTGPHYAQVLKKLAYPTUWS   SLAWHTAMDNYVMEETRICHTSVP-CAGATA PPADDEHCHOGE   PAGAEVTREPS PWRPLVLLIPLELGLIDTINEA YVETLKHICFMMP    GSLGVIGGKPRSAHTFIGVYCEELIYLDHTOLAPVETLKHICFMMP    GSLGVIGGKPRSAHTFIGVYCEELIYLDHTOLAPVETLKHICFMMP    GSLGVIGGKPRSAHTFIGVYCEELIYLDHTOLAPVETLKHICFMMP    GSGGTRRSANGAMPGRHVSRVALIYKRVLQLHRVLIPDLKS    LDQCYKOEFFRENKTVGSDEAGRFLQEMEVYATALLQQANNENG   NSTGKACFGTFLPEEKIADDROEGIGGLQELMQEATKPNRQFSI    SSSMKKKF    GGGYTRRSANGAMPGRHVSRVALIYKRVLQLHRVLIPDLKS    LDQCYKOEFFRENKTVGSDEAGRFLQEMEVYATALLQQANNENG   NSTGKACFGTFLPEEKIADDROEGIGGLQELMQEATKPNRQFSI    SSSMKKKF    GGGYTRRSANGAMPGRHVSRVALIYKRVLQLHRVLIPDLKS    LGQCYKOEFFRENKIKVGSDEAGRFLQEMEVATALLQQANNENG   NSTGKACFGTFLPEEKIADDROEGIGGLQELMQEATKPNRQFSI    SSSMKKKF    GGCVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRKTILNIKVEGEOISAIGE    GICVLLIGTSLEDTOKELEMWRTILNIKUELESPAPGTATSDP    KOLSKLEKQQORKEKTRAKOPSESSKERNTFRKEDRSASSGGEE    DVSSEREP    KOLSKLEKQQORKEKTRAKOPSESSKERNTFRKEDRSASSGGEE    DVSSEREP    ATGRHEGOYFTLOGIIQQUWGITFATTPSLOPHGVLHSHIPPDY    AWAGANGLOAIIITOLIANGPETIGPPADKEKCIAPPTVPTTEHY    GSGLECPVCKDDYALGERVRQLJCHNHITHESILLWSSLVVCYC    GLCASHILLKLUKSIGKOPAPIGNFTRAPARHPHYPTPYTE    GGGTPRKSGGPRRIJPHARIRDCLJPRIMITHESILLWSSLVVCYC    GLCASHILLKLUKSIGKOPAPIGRPARKLIDOLIAPPTVPTEHY    VYRIKDSSILRRHVAAGERGKPIMILLHIGFPEFFFSNRYOLRES    KSEKTWVALDIJGKCYGETDAFHIGKONYLLDCILLPOIGNENGKTAKLIDGEALEMSTANA    GGGTPRKSGGPRRIJPHARIRDCLJPRIMITHESILLWSSLVVCYC    GLCASHILLKLUKSIGKOPAPHEWRITTYKNYKTILLSEALSHITUSA    GGGGREPPILPLSYRLLDGEALIPHOTHINFSILLTSSILLWSSLVVCYC    GLCASHILLKLUKSIGKOPAPHEWRITTYKNYKTILLSEALSHITANA    GGGTPRKSGGPRRIJPHARIRDCLJPRIMITHINFSILLTSSILTSSINGTANA    GGGGREPPILPLSYRLLDGEALIPHOTHINFSILLTSSILTSSINGTANA    GGGGREPPILPLSYRLLDGEALIPHOTHINFSILTSSINGTANA    GGGGREPPILPLSYRLLDGEALIPHOTHINFSILTSSINGTANA				
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6635 . 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAFSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARMGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATTVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGPLV  6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF  6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRIAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSAILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				
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ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTMLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQWQTVPNAGHWIHADRPQDFI AAIRGFLV  6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF  CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREFKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMLKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	6633	1420	470	
LVPCVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV  6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF  CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREFKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	l i			
HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTMLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV  6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF  6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAPSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVMERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	l i			
LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV  SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF  6637  2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRIIAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAPSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALWNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	}			
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DGGDGVF  CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRIAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGKAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALWRERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	<b>[. ]</b>	İ		
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LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	į l	i	8	
DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	i I	,		
CIPICGKIENITAPKTQGLRWPWQAAIYRTTSGVHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	[	.		
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		ł	ļ	TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF	1	]	•	
				TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

			la dignal montida
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, F=Phenylatanine, G=Glycine,
•	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ĺ	to first	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
	1		PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
ļ	1		EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
	1		RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
1			VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
1	1		SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
j	)		PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
1	1	1	TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
			DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
1		1	EDETNFLDEVSRQQELIEKQRREBELKELKEYRNNLKKVGISQE
1	1		NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
		1	KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
1	1	i	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
Į.	1	1	RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
ŀ	1		ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
	1		KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
1	1		NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
l .			LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
		l .	YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
1			ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
1	i		NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
1	l		KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
1	(		APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
1			TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
i	ĺ		GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642	22	1296	PLEERMATKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
·		1	HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
1	İ	1	NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
	i i		KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
			MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
I	1	1	NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV
1	i	1	ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
1			IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
			LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
1			DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
1			HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC
1	I	l	SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
1			CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
		1	DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR
1			LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
ł		1	TVYERLAHASIMKLNQASMDKLYDLMTMAPKYQVLLCPRPKDVL
	[	1	LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
1			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
1	j	1	EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
I		1 '	KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
			LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
	1		EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM
- [		]	DEL
L		<del></del>	

SEO	Predicted	Prodicted - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
<b>.</b>	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
í	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ŀ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6645	6530	4646	FVEGLACYOVE ACCOUNT TO A SECTION (
1		1010	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
1	1		GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
1	1	Į.	GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
l	l	ļ.	GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
1		ì	QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
		ł	MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
1			RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
ı			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
1			AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
1	1		IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
	İ		YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE
j	i		GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
ł	1		VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ IPRTLEEFVGFH
6646	176	890	
1		050	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
ľ	]		EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMOYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
1 .	[		TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
1	1		FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
Į.			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
ĺ			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLFIISFILAWIETWFLD
	·	•	FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
1	į		IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPELQKVME
1 1			KRKRDQVIKQKEEEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ
			EEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
1 1			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
	I		QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
<u>l</u>			KEHREYSTKOLTNLVNVCLGSHINKKAROKLLAAIDDIDRPKR
6650	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
1		İ	QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
1 1			QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
j			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
1 1			VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
<u></u>			KKAWEHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
} {	ļ		CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
1 1	1	į	DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
1 1	İ	1	HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
1			DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
1		Ì	TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
[	į.	,	FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
] [	i		RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
<b>j</b> . [	]		NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
j	ļ		DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
<b>,</b>	ļ	. [	CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTE1EPQHFCQAFHR
] ]	1	!	ENDTLIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
	İ	ł	LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
		l	RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV
		·	

WO 01/53312 PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
			FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
""	] -	2313	PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
1			
i	]		EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1			TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
ł			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
1			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
1	]		TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
i			ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
1			QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
6653	170	1910	CNISVGR
, ""	*′°	1310	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
1	}		RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
1			LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
i			NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
1			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
1			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
1 .			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
1			LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
1			SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA
Į.			SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
l			KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
1			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
6654	1	705	PSMDKKAQ
3034	-	/03	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
1			PODLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
Į			VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
1			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP AISRGPSEYPTKNYV
6655	341	16	
"""	247	το.	KDAYMPKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
			INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
6656	2	1212	YTHVENAGGLKDIAMPKVKG
1 5555	_	1616	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1			DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
1			KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
1			_ = =
1			KEKQPVTGTEGAFYRRQLMHQLPIYDQDPSRCRGLLENELKLM
1	•	,	EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
			TTNGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKQWHP
į .			TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
1			IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT   CSKSKRS
6657	830	2120	
1 223,	0.50	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
			LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
1			HLEAHKNGHANGHLNIGVDIPTPDGSPSIKIKPNGMPNGYRKEM
			IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
1			VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
1			LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
			LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
} i			TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
			AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYPEK
6658	35	<u> </u>	NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
0028	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ	Predicted	1 22-22	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		<del> </del>	FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
			QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
1			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
· f	1	1	IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSS
	·		MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
1	ļ	1	SPPQALLOE
6659	18	523	EPORGDCETWFONCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
}		1	RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
i .	1		CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
Į.			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
1	1		LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL
1	1		NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
ĺ	ĺ		LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
ı			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
ŀ	<b>(</b>		KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
1			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
1			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
			PG PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
			NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAOPGOAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIDTWR
1 1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAOTFAERRER
j j			SFSRSWSDPTPMKADTSHDSRDSSDLOSSHCTLDEAFEDLDWDT
			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
]	1		PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCOGGPGH
			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVTHTM
1 1	]		GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAOGKOMIET
6664	58		YFDFRLYRLWKSRQHSKLLDFDDVL
1 0001	30	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
ł j	j		VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
]			LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
	j		TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
!!			VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
]	1		MPLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
6665	171	1278	SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
.		±2/0	DERRLACRQVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
} }	1		PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
			ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
		1	TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
1	1		EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
J	1		PMEMLKIQLQDAGRLAVHQGSASAPSTSRSYTTGSASTHRRPS
[	1		ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
J	· 1		LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK KGLGEDMYSGITDCAR
6666	498	2868	
ļ		2008	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
ł		·	WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
1		j	NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
- 1		}	CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
	ſ	ŀ	KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
1		į	GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
!			FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED

C-20	Predicted	Decade and and	
SEQ ID		Predicted end	Amino acid segment containing signal peptide
NO:	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ţ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
ł	1		AASRQQRLSALRRYQDKRLLALSNESDSEENVCEVELDTDLFPR
l	ļ	i	PRSPSPEDESSSSSSSSSSEDEEELNERRASTWQRNAMRRRQKT
ĺ	}		TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
ļ	Ì		STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
ļ	Ī	ł	TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
İ			EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
ļ	1		SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP
	1		RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV
Ì	ĺ	l .	AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
į			TDTPATDSSRAVHGHSGLKRORIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPWKWRK
1	1	}	KKSEKFKHTSAALERKISMROSREELIKRGVLKEIYDKDGELSI
			SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLOPS
1	ļ	1	DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
i	1		SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
1			PMHPSGCRMIDELNKTLAMTMORLESSEORVPCSTSYHSSGLHS
1	1	]	GDGVTKAGPMGLPEIROVPTVVIECDDNKENVPHESDYEDSSCL
1	İ		YTREEEEEBDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
į			ELEEKNILPROTDEERLELROOIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
0000	, 11	350	LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
1	].	Ì	NAAPTRTALAHSALSLGLALSLLAVILAPSL
6669	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRLAPKVDVRVVILVS
1 0005	433	1207	ř.
1	1	į	VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
1	į.	ĺ	KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYQKPQICD LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
ł	1		KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
1	{		KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
0070	104	394	VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
I			PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
		l	1
6671	1	763	TTVTV
) 00/1	, •	763	LPAEKPRSAPNMAGGRCGPQLTALLAANIAAVAATAGPEEAALP
1			PEQSRVQPMTASNWTLVMEGENMLKFYAPWCPSCQQTDSEWEAF
1		1	AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAPPHAKDGIFRR
			YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
ļ		Į.	ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
	1 - 35.		ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
1		ļ	GVIFFLALLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG
I	1		PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
1		į.	DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
1		}	LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
			MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
	1		SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG+G+GLNV
1		[	wlcpcvafhrgarpqaeeggarwnslvsspwippnp*hssigae
1			NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK
I			SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
	1	j	ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW
			FGAGHCHSSCDFTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
	1	İ	HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
1	1	ĺ	KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ
İ			PTPC*IGTRVAFFLT
		L	

In   Designing				
No:   nucleotide   coation   corresponding to first   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seq	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cocation   Corresponding   Coffice   Corresponding   Coffice   Corresponding   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffi	1			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	NO:		1	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid te of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the Note of the N	1			H=Histidine, I=Isoleucine, K=Lysine,
amino acid secidue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen				L=Leucine, M=Methionine, N=Asparagine,
maino acid sequence  6675  277  1678  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  277  1678  278  277  1678  277  1678  278  277  1678  278  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  1678  279  16	1		1	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence   Codon, /-possible nucleotide deletion,   Possible nucleotide insertion,   Possible nucleotide insertion,   Possible nucleotide insertion,   CRMPTERRAFILDNETTILDHIRGSHYTEDDTCHCERVLIDHDVD   LEKTHPSHYDORGSSIOGSERTORY VYGOVOITSSUDTRIE   RESHTAGREELERERGHOOTICHT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE		5		S=Serine, T=Threonine, V=Valine,
Apposable nucleotide insertion		i e		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6675  277  1678  GREFTERMSFLONFTILLHERGSHUTSDDTHECEPULINDEVIS GREFT RESHTAGRLERLERKERGNOINCHNIOWERNSKOEDELSJEE RKSILKERPISGSSIGSTGSVYNOSKEPIDOVAND GETATIKKIDVALPLHSSORLLDEFTVYMASARVODLIGLICHO YTSGGEREKLARDENSAYCHLARDGDEVOTHYPLORINDEVING GETLALVEKYSSPGLICKESLEVPELNANGFSLIQUDTWATH REILLGAVERKSGSVIGSGSLIGVELDGEPOLANDEVSPIDOKGHU HYSSFKVSNIHRLEFTTDVOL/GCALPEGUERRAADVICLES ADTHROCOLGCGAGAALASS-NSIKC** EET GERKVELDEPT ADTHROCOLGCAGAACALASS-NSIKC** EET GERKVELDEPT RESHTAGALERLERKERGNUT (CKNI TOMERBAGGELIKLESE KKSLKERPISGSVELGSGSSTGGSNGTGGVVYAQSVDITSSWIDGIR RESHTQARLERLERKERGNUT (CKNI TOMERBAGGELIKLESE KKSLKERPISGSKOSLIGVELDEVTLANDEVGEPTLADHOV TESKERPILGHERTILLHERGNUT GENTGCEPTLADHOVA LEKIHPSMPCDSGSSIGGSNGTGGVVYAQSVDITSSWIDGIR RESHTQARLERLERKERGNUT (CKNI TOMERBAGGELIKLISE KKSLKERPISGKOSLIGVELDEVTLANDEVGEPTLADHOVA TYSSGERPKLANDRVSAYCLHLARDDGSVDTDPPLISNEPTLIK GEFTLALVEKYSSPGLITKSSLIVVELNANGFELGOTHAVOMLSSH HYKSFKVSMIHRIFFTTDVOL/CCALPSPGHERAVDUCLRES ADTHROCOLGCAACAALSS-NSIKC** EEI GGDKVSIDPVTNQ KASTKFWIKGKFISIDSLICAC\DLAEB GEFTLALVEKYSSPGLITKSSLIVVELNANGFSSLIVOMTKVTM KEILLKAVERKSGKVSGSSADGVFEEDGID IATVOMLSSH HYKSFKVSMIHRIFFTTDVOL/CCALPSVELDOMTFVTM KEILLSAVKRRKSGKVSGSSRADGVFEEDGID IATVOMLSSH HYKSFKVSMIHRIFFTTDVOL/CCALPSVELDOMTFVTM KEILLSAVKRRKSGKVSGSSRADGVFEEDGID IATVOMLSSH HYKSFKVSMIHRIFFTTDVOLICAC\DLAEB GFSTLALVEKYSSPGLITKSSLIVVELNANGFSLIDOMTKVTM KEILLSAVKRRKSGRVSSGSRETGGVVXAGSVSGRADGVEEDGID IATVOMLSSH HYKSFKVSMIHRIFFTTTOVQL/CCALPSVELDOMTFVTM KEILLBAVKRRKSGKVSSSSRADGVFEEDGID IATVOMLSSH HYKSFKVSMIHRIFFTTTOVQL/CCALPSVELDOMTPUTSSMPGGIR GFSTLALVEKYSSPGLITKSSLIPVELANDASRVOLLEDOMTTVTM KEILLBAVKRRKGSKVSSSSRADGVFEEDGID TATVOMLSSH HYKSFKVSMIHRIFFTTOVQL/CCALPSGVKELDFVTNO KASTKFWIKGKPISJBULCCC\DLAEB GFSTLALVEKYSSPGLITKSSLIPVELIANDASRVOLLERGSKN HYKSFKVSMIHRIFFTTOVQL/CCALPSGVKELDFVTNO KASTKFWIKGKPISJBULCCC\DLAEB ADTWROCOJGCCGAACAALASS-PISKC** EGISCKVELDFVTNN KEILLBAVKRRAGSGKVSSGSSAGGVFSTEDGGVKELDFVTNNO KASTKRWIKGKSGSSLIVVAGGNGSNOSN DPH PENTAGGSGSTAGAADASPSSORGONSN DPH PENTAGGSGSTAGAADAGGAGGNGSKONSN DPH PENTAGGSGSTAGAADAGGAGGNGSTAGAADAG	l l		sequence	
LEKTHPSSMPODSCSSIGGSNETGGYVTAGASOVOTISSIDDFOIL RESNTAGLEBLIKERGRQUIKCRVIQUKERINSKGAGBLESEFE KKSLLKERP I GGKGS ILGVIKCRVIQUKERINSKGAGBLESEFE KKSLLKERP I GGKGS ILGVIKCRVIQUKERINSKGAGBLESEFE KKSLLKERP I GGKGS ILGVIKCRVIQUKERINSKGAGBLESEFE KKSLLKERP I GGKGS ILGVIKCEPC-QLAUPPRIEVSKFPGKGHV YTSSGREFELADWASAYCHLIADDGGVUTDFPFLDSINSPIHKF GFSTLALVEKYSSFGLITSKESLEVBINAAGGSLIQUMTKVTM KEILLGAVKRKGSGKVGSSGAGBUVFEBEGGILIATVQDMLSSH HYKSFKVSMIHREFTTIVQL/GCALFFGVLEKKRAAVQDLIGEPS ADTWRQEDIGCCGAACAALKS DSIKK-KE ISGIGWEIDPVTNQ KASTKRWIKOXPISIDSLLCAC\DLAEE  GFSTLALDEKSTAGDEFTILLAHRGSHVTSDTTGMCERVLIDHDVD LEKIHPPSMPODSGSIGGSINGTGGVVYAQGVDITSSMPGIR RESNTAQLEELBLEKKERQQUIKCKNI QWKERNSKGSAGELKSLEFE RESNTAQLEELBLEKKERQQUIKCKNI QWKERNSKGSAGELKSLEFE RESNTAQLEELBLEKKERQQUIKCKNI QWKERNSKGSAGELKSLEFE RESNTAQLEELBLEKKERQQUIKCKNI QWKERNSKGSAGELKSLEFE GFSTLALDEKSSSPCLITSKSSLEVBINAAGGFSLIQUDTKVTM KEILLGAVKRKSSGKVSGSRADGVFEEDGIDIATVQDMLSSH HYKSFKVSMIHRIRFTTTVOL/GCALPFFOUKRRAAPVDCLRRS ADTWRGEGIGCCGAACAALSS DSIKK-EGISGKKEIDPVTNQ ASTKRWIKORFISIDSDICAC\DLAEB HYKSFKVSMIHRIRFTTTOVAL/CACLPFFOUKRRAAPVDCLRRS ADTWRGEGIGCCGAACAALSS DSIKK-EGISGKVEIDPVTNQ LEKHPSSWPGDGSGSIGGSNGETGGVVVAQSVDITSSMDFGIR RESNTAQLEELBLEKERGQOIKCKNIQWKERNSKGSAGELKSLEFE KKSLKERPPISGGSSEIGGSNGETGGVVVAQSVDITSSMDFGIR RESNTAQLEELBLEKERGQOIKCKNIQWKERNSKGSAGELKSLEFE KKSLKERPPISGGSESEIGGSNGETGGVVVAQSVDITSSMDFGIR RESNTADRLEELBLEKERGQOIKCKNIQWKERNSKGSAGELKSLEFE KKSLKERPPISGGSESEIGGSNGETGGVVVAQSVDITSSMDFGIR RESNTADRLEELBLEKERGQOIKCKNIQWKERNSKGSAGELKSLEFE KKSLKERPPISGGSESEIGGSNAGTGTGVVAXGDVTITSSMDFGIR RESNTADRLEELBLEKERGQOIKCKNIQWGARGTSTGDFPLDNDFT KKSTRVSDFTATTAGATTTTOVAL/GCALPFGVLKKRAPVOCLRRS ADTWRGGGIGGCGAACAALSE SDIKK-EGISGKVEIDPVTNQ GFSTLALDEKSSSGLIANGKHERPTTTVQL/GCALPFGVLKKRAPVOCLRRS ADTWRGGGIGGCGAACAALSE SDIKC-EGISGKVEIDPVTNG RASTKFWIKKRFISTDTUNGSARPS-INDICTILEVLSSNFGRQ-LR PEPLELLQGGCHLULPANLVSQAPGIGKSCRUCHTINGESSN HYKSFKVSMIHRIBFTTTVQL/GCALPFGVLKKRAPVOCLRRS PPLKSGLDWGGAGALGUNGSALGERGENGGGRAGGAGAGAGARTOV PLEDALSGGGAGAGAGAGAGAARAPPPT-LEFECLEP PLKREPTGGGAPPT-WILLFULLGLEPF PHEHLELLPVOLG GEM-YVHK	6676			\=possible nucleotide insertion)
RESHTAGRIERIRKERONGI KCKNI JOWERNINSKOSAGELKELFE KKSLKERFIPI SCKOS LISVERLEQCP_CLORPEYSKERDECKHV GTATKKIDVI.PLHASGORLL.PHTVUTHASARVODLI.GLI.CVG YTSERGEPKLINNUSAY.CLITAEDDGEVOTI ATVODMISH HYKS FKVSHIRRLERTTDVOL/GCALPFCVLRKRARVDCLRPS ADTWRCDGI JGCCGRACALIAES DENKY SIGHTSKRAPAPDCLRPS ADTWRCDGI JGCCGRACALIAES BOHKYS EIGHVSEI DPVTNQ KESILKAVKYSKYSINGLASS HOHKYS EIGHVSEI DPVTNQ KASTKFWIKOKP ISINSDILCRC\DLAEE GFFILALVEKKYSS POLTSKRS.FVTNARAGPSLIQUDTLYDDVTNG KASTKFWIKOKP ISINSDILCRC\DLAEE GFFILALVEKKYSS POLTSGOTTGOTTGNCERWI.IDHDVD LEKIHPSKWPGDGCSEIQGSNGETCGYVYAQSVDITSSWDFGIR RRSNTAQRLERLRRERQNQIKCHI JGWKSTRISKQSAPLKSLEPE KKSLKERP I SGKQS I LSVIRLEQCPLOLANPFNEYSKPDGKGHV GTATKKIDVTIPLHASGORILPTVVTMASARVQUIGLICVG YTSEGREFKLIDNUSAYCHLAEDDGEVUTDF PLDSNEP IHKK GFFILALVEKYSS FGLTSKESLFVTINAAHGFSILJQUNTKVTM KETLALAVKRRSGGVSCSRADOVE PEDSOJDIATVQDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGVURKRARAPVDCLRPS ADTWRCDGIGCCGRACALRS* DSHKC* BEGIGNKVEIDPVTNQ KASTKRWIKQKP ISIDSDLCAC\DLAEE RKSNTAQRLERLRRERQNQIKCHI JREDDGEVUTDF PLDSNEP IHKK GFFILALVEKYSSFGLTSKESLFVT NAAHGFSILJCUNTKVTM KETLLKAVKRRKGSQVSGSSRADOVEPEDSQIDIATVQDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDTKVTM KETLLKAVKRRKGSQVSGSRADOVEPEDSQIDIATVQDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQVDMLSSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIQTHTCHERSH HYKS FKVSHINRLEFTIDVOL/GCALFFGSTIGTSTIDLSERRFHVOL  6679 20786 GFFTILLSERGGSTINGTSTILLSERRFHVOL LLEILBAVSQUSSTILLSERGGGGGALFTTILLSERGR	00/3	2//	1678	
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WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR	1 1			
FQGGGGG	<u> </u>	<del></del>		PQGGGG

SEQ T	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
1			KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
] [			LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYO
1 1			TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
1 1			SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
			S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
]		·	VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
1 1			YOLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
1			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
1			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
1 1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1 1			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
1 1			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
6683	109	1238	GPAPRWCSFLDNLTEELEENPESNE
	205	9621	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
i i			VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
1 1			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
1 1			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
1 1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1 1			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
1			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
			GPAPRWCSFLDNLTEELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
1 1	i		PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
1 1			ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
6685	250		RNIVQNYR
0005	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
1 1			QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
1 1			ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1 1			LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQBYICQ
1	·		IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
			VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
		ļ	ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
		j	RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL
			TASRQGVTST
6686	310	927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
1			QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
	)		LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
	ł		SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
<u> </u>			VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
	1		IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
	1		SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
	ł		IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
[ }	į		PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
<u>  </u>			LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
		i	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
		į (	LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
l t		1	
	}		STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
			STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
			STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
,	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del></del>	<del></del>	SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS
į	i		FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK
	1		QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF
	1		GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGP
1	1	1	QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ
	1		YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
	}		GDGLAIWYTKDRMOP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
	i		DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
i			LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
1			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
ł			GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSOF
1	ł		ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
			CSLCEKAPSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
}			/GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
	-		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
	•		DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCOVE
1			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
5550			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
1 1			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
6695			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
0035	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
1 (			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
i l			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
6696	1	700	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
""	-	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFQLCAD
1	1		LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
1 [	1		DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
1 1	1		RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
1	ľ		TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
6697	3	782	LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKQIKSS
,	,	182	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
; I	1	i	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
, I	İ		LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
į į	· [		WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
1 1	]		IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
6698	668	754	SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6699	325		VGSCACAGSCKCKECKCTSCKKSECRAFP
1 1		492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
		•	LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
٠			NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	bequence		ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1300	
8700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
			FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
	<del> </del>		LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
1	l .		RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
l .	}		IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
1	1		FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
l			QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
]	1	į	ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
1			KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
ł		ł	STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
1		i	LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
1		1	SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
1		1	VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
		1	LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
1		}	RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
i		}	NNTYRSAQHSQALLRGLIALRDSGILFDVVLVVEGRHIEAHRIL
1		I	LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
1			ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
1		1	YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
1			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
1	ſ	1	VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
		1	SPOTELRSDFOCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
1			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
1	ŀ		RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGOHPCFIIAEIGONHOGDLDVA
ŀ	l		KRMIRMAKECGADCAKFOKSELEFKFNRKALERPYTSKHSWGKT
1	1		YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
1	1		LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
1			TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
1		1	VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
			IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKOLLPCEMACNEKLGKSVVAKV
1		1	KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
	i	I	TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDOREG
1 2,03	3.2	1007	
			LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
1		1	LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
	1		YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLQE
1			NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
		]	MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
1		1	RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
6705	<del> </del>		GI
0,05	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
1		İ	SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
	ł	[	LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
1	1	l	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
1			VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
		1	PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
1	1	}	AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
J	1	j .	LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
L		<b>I</b>	EK

Designing mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleotide   mucleo	SEO	Predicted	180 1	
NO: nucleotide location corresponding to first amin acid residue of amin acid residue of amin acid residue of amin acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence			Predicted end	Amino acid segment containing signal peptide
Cocation   Corresponding   Coffee   Corresponding   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Cof				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid amino acid sequence companies to first amino acid sequence companies to first amino acid amino acid sequence companies to first amino acid sequence companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies to first companies	1.0.			Glutamic Acid, F=Phenylalanine, G=Glycine,
amino acid maino acid mesidue of maino acid mesidue of maino acid sequence  6707  2233  1343  1343  YESCIME, T-THYRONINE, NANDAME SEQUENCE  6707  2233  1343  YESGIGVELO/IFMERFIFERKORPENESSERRPITS- GWYVKGHAVNOSH GOGLGC/CVCTSHSSDSTRESSERRPITS- GWYVKGHAVNOSH GOGLGC/CVCTSHSSDSTRESSERRPITS- GWYVKGHAVNOSH GOGLGC/CVCTSHSSDSTRESSERRPITS- GWYVKGHAVNOSH GOGLGC/CVCTSHSSDSTRESSERRPITS- FFILSO-KT'S-SKENNVPARYSTITS-GIGSCKORD-SPKCHN SOAR-SRF-GILCHPECHGGLDININGGSSPHTDKHSC/URNIL- CREMPFSHLAGEGFECH/CQACACEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGEGFECH/CQACACEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGEGFECH/CQACACEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGEGFUCAGAACEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGEGFUCAGAACEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGEGAAAS-FGLGSAAB-FHELCEH TD-LPK-GGGYIGHFECDSHLCILINISFRIPS-SPF-GWARYA C-RCHWFSHLAGH-MARCHALGEN-FALAGEW-GOPPUL- EMFTSEAAFIEN.GRERRFERHLIYTIGFUL/SWRFYRGMARYA- GRITAW-HIN-FRICKALAGS-GWARGA-WGCH-LISH-HILL- EMFTSEAAFIEN.GRERRFERHLIYTIGFUL/SWRFYRGWARYA- C-RCHWFSHLAGE-AAAG-FULGH-SER-WGWARYA- GAGKTDATKELL- EMFTSEAAFIEN.GRERRFERHLITH-HILL- EMFTSEAAFIEN.GRERRFERHLIYTIGFUL/SWRFYRGWARYA- C-RCHWFSHLAGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-MARCHALGH-M				H=H1Stidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid amino acid sequence amino acid sequence amino acid sequence amino acid sequence companies are acid and acid sequence companies are acid as acid sequence companies are acid as acid acid acid acid acid companies acid acid companies acid acid acid acid acid acid acid acid			1	L=beucine, M=Methionine, N=Asparagine,
residue of anino acid sequence  6707  2233  1143  1143  Veyossible nucleotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide deletotide	i			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s				S=Serine, T=Threonine, V=Valine,
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	1			W=Irypcopnan, Y=Tyrosine, X=Unknown, *=Stop
1343   YWEGIGYELQHIPHRETSTERKRIPTOR CORRIVESREMPCIS- GRYVOGNA-VANGEN-GGQLRC-VC-VCSHSSDSTRSSGRAKCHS FFILSO NA'S SWERMVPAKTSKI TSK-GISSESSGRAFO DEK-NV SOAN-SRFCGLCNP-COHCCLIDILRGGSSFWTDKISC-VHINLLC BREVFSILGEGEGERCHGCACREAGRASGESGRAFD DEK-NV SOAN-SRFCGLCNP-COHCCLIDILRGGSSFWTDKISC-VHINLLC BREVFSILGEGEGERCHGCACREAGRASGESGRAFD DEK-NV SOAN-SRFCGLCNP-COHCCLIDILRGGSSFWTDKISC-VHINLLC BREVFSILGEGEGERCHGACACREAGRASGESGRAFD PEK-NV SOAN-SRFCGLCNP-COHCCLIDILRGGSSFWTDKISC-VHINLLC BREVFSILGEGEGERCHGACACREAGRAGE COMBANA TO STANDAM SHE STANDAM SHE STANDAM SHE SEE TO STANDAM SHE SHE SHE SHE SHE SHE SHE SHE SHE SHE			sequence	Codon, /=possible nucleotide deletion,
GMYVVOSTAVINGEN*GGOLRC-VCVTSHSSSTRSSORASKCHS FFILSON N° SSKENWYPAKTSRITYCHSCSSKGROP DEK*NV SOAR*SFILORGO/GGLUBLIRGGSSEWTDKISCYHNILG SERVESULGEG/GRIV CGGCULILIRGGSSEWTDKISCYHNILG SERVESULGEG/GRIV CGGCULILIRGGSSEWTDKISCYHNILG SERVESULGEG/GRIV CGGCULILIRGGSSEWTDKISCYHNILG DP*LPB (10 FIFTOS) GUT GGROVERACAAS GGLDSAAEPHLCEH DP*LPB (10 FIFTOS) GUT GGROVERACAAS GGLDSAAEPHCEH C**CHWYPSHLAMENCOT LLANGLY GROVERACAS GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER GGROVER G	6707		1343	\-possible nucleotide insertion)
FFILSO*KT*SSWEMWYRAYSRITSYCHSCKSKORP DYKNNLL SOAR*SRYCICLONGGGGCGLDININGSSSFWTDKKSCVINNILLC NRAWFSLLCEGOSHCYGGAVCREACAAASGGLDSAABFRICCH TD*LPK*GGPYICHHCDSNILCILNINISYSF*GYARYA C*RCHWYFSLLCHOSCHIUCLANISHSYSF*GYARYA C*RCHWYFSRLLYNICGDLUACL*RROL*SSO GTOST TYGSWINGSGSPYOTGGGLUAGAGGAGGGGGALQUPLUFT TYGSWINGSGSPYOTGGLUAGAGGAGGGGGGALQUPLUFT GSITAVHPHRPCKLALGSGGVRYMESALTARDRUVODFVLL HFTSEAR*I FEILKRERFERRILTYTIGPLICSNDVLEAFGN GGITAVHPHRPCKLALGSGGVRYMESALTARDRUVODFVLL HFTSEAR*I FEILKRERFERRILTYTIGPLICSNDVLEAFGN AKTURNINNSSRIGKYMDVOFDFKGADVGGFLISYLLEKSRVANO NINGSRNFH FYQLLECGEBETLRRILGHRULGSNDVLEAFGN AKTURNINNSSRIGKYMDVOFDFKGADVGGFLISYLLEKSRVANO NINGSRNFH FYQLLECGEBETLRRILGHRULGSNDVLEAFGN AKTURNINNSSRIGKYMDVOFDFKGADVGGFLISYLLEKSRVANO NINGSRNFH FYQLLECGEBETLRRILGHRULGSNDVLEAFGN AKTURNINNSSRIGKYMDVOFDFKGADVGGFLISVLEKKRUNDA NINGSRNFH FYQLLECGEBETLRRILGHRULGSNDVLEAFGN AKTURNINNSSRIGKYMDVOFDFKGADVGGFLISVLEKKRUNDA SEPSWRSTYLGLLDIVGGEVFROGUNTFORGUNTALHAGUN EELLISPINLEOAAYARDALAKAVYSRFFTKKUGKINSKLASKOV SSSNDKSDWKVADVAVRANDALKAVORGGGREYKRUNDALHAGUND EELLISPINLEOAAYARDALAKAVYSRFFTKKUGKAREKTROAER FAMMERSKYNDSVRSRSKREBELDALLAHIGTUNCHELQUTNINK EELLISPINLEOAAYARDALAKAVSRSTREBERIALHAGUNTALTOTULPCPP PSPRLANSLSVPRSKOBENSKURDVANDVANGGGGLWFYGGGFASPNGGO FYHYKKULBYSPPRRCALDHAALTOTULPCTPVLLECTP PSPRLANSLSVPRSKOBENSKURDVANDVANGGGLWFYGGGFASPNGGO FYHYKKULBYSPPRRCALDHAUVNORGGGLWFYGGGFASPNGGO FYHYKKULBYSPPRRCALDHAUVNORGGGLWFYGGGLAFYGGAPAGGG FYHYKOLWANAHALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGUNTALAGU			1343	TWSGIGIEDQHFHWKKFHFEKKGPPSTCQBRLYESRSRWPCIS*
SOAR*SRFCGLCNPGGEGGLDININGGSSSWTDKSCVINNLLC   NRRVFSLLGEGGHCYGGAVCREACAAASGGLDSARFRELCEH   TD*LPK*GDGYICHFECDSNILCILIVNISFNIFSYS*GVARYA   C*RCHWYFEWLLYNNCGULIVACL*RRD\SSO   TVGSSKSGRSDPVGROLLLVGCK*RGX\SSO   TVGSSKSGRSDPVGROLLLVGCK*RGX\SSOQRYTMSALTARPUGVODPFVLL   EMFTSEAFIENLINTYTIGPVLVSVMPYBDIQIVSR   GRITAVVHPHRPCKLALGSGGVRYTMSALTARPUGVODPFVLL   EMFTSEAFIENLINSFRCKNWDYDFVLALARPDGVODPFVLL   EMFTSEAFIENLINSFRCKNWDYDFVLALARPWGVODPFVLL   EMFTSEAFIENLINSFRCKNWDYDFVLALARPWGVODPFVLL   EMFTSEAFIENLINSFRCKNWDYDFVLALARPWGCAVDFVLLERGG   ARTULRINDSSRGXYMDVODPFVCALAVGUNGCAVENPULGERGG   ARTULRINDSSRGXYMDVODPFVCALAVGUNGCAVENPULGERGG   ARTULRINDSSRGXYMDVODPFVCALAVGUNGCAVENPULGERGG   ARTULRINDSSRGXYMDVODPFVCALAVGUNGCAVENPULGERGG   ARTULRINDSSRGXYMDVODPFVCALAVGUNGCAVENPULGERGG   ARTULRINDSSRGXAVATENDLAVATENDICTTENSLAGGUNGCAVENPULGERGG   FANNSTTVAGUNGCAVENPULGEGEBETTERLGLERNPGSTLYLLKGGCAVENPULGEGEPABAGGAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGEGENFALLARGUNGCAVENPULGARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNGCAVENPULGATARGUNG	ļ <i>.</i>	i		FELL COLUMN TAVINGSW "GGQDRCVCVCTSHSSDSTRSSQRASKCHS
NRRVYSLLCGGCHCYGGAVCREAGAASGGLDSAABPRILCEN   TD-1_DK-8_GOPY1_GHHCDSNILCILINGSTB_SYS_F_VGARYA   C-RCHWYFERLLYNNICGDLUACL-RROL-SSO    TVGSWSKSGSS_PVGCGGLLUTGRGAGAAGGFGGGSAALQVELUFT   TVGSWSKSGSS_PVGCGGLLUTGRGAGAAGGFGGGSAALQVELUFT   GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLL    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLLQ   GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    GEITAVHPHRPCKLALGSGVRYTMESALTARDRUGUDFVLQ    ALTCHNOMS RPGKYMDVQFDPKGAPVGGLAUSHVLAGGCAK   VSSINDKSDNKVRKADTUDFTEDEVELISIAASVLLIGNIH   FAAMESSNAQVTTERQLKYLTPTLSVEGSTLREALTHRKI IAKG   EELISPILUAGAAYARDALAKAVYSRTFILUSLINGKGCKK   ESPSNRSTTYLGLLDIYGFEVFGINSFEGFCINYGKIKQGCFI   ELILKSGSGEVFABGGIAMPVQYPNIKI ICOLVERKFKGII VS   ESPSNRSTTYLGLLDIYGFEVFGINSFEGFCINYGKIKQGCFI   ELILKSGSGEVFABGGIAMPVQYPNIKI ICOLVERKFKGII VS   ESPSNRSTTYLGLLDIYGFEVFGINSFEGFCINYGKIKGKKKEKKGRGAEK   TAAMBEKVSKRSRKEEEDLEALIAHFQTLOAKKTGVELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGFTNANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGGGGLWANGRANANEQUELPCPP   PSPRLANSLSVHPEKDELIHPGGSYYNGGGGGLWANGRANAY IVELI   GGFHESTRDY1YNDVARNILATARGAPALALGYLDFENTATO   GAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	{		SOAPA SERCCI CARCOLOGI PANI PROGRESS KGRGD*DFK*NV
6708  115  1729  1739  1749  1759  1759  17598888685P9VGRQLLINGER, SSQ  17598888685P9VGRQLLINGER, SSQ  17598888685P9VGRQLLINGER, SSQ  GEITAVVHPRPCKLAISESGWAYTMSALTARDRUGVOPFVLL  EMFTSEART IELLERERERENLIYTIGPULWSVMPYRDIQIVSE  OMERYRKOSYFEEPPHLAWADTVYRALTERDOAWHISVES  GAGKTDATKRLLOLVAETCHAPGRGAVERLLOSDPULEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILISSUPLLEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILISSUPLLEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILISSUPLLEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILISSUPLLEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILISSUPLLEARVIN  ARTURNINSSRIPKYMROVOPPKGAPVGGILIASVLLIKURQCAK  VSSINDKSBRIVATRALTVIDETEDBEVBLIASVLLIKURQCAK  VSSINDKSBRIVATRALTVIDETEDBEVBLIASVLLIKURGCAK  VSSINDKSBRIVATRALTVIDETEDBEVBLIASVLLIKURGCAK  VSSINDKSBRIVATRALTVIDETEDBEVBLIASVLLIKURGCAK  SESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  ESPARSTTVLGLLDIVGFEVFORNSTEFTKILVGKINKSLASKOV  TAAMMEKVUSKRSKREEBEDLEALIAHFQTLDAKTTQTVLELPCP  ESPARASILSVIPEKODLILINGGSFROGKTFILVYNIKK  BURKVUSINSTERDIVTYTYNOVARANTALTOTIVKSLESTGFTPTRSCCO  158  980  ERMITTMYRVESSSGRAARMILAMGPAPLAALGYIDPGEFATM  1QAGASFGYGLAVVVVONNIMAMILOILSAKLGIARGALGEVYNIKE  ESPARLAGICKOV STANDAVIVVONNIMAMILOILSAKLGIARGALGEVYNIKA  6710  158  980  ERMITTMYRVESSSGRAARMILAMGPAPLAALGYIDPGEFATM  1QAGASFGYGLAVVVVONNIMAMILOILSAKLGIARGALGEVYNIVY  WESLATCHININGENKONGARHALDOTTSAKLOURGHPOTTAT  1QAGASFGYGLAVVVVONNIMAMILOILSAKLGIAGALGHVIVYY  WESLATCHININGENKONGARHALDOTTSAKLOURGHPOTTAT  1QAGASFGYGANGARHALDOTTSAALGARANTALGEVAL  ESPARLIASITUM STANDATATATATA  ELUTELINININGENKONGARHALDOTTSAALGARANTALGIPTUM  MAMILTASVHDIMIHDADVGPGOOIREP  EPGGKATRYRVONNAGORA-**HMEDLICHANDITATATATA  EPGGKATRYRVO		İ		NEBARA SEL CECOCHOCOCA MODES OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL SELECTION OF A COLUMNICAL
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EMFTSEARFIENLRTRYTGEVILVSNPYRDIGIYSR OMMERYRGVSYEVEPHILAVADTRAIRTERQDAWMISUSE GAGKTDATKRILQLYAETCPAPORGGAVERLIGENDPULEAGN ARTLENDNSSRFGKYRDVOPPDEKGAVERLIGENDPULEAGN NIGERNFHIFYQLLEGGEEETLRRIGGERNPOSYLVILVKGQCAK VSSINDKSDMKVVMKALTVIDFTEDEVEDILIGIASVULHLENIH FAANESSNAQVTTENQLKYLTRLISVEGSTLREALITHRKHITAKG EELLSPINLEQAAYARDALAKAVSRTFIKUGKINRSLASKDV ESPSMRSTTVIGLIDITGFEVFGHISFEGFCINYCREKLQQLFI ELTIKKSEQBSYRAEGIAMEPUQYFNNKIICDLVEEKFKGII\SI LDE\ECCURPGE  PHEHLIFFSGERGPFFLVSRRGLGFGKMKKKKKGKGAEK TAAKMEKKVSKRSRKKEEKLEALITHRGTLDAKRTQTVELPCPP PSPRINASLSVHPEKDELILFGGEYFNGGKTFLYNELVYYNIRK DTWTKVDIPSPPPRRACHQAVVVKDUKSTGFSGRSGRHMVAMKROLILF GGFHESTRDYIYYNDVAPNLDTFSKLSPGSTGFFPRSGCO 1PSLDRAASSVYGGYSKGRVKKDUKSTHSDMP FYHYKDLMVLHLATKTMEGVKSTGGPSGRSGRHMVAMKROLILF GGFHESTRDYIYYNDVAPNLDTFALSYLSPGSTGFFPRSGCO 1PSLDRAASSVYGGYSKGRVKKDUKSTHSDMP FRHYMTYRVESSSGRAARKMRLALMGPAFTAAGIYIDGGNFATN 1QAGASPGYQLLMVVVANLMAMLIQILSAKIGIATGKNLAEGI RDHYPRVVWFWWQABIIAMATDLAEFIGAAIGFKLILGYSLL GGAVLGIATFILLHQERGCKELERVIGGLLEVAAAYIVELL FSQRNLAQLGKGMVTPSLPTSEAVFLAAGUL/GATIMPHVI/YI WHSLIGHHLGGRGGKELERVIGGLLEVAAAYIVELL FSQRNLAQLGKGMVTPSLPTSEAVFLAAGUL/GATIMPHVI/YI WHSLIGHHLGGRGGKENGVASTKWDVALAMTIAGPVNIAIMATAA SELNFYGHTGVA  6711 3 347 VTEKKTMTCKMSQLERNI-TMINTLHYSVKLGHEDTLIHGEFK ELVRTDLHNILMKENKNDQAI-*HIMDLDTNAHMQIIFKELIML MAMINSYHDNHUBADVOPGOGNEG FPEOTOGRELYKKAQASLKSGLDLSVVRLEPGRIIDDMIAVVV VDFFNRINLIYGTMARRCS-TSCPUVAGGPRYETWODERGVAR PARLISAPRYMALLMMMIESII  6712 118 578 PHGGKRTRYEQVRAPGOGPOAQLAMALCLKQVFAKDKTFRPRKR FPEOTOGRELIYKKAQASLKSGLDLSVVRLEPGRIIDDMIAVVV VDFFNRINLIYGTMARRCS-TSCPUVAGGPRYETWODERGVAR PARLISAPRYMALLMMIESII GRATILSPTREIALGTLKFFKELGKFTGLKKAGYKVPTPI GRATIFVILDGRGGVAVAARTGSGKATCPLLEMFERLKHISAOTG ARALILSPTREIALGTLKFFKELGKFTGLKKAGYKVPTPI GRATIFVILDGRGGVAVAARTGSGKATCPLLEMFERKHISAOTG ARALILSPTREIALGTLKFFFKELGKFTGLKKAGYKVPTPI GRATIFVILDGRGGVAVAARTGSGKLGLENTLARFKHISAOTG ARALILSPTREIALGTLKFFKELGKFTGLKAVANDNAQOQ YUKSRFARSPESIKRAKGEDLIVALGHLEFSSFREEEELGGLRK UNDSKNYRSRATIFEINASSRDLCSGVARAKRGKDRKATARPOQ GOGGGGGOGOGOGOGOGOGOGNARARGKGRKATARPOQ	}			GEITSWHPHPPCKLYLGEDERBARMEGAL TARDOMALGVEDAL
OMMERYROUS SYEEPPHLLAUDTUYRALETERDOAVMISUSES GAGKTOATRIKLICJUYAETCPAPORGAGVERDILOADRILABAGN ARTIENNINS SEFGKYNDVOFDEKGADVIGELISYLLEKSRUVHO NIGERINFHIFYOLLEGCEBETLERIGLERINPOSYLYLVKOQCAK VSSINDKSDMKVVRKALTVIDFTEDEVEDLISTASSVLHIGNIH FAANEESNAQVTTEKOLKYLIRLISVEGSTIKEALTHEKIITAKG EELLSPINLEQAAYARDALAKAVYSREFTIKUVGKINRSILASKUV ESPSWRSTTVIGLDIYGFEVFORINSFEGFCINYCNEKLOQLFI EITLKSEQEBYEBEGIABEPVOYYNKIT ICDLVEEKFKGIIT\SI LDE\ECCUPECE  6709 3 894 PPHEHLP FSGERGFFFIVSRRGLGFEKMKKKKKKEKKERGGAEK TAAKMEKKVSKRSRKEEEDLEALEHAPTLDAKRTQTVELPOPP PSPELNASLSVHPEKDELILFGESTMOKTFLYNELVYYNIKK DTWKKVDIPS PPERCAHOAVVVPQGGGLWVFGGERASMIGE FYYKKDLWIHLATKTMEOVKSTGGPEGREGRWVAMKROLILF GGFHESTRDYIYYNDVAFNLDTFNSKDSFGTEPTFRSGCO) 1PSLPRAASSVYGVSKGRVKKDVDKSTHSDMF FYHKKDLWIHLATKTMEOVKSTGGPEGREGRWVAMKROLILF GGFHESTRDYIYYNDVAFNLDTFNSKLSPSGTEPTFRSGCO) 1PSLPRAASSVYGVSKGRVKKDVDKSTHSDMF FYHKROLINGARGKPLEKVIGGLLLFVAAAYIVELI GGAVLTGIATFILIMLORRGKPLEKVIGGLLLFVAAAYIVELI FSOPNLAOLGKKGMVFSLFTSERGFGAAIGKLLGVSLL QGAVLTGIATFILIMLORRGKPLEKVIGGLLLFVAAAYIVELI FSOPNLAOLGKKGMVFSLFTSERGVAAAYINGATIAMTAA SELMFYSHTOVA SELMFYSHTOVA SELMFYSHTOVA SELMFYSHTOVA  6711 3 347 VTECKTHTCKMSQLERNI-TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHHILMKERKKNODAI-*HIMBDLDTRAHMQIIFKELIML MAMILTSYIDNHUBADVGPQQOMEX FEPTGTGRELYKKAGASLKSGLLBAVVLPEGREINDUM LAVWI VDFFNRINLIYGTMAERGS*TSCPWARGPRYEYRWODERQYRR PAKLSAPRYMALLIMDWISSLI QARGSDEEGEFEIQAEDDARARKLGFGRFLPTFPFTSECTSDVE PDTREMVRAQNKKKKKSGGPOSMGLSYPVTREGINKKGYKVPTPI QRRTIP VILDGKGUVAAARTGSGKATACPLLEMFERKHTBAQTG ARALLISPTRELALGTLKFFFKELGKTGLKATALLGGDRMEDOF AAHLENPDIIIATGRUNVAARATGSGKALVHLHLIBINVAPODOTV VFVATKHHAPUITELLATQRVGCAHIYSALDPTARKINLAKFTL GKCSTLIVYDLAARGCLISPTVLDSARKLHIBLAGTRENVAPODOTV VFVATKHHAPUITELLATQRVGCAHIYSALDPTARKINLAKFTL GKCSTLIVYDLAARGEDLOSTLABLELIGGLARVANDNAQOQ VVKSRFARSPESTSIKRAKEDDLUGLGLHPLFSSFFEEEELQERIK VDSIKNYRSRATIFEINASGRICGGVGRAGKGRKKAKARALHRIPOO GOQGRGGOCGPOVGROOPPARSPRALCEGOPKEEEPEEGEGERIK VDSIKNYRSRATIFEINASSRICHESSFFEEEGORIKG	1	1		ENFTSEARF FILL REPERENT TYTYLCOUT USIND PROTECTION
GAGKTTDATKRILQLYAETCPAPGGGAVEGLIGSTLEKSRUVHO NIGERNFHIFYQLLEGGEETLRRIGGERNPGSYLVLUKGQCAK VSSINDKSDHKVVKALTVIDFTEWDULLSIAASVILLENIH FAANEESNAQVTTENQLKYLTRLISVEGSTLREALITHKRILAKIH FAANEESNAQVTTENQLKYLTRLISVEGSTLREALITHKRILAKIH FAANEESNAQVTTENQLKYLTRLISVEGSTLREALITHKRILAKIH EELLSPINLRGAAYARDALAKAVVSRTFIKUGKINRSLASKUV ESPSMRSTTVIGLIDITYGFEVGHOSFEGGCINYCHKIQQLFI ELTUKSEQBEFFAEGIAMEPVQYFNNKIICDLVEKFKGII\SI LDE\ECCLPGE  PPHEHLFFSGERGPFFIVSRRGLGFGKMCKKGKKEKKGRGAEK TAAKMEKKVSKRSRKREEDLEALIHPCTLDAKRTOTVELPCPP PSPRLNASLSVHPEKDELILPGGEFFNGKRTFLYNELVYNIKK DTWTKVDIPSPPPRRCAHQAVVPQGGGLWYFGGEFASPRGEG FYHKKDLWHLHAIKTMEOVESTGGRSGIRMWAMKQOLLE GGFHESTRDYIYYNDVYAFNLDTTTWSLTSPSGTGPTRSGCO\ 1758/PRAASSYVGGYKKOVKWOKMAKRQOLLE GGFHESTRDYIYYNDVYAFNLDTTTWSLTSPSGTGPTRSGCO\ 1758/PRAASSYVGGYKKOVKWOKMAMMANICLIAKICIATGKNLAEQI RDHYPRVWFYWVQABILAMATDLAEFIGAAIGFKLILGVSLL OGAVLTGIATFILIMLQRRGQKFLEKVIGGLILFVAAAYTVELI FSQPNLAQLGKGMVTPSLPTSEAVFLAAGVULQATHTHGFVNLATMATAA SEINFFYGHTGVA  SEINFYCHTGVA  6711  3 347 VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHEDTLIHGEFK ELVRTICHHILMGGSRCQKYSATKWDVALAMTILGFVNLAIMATAA SEINFYCHTGVA  MAMLTWSYEIDNHDADVGPGGOHRBG  6712  118 578 PHGGKRTRYFQVRAFGGOPQAGLAMALCLKOVFAKDKTFRFRKR FERGTGRFELYKKAQASLKSGLDLRSVVRLEPGENIDDHIAVWR VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYETRMODERQYRR PAKLSAPRYMALLMBWIESLI QRATISVTLDGKGVVAMARTGSGKTACPLLPMFFRLKTHSAGTG ARALLSPTREIALQTILKFFKELGKTSLKATALLGGDRINGDQF AALHENPDIIIATGFLAUTLUFTLARGLYVPPFPTFTEGCTSDVE PDTREMVRAQNKKKKKGGGPOSMLSLYPVFRGINKKGVKVPPTI GRKTIVVILDGKDVVAMARTGSGKTACPLLPMFRLKTHSAGTG ARALLSPTREIALQTILKFFKLIGKTSLKATALLAGDINGDOP VFWATKHAPKLITELLTTGRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVVDLAARGLIPPLLOTILFPREKKTHSAGTG ARALLLSPTREIALGTLIVTLAFBKLLGGENYFPPVAG GKGSTAYSLVAPDEIPYLLDLHLHLINVYPPDQTOV VFVATKHAPKLITELLTTGRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAAGGLIPPLLOTSPPPAKGKLPHLVVA RAGRSGTAYSLVAPDEIPYLLDLHLHLENVYPPDQTOV VFVATKHAPKLITELLTTGRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAAGGLOPSTEPARKGHLDUGGLGHEFFSSRFEEEELQRIRL VDSIKNYRSRATIFEINSSEGLGGVGRARKRORDKATAAROOQ YVKSR PASPSES IKRAGEMDLUGGLGHEFESSRFEEEELQRIRL VDSIKNYRSRATIFEI	1	1		OHMERYRGVSFYEEPPHIJAVADTUVDALDTEDDDOALMIGUEG
ARTIERNDNSSRFGKYMDUGPFKGAPUGGEILSYLLEKSRYUVHO NIGERINFHIFYOLGGGEETHERIGGERINPOSYLYLVIKGGCAK VSSINDKSDMKVURKALTVIDFTEDEVEDLISIAASVLHLGMIH FAAMEESRAQUTTEROLXYLFELDKSGSTLREALTHRKI TAKG EELLSPINLEGANYARDALAKAVYSRTFTWLVGKINRSLASKDV ESPSMRSTTVIGILDIYGFVFGINSFGGFCINYCNEKLQQLFI ELTILKSEQBEYBAEGIAFPVQYPINKIICDLVEEKFKGII\SI LDE\CCLRPGE  894 PPHEHLPFSGERGFFFLVSRRGLGPGKMKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	1	ł		GAGKTDATKRLLOLYAETCPAPORGGAVPDPLLOCNDVLEAECN
NIGERNFII FYQLLEGGEETLRRIGLERNPGSYLYILVRGCAK VSSINDKSDMKVVRKAUTVIEDEVSCHLSIAASVLHLGNIH FAANESSAQVTTENQLKYLTRILSVEGSTEREALTHRKITAKG EELLSPINLEGAAVARDALKAYLTRILSVEGSTEREALTHRKITAKG EELSPINLEGAAVARDALKAYLTRILSVEGSTEREALTHRKITAKG EELSPINLEGAAVARDALKAYRTFIKUVGKINSLASKUV ESPSWRSTTVIGLLDIYGFEVFOHNSFEQFCINYCNEKLQQLFI ELTIKKSEQBEYEARGIAWEPVQYFNNKIICDLVEEKFRGII\SI LDE\ECCLEPGE PHEHLIPPSGERGFFSFLVSRRCLGFGKMKKKKKKKKKKGRGAEK TAAKMEKKVSKRSKSEEDLEALIAHFQTLDAKKRQTVELDEOP PSPELNASLSVHPEKDELILFGGEYFNGGKTFLVNELLYVNIRK DTWTKVAUDIPSPPPERCAHQAVVENOKTGGPSGRSCHRNVAMKRQLILF GGFHESTRDVIYYNDVYAFNLDTFTVSKLESSGTGPTPRSGCO\ FYHYKDLMVLHLATKTHEOVKSTGGPSGRSCHRNVAMKRQLILF GGFHESTRDVIYYNDVYAFNLDTFTVSKLESSGTGPTFRSGCO\ FYHYKDLMVUHLATKTHEOVKSTGGPSGRSCHRNVAMKRQLILF GGFHESTRDVIYYNDVYAFNLDTFTVSKLESSGTGPTFRSGCO\ FENHYRPEVWFYWQABIIAMATDLAEFIGAAIGFKLILGYSILL GGAVLTGIAFFLIHLMORRGGKTEKVJOKGLEFASNGEY GGAVLTGIAFFLIHLMORRGGKEKVJOKGTHSDMF FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/VI WHSSLTQHLHGGSRQGRYSATKWOVATAMTIAGFVNLAIMATAA SELNFYCHTGVA SELNFYCHTGVA  5711 3 347 VTECKTMTCKMSGLERNI*TMINTLHYSVKLGHPDTLIHGEFK ELVETDLHNILMKRNNDQAI*HMEDLDTNAHMQIIFKELIML MAMITMSYHDNMIDADYGGQOHRG  6712 118 578 PHGGKTRFPQVEAPGOOFQAQLAMALCLKQVFAKKTFRPRKR FEPGTQRFELYKKAQASLKSCLDLRSVVRLPPGENIDDHIAVHV VDFFNRINLIYGTMAERGS*TSCDVMAGGRYEFTRPOKECTSDVE FPREWARAONKKKKSGGFORGLSYPVFKGIMKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACPLLPMFPRIKTHSAGTG ARALILSPTREIALQTLKFTRELGKFTGKKTALLUGGDRMEDQF MGFACQLGEIIARIJGGGRANLOFSEKLUGSVETVYDEADRIJFE MGFACQLGEIIARIJGGGRANLOFSEKLUGSVETVYDEADRIJFE MGFACQLGEIIARIJGGGRANGLOFTLESATLPKLUVFPARAGLTEPUL RLDVTKLREGGLYTSFLVERGDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEVLTELLTTORVSCAHIYSSALDPTARRINLAKFTL GKCSTLVTDLAARGGLDIPLDVNINYSPPAKGKLFHEVGRVA GAGGSGTAYSUAPDEIPYLLDLHLFLGRSLTLARPLKGPSGVA GVOGMLGRVPGVVUDEDSGLGSTLGSSTLERGLERGLARVADNAQO VYKSRPAPSPESI KRAKEMDLVGLGLHPLFSSTPEEELLQRIRL VDSIKNYRSRATIFFINASSRDLCSQVMRAKRQKORKALARPQO GQCGQOGEQOGGPGAPSPAPSADGGSSPGEGESUPDIFS	}			AKTLENDNSSRFGKYMDVOFDFKGA DVCCHILSVI LEVERINGIO
VSSINDKSDWKVVRKALTVIDTEDESVEDLISIAASVLHLGNIH FAANESSNAQVITEROLKVITERLISVEGSTLERABLIHKRII NIK EELLSPINLEGAAVARDALAKAVYSRTFTWLVGKINRSLASKDV ESPSWRSTTVIGLLDIYGFEVFOHNSFEDÇTINYCNEKLGQLFI ELTIKSEQBEVEARGIAWERVOYFNNKIICOLVERKFGGII\SI LDE\ECLEPGE  894 PPHEHLFPSGERGFFSFLVSRRGLGFGKWGKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEEEDLEALIAHFOTLOAKRTOTVELPCPP PSPELNASLSVHPPEKDELLIFPGKTFLVANELYVINIRK DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEC FYHYKDLMVLHLATKTHEOVKSTGGPSGRGHRWAMKRGLILG GGFHESTRD'IYJNDVYARNLINTFTWSKLSPSGTGPTPRSGCOI 1PSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF FHRWTNVRVESSSGRARKERLAMGPAPLAAIGYIDFGNFATN 1QAGASFGYQLLWVVWARLMAMLIQILGAKLGIATGKNLAEQI RDHYPRPVVWFYWVQABILAMATDLAEFIGAAIGFKLILGVSLL GGAVLTGIATFLILMIQRRGGKPLEKVIGGLLLEVAAAYIVELL FSQPNLAQLGKGWVIPSLDTSSAVELAAGVU\GATIMPHI/YI WHSSLTCHLHGGSRGOCKYSATKUGGLLEVAAAYIVELL FSQPNLAQLGKGWVIPSLDTSSAVELAGGU\GATIMPHI/YI WHSSLTCHLHGGSRGOCKYSATKUGGLLEVAAAYIVELL FSQPNLAQLGKGWVIPSLDTSSAVELAGGU\GATIMPHI/YI WHSSLTCHLHGGSRGOCKYSATKUGGLLEVAAAYIVELL FSQPNLAQLGKGWVIPSLDTSSAVELAGGU\GATIMPHI/YI WHSSLTCHLHMGSRGOCKYSATKUGGLLEVAAAYIVELL FSQPNLAQLGKGWVIPSLDTSSAVELAGGU\GATIMPHI/YI WHSSLTCHLHMGSRGOCKYSATKUGGLLEVAAAYIVELL FSQPNLAQLGKGMVIPSLDTSSAVELAGGU\GATIMPHI/YI WHSSLTCHLIMGRAGGPQALMALCLKQVFAKDKTFPRRK FEPGTRFELYKKAQASLKSGLDLRSVURLDFORNIDDITAVEV VDFFNRINLIYGTMARGCS*TSCWMAGGPRYERYRQDERQVR FPPGTREBLYKKAQASLKSGLDLRSVURLDFGRENIDDITAVEV VDFFNRINLIYGTMARGCS*TSCWMAGGPRYERYRQDERQVR PAKLSAPRYMALLMDWIBSLI  6713 2485 3 QARGSTBEBGEFEIQAEDDARARKIGDGRFLPTFPTSECTSDVE PDTREWVRAQNKKKKSGGFQSMLSYVVKGJMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLHPERRIKTISAQTG ARALILSPTRELALDOTHFTELGKFFGLKFTALLVGFRAAGTEPVL NGFAEQLQEI IARI.FGGHQTVLFSATIPKLLVEFRAGGTEPVL WGFAEQLQEI IARI.FGGHQTVLFSATIPKLLVEFRAGGTEPVL UFVATHHHEVLTFELLTTQRVSCAHIYSALDDTARRINIAKFTL GKCSTLVTDLAARGLDIPLLDVINIYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPSLLDCHLGLHPUNFSSFPEELLGRIRL VVSIKNYRSRATIFFINASSRDLCSQVMRAKRQKDRKALARRQO VVKSRPAPSPESI KRAKEMDLVGLGGLDPLFFSSFPEELLGRIRL VDSIKNYRSRATIFFINASSRDLCSQVMRAKRQKDRKALARRQO GQQGCQOGCQOGEQOGGPGPAPSPSRAUCGGPASPERALDGGGSVSUDIFS	1			NHGERNFHI FYOLLEGGEEETLRRIGLERNPOSYLVI NKGOCAK
FAMNESSNAQVITENQLKYTERLİSEVEĞİLREALITHRKITAKĞ EELLİŞPILNEĞÖNAYARDALAKAYSRIFTİKLÜĞKİRNİSLASKÜV ESPİNRESTIVLĞLLDIYĞFEVPÖHNSFEQFÇINYCNEKLÖĞLİF ELTİKKEQEBYEAĞİLMEPVÜYFINKITLÖLVEBKERĞİLİŞİ LDEVEÇLRPĞ  894 PPHEHLIFTĞĞERĞFŞFLVŞRRÇLĞFĞKMĞKKĞKKEKKĞRĞAEK TAAKMEKKVŞRRŞSKREEDLİBALIAHFÇTLDAKRRÖTVELPÇPP PİPHENLIFTĞÖRİNDEN KIRKEKÇIN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜN ÇÜNÜ	ł	)		VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVIHLGNIH
### RELISPINIEQNAYARDALAKAYUSRTFTKIUGKINRSLASKDU  ### SEPSKRSTTYLGLLDIYGFEVQGINSFEQGCINYCNEKLQGLFI ### ELITLKSEGEEYEAGGIAMEPVQYFNNKIICDLVEEKFKGII\SI LDE\# ECLRGE ### PHEHLFPSGERGPFSFLVSRRGLGFGKMCKKKKKKKKKKKKKGRGAEK TAAKMEKKVSKRSKREEDLEALIHFQTLDAKRTGTVELPCPP ### PSPELNASLSVHPERDELLIGEGYFKGGKTFLYNELYVYNIRK DTWTKVDIPSPPRRCAHQAVVVPQGGGGLWVFGGEFAS PNGEQ FYHYKDLWVLHATKTHEQVKSTGGPSGRSCHRWAMKRQLILF GGFHESTRDYIYYMDVTAFHLDTTTWSKLSPSGTGPPSRGSCQ\ 1PSLPPAASSVYGGYSKQRVKKUDVKSTRSDMP ### PROPARSSSGRAARKHALMGPAPTAATGYIDPGNFATN IQAGASFGYQLLWVVWANLMAMLIQILGAKLGIATGKNLAEQI RDHYPRPVWFWYWQABILMATCLAGFVLIAAGVLIQFAFTAN GAQALTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATTMPHVI/YI WHSSLTQHLIGGSRQQKYSATKWDVAIAMTIAGPVALAIMATAA SELNFYCHTGWA  ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ### SELNFYCHTGWA ##	ı			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKI LAKG
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ELTIKSEGEYPAGIAWEPVQYFNNKIICDLVEEKFKGII\SI LDE\ZCLRPGE  894  PPHEHLFPSGERGFFSFLVSRRGLGFGKMGKKKKKKGRGAEK TAAKMEKKVSKRSRKEEDLEALIAHFQTLDAKRTQTVELPCPP PSPRENASLSVAPEKDELHGGEYFNGQKTFLYNELYVNIKK DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ FYHYKDLMVLHLATKTHEQVKSTGGPSGRSGHRMWAKKQLILF GGFHESTRDYIYINDVAFINLDTFTWSKLSPSGTGFPRSGCQ) IPSLPRAASSVYGGSKGRVKKDVKGTHSDMF  6710  158  980  RHKMTNYRVESSGGRAKRWRIALMGPAPLAAIGYIDFGRFATN IQAGASFGYQLLWVVWANLMAMLIQILSAKLGIATGKNLAEQI RDHYPRPVWPYWVQABIIAMATOLAEFIGAAJGFKLLIGVSLL GGAVLTGIATFLIIMLGRGKPLEKVIGGLLLFVAAAVIVELI FSQPNLAQLGKGMVIPSLPTSEAVELAGGVLKGATIMPHVI/YI WHSSLTCHIHGGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA SELNFYGHTGVA  6711  3  347  VTECKTMTCKNSQLERNI*TMINTLHYSVKLGHPDTLIHGEFK ELVETDLINILIMKSNKNDQAI*HIMEDLDTNAHMQIIFKELIML MAMMINSYHDDMHDADVGPGQOHRPG  6712  118  578  PHGQKRTRYPQVRAPGQOPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRMQDERQYRR PAKLSAPRYMALLMDWISSLI  GRALILSPTRELAQTLKFTKELGKFTGLKTALLIGGDRMEDQF AALHENPDIIIATFGRVHVAVEMSLLQSUSYVYPDEADRLFE MGPAEQLOLGIIARIPGGRQTVLFSATLPKLLVFPARRALTEPUL IRLDVDTKLMEQLKTSFFLVREDTKAAVLLHLLHNVRPQDQTV VFVATKHAEYLTELLTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLDDNVINYSFPAKGKLFHRVGRVA RAGRSGTAYSLVAPDEIPYILDLHLFLGRSITLARPLKEPSGVA GUPGMLGRVPQSVVDEEDGLGSTLEASLELRGLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSFFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLFSSRFEEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSEFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSEFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSEFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSEFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSEFEELGRLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGSHPLSSUFEFEILGRLARVADNAQQG COQCREQEQGEOFUPAPSPR		<b>(</b>		ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLOOLFI
B94  PPHEHLEP SEGERGPF STLVSRRGLGFGKMCKKKKKEKKGRGAEK TAAKMEKKVS KRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP PSPRINASLSVYHPEKDELILFGGEVFYNGGKTELYVENIKK DTWTKVD1F SPPRICANGAVVVPQGGGGLWYFGGEFASFNGEQ FYHYXDLWVLHLATKTWEQVKSTGGPSGRSGHRWAMKRQLILF GGFHESTRDY 1YYNDVLANLTFTWSKLSPSGTGPTPRSGCQ\ 1PSLPRAASSVYGGYSKQPVKKDVDKGTRHSDMF  6710  158  980  RHKHTNYRVESSSGRARKMRELALMGPAF LAALGYIDPENFAN IQAGASFCYQLLWVVVWANLMAMLQILGAKLGIANFGKNLAEQI RDHYPRPVVWFYWVQABIIAMATDLAEFIGAALGYLDPENFAN IQAGASFCYQLLWVVWANLMAMLQILGAKLGIANFGKNLAEQI RDHYPRPVVWFYWVQABIIAMATDLAEFIGAALGFKLILGVSLL GGAVLTGIATFLILMLQRRGQKYLEKVIGGLLLFVAAAYIVELI FSQPNLAQLGKGMVIPSLPTSEAVELAAGVL\GATIMPHVI/YI WHSSLTCHLHGGSRQQKYSATKWDVAIAMTIAGFVNLAIMATAA SELMFYGHTGVA  6711  3  347  VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLINILMKENKNDQAI*HMEDLDTMAHMQIIFKELIML MAMLTWSYHDNMHDADVOPGQOHRPG  6712  118  578  PHGGKRTRYPQVRAPGQOPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTORPELYKKAQASLSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQVRR PAKLSAPRYMALLMDWIESLI QARGSDSEDGEFETQABEDDARARKLGPGRPLPFTPTSECTSDVE PDTREMWRAQNKKKKSGGPQSMGLSYPVFRGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALISPTRELALQTLKFTKELGKFTGLKTALLLGGDRMEDQF AALHENPDIIIATPGRJVHVAVENSLKLQSVEYVYFDEADRLPE MGPACLQEIIARIPGGHOTLFSATLPKLLVEPARAGLTEPUL IRLDVDTKLAEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLDINVINYSFPAKKCIPHTWQRVA RAGRSGTAYSLVAPDEIPYILDLHLIFLGRSITLARPLKEPSGVA GUPGMLGRVPQSVVDEEDSGLQSTLEBASLELRGLARVADNAQQQ VVRSRPAPSPESIKRAKEMDLVGLGHPIPFSSKREEEELGRIAR VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKORRAIARFQQ GQQGRGEQQGEPUGPAPSRPALGKEGEFEELGRIARI VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKORRAIARFQQ GQQCGCGCQCQCGCGPUGPAPSRPALGKKGFEELGREREL	1	[		ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
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1 PSLPRAASSYYGGYSKQVVKKDVDKGTRHSDMF RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDFGNFATN 1 QAGASFGYQLLWVVWANLMAMLIQILSAKLGIATGKNLAEQI RDHYPRPVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL QGAVLTGIATFLILMLQRRQQKPLEKVIGGLLHFVAAAYIVELI FSQPNLAQLGKGMVIFSLPTSEAVFLAAGVIL\GATHMPHYI/YI WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA SELNFYGHTGVA SELNFYGHTGVA  6711 3 347 VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML MAMITWSYHDNMHDADYGFQQOHRPG  6712 118 578 PHGGKTRYFDVAPFQQOPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI  6713 2485 3 QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE PDTREMVRAQNKKKKKSGFQSMSLSYPVFKGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSFTRELALQTLKFTKELGKTGLKTALLLGGRMEDQF AALHENPDIIIATFGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLIEGUKTSFFLVREDTKAAVLIHLLHUVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDFTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEFSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVWRAKRQKDRKAIARFQQ GQQGRQDQDGEDVGPAPSRPALQEKOPEKEEEELEGESVEDIFS	1	}		FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
RHKMTNYRVESSGRAARKMRLALMGPAFIAAIGYIDFGNFATN IQAGASFGYQLLWVVWANLMAMLIQILSAKLGIATGKNLAEQI RDHYPRPVWWPYWQABIIAMATDLAEFIGAAIGFKLILGYSLL GGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI FSQPNLAQLGKGMVIPSLPTSEAVFLAAGGU\GATIMPHYI/YI WHSSLTQHLHGGSRQORYSATKWDVAIAMTIAGPVNLAIMATAA SELNFYGHTGVA  6711 3 347 VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML MAMLTWSYHDNMHDADYGPGQOHRPG  6712 118 578 PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR FEPCTQRFELYKKAQASIKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI  6713 2485 3 QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE PDTREMVRAQNKKKKKSGFQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACPLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPPIIIATFGRLVHVAVEMSLKLQSVEYVVFDEADRLPE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEPFARGLTEPVL IRLDVDTKLNEQUKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINTSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRPLCSQVWRAKRQKRKAIARFQQ GQQGRQCQCQCGCQCGCGCGCGCGCGCGCGCCGCCGCCCCCCCC	1	!	•	GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
IQAGASFGYQLLWVVWANLMAMLIQILSAKLGIATGKNLAEQI RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL QGAVLTGIATFLILMIQRRGCKPLEKVIGGLLLFVAAAYIVELI FSQPMLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGPVNLAIMATAA SELMFYGHTGVA  VTECKTMTCKMSQLERNI+TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML MAMLTWSYHDNMHDADYGPGQQHRPG  6712  118  578 PHGGKRTRYPQVRAPGQPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI  6713  2485 3 QARGSDSEDGEFETQAEDDARARKLGPGRPLPTFPTSECTSDVE PDTREMVRAQNKKKKKSGFQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALLLGGDRMEDQF AALHENPDIIATFGRLUHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLLVTDLAARGLDIPLLDNVINTSFPAKGKLFLHRVGRVA RAGRSGTAYSLUVAPDEIPYLLDLHLFLGRSLTLTARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL VDSIKNYRSRATIFEINASSRPLCSQVWRAKKQKRKAIARFQQ GQQGRQCQCQCGCQCGCVGPQPAPSRPALQEKQPKEEEEAGGSVEDIFS	6710	158	980	DUMMENURGAGON
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PAKLSAPRYMALLMDWIESLI  QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE PDTREMVRAQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI QRRTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRIRIL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQCEGPVGPAPSRPALQEKQPEKEEEEEAGGSVEDIFS	] 1		-	VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
PARGSJEEGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDUE PDTREMVRAQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI QRRTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRIL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEFEAGESVEDIFS	1			PAKLSAPRYMALLMDWIESLI
PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIAFFQQ GQQGRQEQQGEGPVGPAPSRPALQEKQPEKEEEFEAGESVEDIFS	0,772	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF ARLHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLPE MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQGEPVGPAPSRPALQEKQPEKEEEFEAGESVEDIFS	[ ]	1		PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKILLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRYGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRI. VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS	1 1			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAOTG
AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE MGFAEQLQEIIARI.PGGHQTVLFSATLPKILLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRYGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRI. VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS	j			ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLIHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSFESIKRAKEMDLVGLGLHPLFSSRFEEEELQRIRIL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQOEGPVGPAPSRPALQEKQPEKEEEEEAGGSVEDIFS	1 1	ľ		AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGHHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS		1		MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIAFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS	; l	1	ļ	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRI. VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESYEDIFS	! I	Ì	Į	VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS		ĺ	Į.	GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS	1	}	Í	KAGKSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS		ļ	i	GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS	1	<u> </u>	į	IVKSKPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS EVVGRKRQRSGPNRGAKRREEARQRDQEFYIPYRPKDFDSERG	1		ĺ	VUSIKNYKSKATI FEINASSRDLCSQVMRAKRQKDRKAIARFQQ
EVVGKKKQKSGPNKGAKRREEARQRDQEFYIPYRPKDFDSERG		<u> </u>		GQQGKQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS
	<del></del>		<del>-                                    </del>	EVVGKARQKSGPNKGAKKKEEARQRDQEFYIPYRPKDFDSERG

SEO	Predicted	Predicted end	
- ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
1	İ		FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
ł		1	GRRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPLOAESA
			LELKTKQQILKQRRRAQKAALSLQRWWPQAALCPO
6714	169	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS
1	1		GQNLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNLNPAF
1			SKKFVLDYHFEEVQKLKFALFDODKSSMRLDEHDFLGOFSCSLG
1	1		TIVSSKKITRPLLLLNDKPAGKGLITIAAQELSDNRVITLSLAG
1	İ	İ	RRLDKKOLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW
i	i	[	KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEFOTSVSO
ı			MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS
I	1		FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYI,
	İ		SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP
6715			TNPFCSGVDGIAQAYSACLP
6/13	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
l l			GKPKHLGVPNGRMVLAVSDGELSSTTGPOGOGEGRGSSLSIHST.
1			PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
6716	1	175	AENVTFWKACERFQQIPASDT
0.120	<u> </u>	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ
6717	115	006	HTVTLHRVSLCCSK
	113	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
1	•		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
	Î l		FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
1			PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
1			GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
6718	290	599	WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
i		-55	VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
			LEKEKKLDIMKTATQ
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
1			DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
1 .			QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT
			RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
			RKSSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
	i J		VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
1			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
	İ		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1 1	ł		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
-			SVVTLISE
6721	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
	j		VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGOALSTY [
1	i		QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
1			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
]	-	İ	IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
į į	l		vlvgfnpvsmarhpfppprilrsltvfpslraphyqitsllfsm
6722	<u></u>		SVVTLISE
0'22	1	390	RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
1	1		LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
1-6733 1			PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYONW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLOALT
		i	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
LL	<u></u>	i	AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

SEQ	I Description		
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	\A=Alanine, C=Cysteine, D=Aspartic Acid P-
1	location	location	Glucamic Acid, F=Phenylalanine G-Glyging
1		corresponding	H=H1Stldine, I=Isoleucine K=Lycine
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
İ	1	amino acid	P=Proline, O=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +=Cton
	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		<pre>{ \=possible nucleotide insertion}</pre>
			VEVKELQREPLTPEEVQSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGOFVAVVNDKSSPVEALKGLVDKLOALT
1		1	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
ŀ	•		AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
ļ	<u> </u>	1	VEVKELQREPLTPEEVQSVREHLGHESDNL
6725	356	722	RRRTPPVILATMODDLMLALRLQEEWNLQEAERDHAQESLSLVD
J	1		ASWELVDPTPDLOALPVQFNDQFFWGQLEAVEVKWSVRMTLCAG
L	Į		ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG
	1		GVI.VITOKOTI TKVIDERI POZVINISTE TO TO TO TO THE TIME INVO
Ī	i	•	GYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRDGL
	1		LFRHVLNFLRNGELLLPEGFRENQLLAQEAEFFQLKGLAEEVKS
l			RWEKEQLTPRETTFLEITDNHDRSQGLRIFCNAPDFISKIKSRI
6727	1	831	VLVSKSRLDGFPEEFSISSNIIQFKYFIK
l		031	FRGMGDERPHYYGKHGTPQKYDPTFKGPIYNRGCTDIICCVFLL
f :	! !		LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP
			YLFYFNIVKCASPLVLLEFQCPTPQICVEKCPDRYLTYLNARSS
			RDFEYYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF
	· i		PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA
	]		RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG
6728	486	02.5	RGMIIMGILVLGY
	400	935	FCSSWLRSLADSSLSWKMFLVGLTGGTASGKSSVIQVFQQLGCA
,			VIDVDVMARHVVOPGYPAHRRIVEVFGTEVIJENGDINDVULCD
	1		LIFNQPDRRQLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK
6729	259		HVPSALKEADSLMRRDT
0,25	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV
l	i		LAGVKKFDVPCGGRDCSGGCOCYPRKGGRGOPGPVGDOCYNGDD
	Į.		GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGRDCADGT
l	ĺ		PGHPGQGGPRGRPGYDGCNGTOGDSGPOGPPGSEGFTGDDCDCC
i			PKGQKGEPYALPKEERDRYRGEPGEPGLVGFOGPPGPBGHVGOM
l	ļ		GPVGAPGRPGPPGPPGPKGOOGNRGLGFYGVKGEKGDVGOPGDN
	1	1	GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE
6730			GIM
6/30	784	1015	NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE
6731			RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF
6/31	1	446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGG
1	1		LDIYAGLDSAVSDSASKSCVPSRNCLDLYEETLTREGTAKEATV
(	1	1	NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA
			LIKTARVEINRKDEEI
6732	102	1205	GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW
			AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN
[		i	LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE
ļ		<u> </u>	GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE
ļ		1	PLVAKERS PVGKRTRLEEFRS DSAKEEVRESAYYLRS RQRRQPR
ŀ		1	PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE
l	1	ĺ	DEASSOTDI SOTI SYNTRES TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE STORE TO DE S
1	j		DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVOOKUMESEECHTESPROPROMEEN
	l		YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW
6733	613	1311	
ĺ			RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK
Į.			KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI
			QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVIR
j		j.	VLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETVRRMI.FOL.
- 1	[	1	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEOERERLKK
6734	189		LLEQEKAYQARKE )
-	10,7	551	SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD
		<u></u>	AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
ı	1	· ·	QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
1	ļ.		XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
1			SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
ı	j.		KHAKEIEEESETTVEADLTDKQKHQLKHRELFLSRQYESLPATH
[	1		IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
	ł		EIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
1	1		REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
	1		REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
1	i		CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
1	}		PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
	-		ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
i			RQFLELLQFNINVPSSVYAKYYFDLRSLAEANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
ł			WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
1	ľ		QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
			KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
6739	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
Į.	<b>,</b>		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
1	<b>!</b>		VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1	1		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
1			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
i	f .		REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
6741			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
0/41	141	960 -	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1	ļ		YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
1			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
l	i i		PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
6742	141	960	LIPKTKIP  DI TI DECCEDENCIMENTE DETENCIONALI AMA GUALINA
	~	200	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
I	l l		HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1			YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
1			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
1			ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
1			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
			LONIR .
6744	95	1343 -	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD
J i	_		RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT
l i			DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
[			LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE
1			VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAEGQLRFWNP
L			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEO	Predicted	T 50	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
İ	ļ		CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
1			PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
			DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
6745			TLALENELLVTKNSIHQACI
0745	1	588	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
1	1	1	AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERREDP
Ì			ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
1		1	PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
		ł	RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
ľ	1		SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
			VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
			QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKOVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
1			LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
1	ĺ		VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
L			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
			SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
1	ļ		VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
	ļ ļ		INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
L			HAKTGQSADSGTIKAKLSGPSVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
i			TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
<b>1</b>			EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
<u> </u>			RSSQLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
			NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
1			QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
1 1			FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
1	1		HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
1	1		SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
) )	j.	•	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
			FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
[ · ]	İ		YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
<u></u>			ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKOREAGFL
1	1	ł	CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ
1 I			VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
1 1	İ		KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK
] [	j		SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
, ,	j		PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
] [			TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
1 1			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
	1		CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
]			HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
1 1	1		CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
ļ Ī			KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
{			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
	·		TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
6753	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
		1	PFGIKLRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
j Ì		ļ	SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
L		ŀ	AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	"	\=possible nucleotide insertion)
			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
İ			GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
			KPMLQSRHSLDGSKLTEKVETAQPLWITLALOKOKGFREOOATR
1			EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALD
1	<b>l</b>		EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAADIJVKE
- C3EA			VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFODVLKEPSTALEKT.PE
1	1		LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKORELYAO
			FLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
6755	298		NEALT
0,55	230	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
1			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
			VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
l .			KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
			LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
İ			LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELILTE
			REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
			KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
7000			PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
1			TRGIKHRIKWNRKALPSTAQITEAOVAENRPGAFIKOGRKLDID
	ļ		FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATO
6758	1		AANQGEFQKPDNKLHQQVLW
0,55	*	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
i l	j		LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
	Ţ		PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
l i	i		TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
	Į.		VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
	[		WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
	J		LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
	. 1		NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFV
6750			SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIOVVCVI.
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFOLKDLEKIADKEKGTT
1			AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
6761			VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
0,01	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS
İ	1		SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACND
			NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGETGKG
1	1		MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
	į		RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
J	Ī	İ	LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
- 1	Ī		SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
}	·		NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGI IADATVRSLEG
j			RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
			AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
ŀ	ļ		ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
			PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL

SEQ	Predicted	1 h - 1/2 - 1	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sedgence	Codon, /=possible nucleotide deletion,
6762	3	613	\=possible nucleotide insertion)
1 0,02		613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
1	]	{	QVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIG
	1		LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
1	1	j	LVVVNHYLAFQFFAEEYYPFSEVLAYFTFCLWIIPFAFFVSLSA
6763	2	750	GENVLPSTMQPGDDVVSNYFTKGKRGK
1 0,03	_	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
			RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
	1		SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR
1	1		ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
6764			YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6,04	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
1			KKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
6765			RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
0,763	3	550	ARYSRVDHFCRRCCRAVARAPRFLLQFPSGPSRHFLAACVARWL
Í			RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
1			NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
			VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
6766			PHLRNQ
6,00	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
	ľ		KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
			QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
1 1		•	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
1 1			LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
1			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
1 1			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
6767	336	010	AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
""	330	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
1 1	1		GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
] 1	]		RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
1 1	i		PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
6768	2	353	NPDATEILHVKKKKALLL
1	2	363	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
, [	ļ	•	LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
6769	284	396	ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6770	1	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
****	<b>-</b>	397	QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
[ [			ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
6771	3	220	KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
"''"	,	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
1			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
6772			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
"''"	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
	i		CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
	1	1	P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGOFL
1	1		HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
			LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
			AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
	İ		IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
	1	ļ	QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
		Ī	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
[		1	TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
	[.		QKVYRDCSCIPQNLSSGFGHATAGKCTST
			<del></del>

SEQ	Predicted	Predicted end	I Amino and A
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
İ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
[	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
6773	1		\=possible nucleotide insertion)
1 3773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
			RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
			CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
			EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGCRCLEVEGHRL
6774			CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
		<u>L</u>	GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS
1	1		GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
	i		HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
L	<u>L</u>		QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
1			LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
1	1		TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
			CAALAPTFLIYCSLRFLSGIAAMSLITHTIMLIAEWATHRFQAM
1			GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
1	1		CMILECARMITAMENTE COLUMN PUR AND
1			SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
]			KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA
	Ì		YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
6777	779	63	RVSSRGRVNCLGLFVLQVW
	,,,,	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
			GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD
1			AELLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
			SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
1			HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
6778	311		GGGARLQHP**SPRARKGR
1 ""	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EBTAGDSE/ERSPEEE
1			VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
			KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNOSNVRRMH
6330			T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRROPRILAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
[ ]	•		MAKCAWKGPREPPQDARAEAESPGGASESDODGGHESPPKKKAV
			AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1 1			SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
			V
6780	3	403	HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
1			SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
		•	LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
L		•	K K
6781	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
1 1	1	• •	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
1 1	l	1	SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
1	ĺ		TPVFINSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
1 1		İ	HTPONTKEGG BUDDNAL GGDD DNI OTGDD IN GGD TOTGDD OTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD TOTGD
1	i	J	HIPONIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP
	ľ		SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ
]	ŀ		STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC
1 1	ł		KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
1			KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
6782	3		LVPSELISAVPTTKSNHGGIASESLAG
~.62	ا د	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
1		i	NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTOOPPTK
1		}	VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLOKKOSNLATGLS
] [		İ	KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSO
j l	j		NPGELSCKRGDVLVMLKQTENNYLECQKGEDTGRVHLSOMKLIT
<u>                                 </u>		į	PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ı	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion
<b> </b>	sequence		\=possible nucleotide insertion)
Į.		1	DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
Í			PEGGNGKRECVSSHCVKGSRCVARFEYIGEOKDELSESEGETTT
!	1	1	LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
	İ	ļ	PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
6783	3	1750	I
		1/50	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1			TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
1			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
ı			LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
İ			PQKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVPE
1	]		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
1			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
	1	•	KEEAIPWPGTLAIVHSYIAYKAAKEEEKOKLLKWSSDLKOEREO
			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKOLIRLIH
	1		GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSOSCT
6784	3		ANCNOGEETK
0,04	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
			TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLOTSSKVT
Į.			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1	[		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
1			PTSQNS IHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1			PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVFE
j			PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
1	!		RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
1			KEEAIPWPGTLAIVHSYIAYKAAKEEEKOKLLKWSSDLKOEREO
]			LEQKVKQLSNSISKCMEMKNTILAROKEMHSSLEKVKOLTRLTH
1			GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
6785	1		ANCNQGEETK
1 4,00	*	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
1			LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
i			KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
6786	1820	1397	GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
]		2337	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
1			DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
i i	1		YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
i i	. 1		VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
			EITLKGFREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
<u> </u>	1		YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
[ ]	ļ		VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAORLIEEKGAV
, ,	1		DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIODVSC
}	j	· i	AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERIOAR
]			WHDSDWILSVPAKLPEIEEYYDGNTSSNSRORSGWSSGRSGRSG
	İ		RSGGRSGGRSGRQSRQGSRSGSRODGRRRSGNRNRSRSGGHKRS
	ļ		PD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
6787	3545		SVWN
3,0,	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
1			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGITGTCHHAWLT
6788	16		LVFLVEMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLOT
	***	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
·			REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΙD	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, TaThreonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	} -	\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATQE\
ŀ	ļ	ļ	FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS
		ł	NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG
1		} ·	AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG
		<u> </u>	GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
l	į	1	GHK
6789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
l	ì	į	GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
	1	1	GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLOHYAVNSAD
ļ	1		PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
İ		<u> </u>	MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
l	į.	ĺ	TLGVQSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
			EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
1	<b>,</b>	1	HYOWLOVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
ŀ		ļ	KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
i	ļ	Ì	EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
Ì	İ	]	ALNFKTSESEGVILHGEGQQGDYITLELKKAKLVLSLNLGSNQL
1	}		GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR
l	1	(	TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
l		1	VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG
į	Į.		RLNODLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
l			VHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFAILTIDG
	1		DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQGC
l	1	j	MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
1	}		HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
ĺ		-	SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
ł			YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
1	!		NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
ł	ł .		YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
l			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
ļ	1		TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR
			SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
l	1		ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
	1		VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDQONSHPDLAO
	l		EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
	]		GTREPYNIDVDHRNMANGOPHSVNITRHEKTIFLKLDHYPSVSY
			HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS
			RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM
	1		SSATDPWHLDHLDSASADFPYNPGQGQAIRNGVNRNSAIIGGVI
ł	ĺ		A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSRQK
	}		KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW
			SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ
			NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
			EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
			LRMGNGALHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
			PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
			CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
			TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
			ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
			CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
			APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
	<u> </u>		AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG

SEO	Predicted	Predicted end	Dimino solid assessment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
· I	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	<u> </u>	\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
			LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
1			YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
			VIVLWTANTERFCEVIPGLNDTAENLLRTIBLGLEVSPSTLFAV
1	]	·	ASILEGCAFLNGSPONTLVPGALELAWQHRVFVGGDDFKSGQTK
l.			VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
1			SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
1	<b>,</b>		CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRORSCI
1	1		ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
1			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
1			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
1	!		EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
İ			NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
			FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
	i i		RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
J	]		MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
6795	1740	1010	HEEEHRRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
	1,40	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1 1			VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
1			FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
			DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
1			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
1			SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
<u> </u>		•	HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
6797	1630		SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
6/9/	1620	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
1	<b>i</b>		TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
	1		ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
	Į.		LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
	1		TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
]	ĺ		RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
ļ l	İ		PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
]	İ		CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
ļ ļ	1		ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
L			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
[ ]			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\POIA
1			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
'			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
		ļ	VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
] · ]			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
			ENKRRTLFKLASETEDNONSLGDILQASDNLSRVINSYKTIIEG
[ ]			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSQAEATLGPSSTSNAL
	1		SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PPPGTAACGASDADLLOPSADSSSSSSSADLDPPRAACGASDADLLOPSADSSSSSSADLDPPRAACGASDADLLOPSADSSSSSSADLDPPRAACGASDADL
	1		PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
[			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFO
		·	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	<u>-</u>		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
	1	ļ	RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
	ŀ	]	MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
		1	LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
0.55		1	ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
	i	Ì	VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
	1		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
		l	TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
			ENKRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
	j		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
	l .		PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
		1	SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
		1	PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
1			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
•	1	1	DOLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
l	1		PLSFQSQSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
ì	1		RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
1	1		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
ŀ	Į.	Ì	LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
1 0000	101	1040	*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
Ì		1	SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
l		1	RATRARRAVOKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
ł	1	1	AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
}	1	1	IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
Į	1	1	TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
Ì	i	1	NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
ļ		1	FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
l			VKVGKFMAKLAEHMFPKSQE
6801	1 2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
	_	1 2/02	YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
1			RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
			VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD
1		1	YLEGLLTKPIVKKYCLDVIEGALOMRYGDLLYKSLVPVPNSSSS
1	1		/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
			SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
Į			VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
[		i	LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
l			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
1		1	PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1			VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
j			QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
			VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
			PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
1	İ		RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
1			EIKRLNKALODALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
[	1	}	OOVOIYEEDFKKERSDRERLNOEKEELQQINETSQSQLNRLNSQ
			IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
l			KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
			TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
l			G G
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
	_1	L 2203	THE CALL HAMPOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=beucine, M=Methionine, N=Asparagine,
l l	to first	amino acid	
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1	1	1	KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
İ	1	<b>{</b>	SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
	1		GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
ŀ			AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
			NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
ĺ			QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
ŀ		•	ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
1	)		TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
	Ì		SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIOVMATELA
			HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
			PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
	. 1		ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
ì	]		ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
I	1		FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
1			AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
1	1		SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
	_		GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLONSRAKDR
· I	1		KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
			LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
	1 .		SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
			QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
	1		KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
ı			QQKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
			VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
	į į		KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
1			DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
1	1		CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
1			LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
1			KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
1			AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
			EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
L			VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
1			GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1			SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
1			MHVVSVPYALMKANPLSWIQKVCPYKARAALVKSRDMHWSLLAQ
j ·	l	•	RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
1	ľ		ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
1			TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
			SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
1	1		FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
.	<b> </b>		RGRIAVFSVTVLHDDRIVLVAEORPDASEEDSFOWMSRVLOAID
	[		SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
1			VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
			ELAHLEDSDOARKFLFLADVLOWRAHTTPDHPLFLLLNAKGTVT
1		•	STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
1 1	-	•	FYGCLYCGCVPVTVRPPHPONLGTTLPTVKMIVEVSKSACVLTT
j			QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
[ .	ĺ		DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
1 1	į		IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
i i	ł		AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC
]		-	MVVAEERP\RIALTQSFSKLFKDLGLPARAVSTTFGCRVNVAIC

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Deginning nuclectide location corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:		ř .		Amano acta segment containing signal peptide
Cocation   Cocresponding	3		1	(A=Aldnine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first anino acid anino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence  8-Serine, T-Threonine, V-aValine, w-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop Coden, Y-possible nucleotide deletion, V-possible nucleotide insertion) VOGTAGEPETYVVVMPALEMENEVETVVEGER HADHESARLSFOTOTO INARTORIGHESPETTYVGGER HADHESARLSFOTOTO INARTORIGHESPETTYVGGER HADHESARLSFOTOTO INARTORIGHESPETTYVGGER HADHESARLSFOTOTO INARTORIGHESPETTYVGGER VOGENCHEDALOLVALVETVVILGENTIANS TRECAPETYGGER HADHESARLSFOTOTO INARTORIGHESPETTYVGGER VOGENCHEDALOLVALVETVVILGENTIANS TRECAPETYGGER VOGENCHEDALOLVALVETVVILGENTIANS TRECAPETYGGER VOGENCHEDALOLVALVETVVILGENTIANS TRECAPETYGGER VOGENCHEDALOLVALVETVVILGENTIANS TRECAPETYGGER SVFOAGOFOLALANICARRESIGALSSFOTOSSEPSTULTEGAGER RITOAQVAAF RESEALRISSEDOTOSSESSESSESSESSESSESSESSESSESSESSESSESSE	1.	l .		H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of amino acid sequence  Sequence  Sequence  Lografoptopin, Y-Tyrosine, X-Unknown, *=stop Codon, Y-possible nucleotide deletion, Y-possible nucleotide insertion Lografoptopitryvpmpangroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroyngengroynge		corresponding	to first	
amino acid residue of amino acid sequence  sequence    WeTryptophan, Y-Tyrosine, X-unknown, *=Stop Codon, /=possible nucleotide deletion,  -possible nucleotide dissertion   LogTaGepDPTTVTVOWRALREDEWTLYREGSPHSLEDESGKI   POWAYI LAHITETREPLOSHIGE HWWS.PHRATGYTYTVGERE   HABHFSARLSFOTDT HARRGYLGFLERTELTDASCRUBDA   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYTY   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYTYVGERE   HABHFSARLSFOTDT HARRGYLGFLERTELTDASCRUBDA   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYTYVGEN   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYTYVGEN   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYTYVGEN   VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVGENYA     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVGENYA     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVGENYA     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVGENYA     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVLYGGEN     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVLYGGEN     VWSLDETLERGENYH DIDETSVITAMES IAECAVETYVLYGGEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIDETSVITAMEN     VWSLDETLERGENYH DIVERSE     VWSLDETLERGENYH DIVERSE     VWSLDETLERGENYH DIVERSE     VWSLDETLERGENYH DIVERSE     VWSLDETLERGENYH DIVERSE     VWSLDETLERGENYH DIVERSE     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN     VWSLDETLERGEN	1	to first	amino acid	
### Residue of amino acid sequence code, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide	l .	amino acid	residue of	
amino acid	1		1	
Sequence		ł		w=11ypcopnan, 1=1yrosine, x=unknown, *=Stop
OGTAGEDETTVYDMRALRHDVRIDVERGS PHEID LIMESCRI   POYKVI I ANTETKOP LODSHLOE LWSS PHEATOTYTY VIGERS     IAAHEFSARLS RODTOT I WARTCYLOF LRYSTER TELIDAS GGRIDAL     VVOSLDETLELRGWRYHPT DIETS VIRAHES I LACAVITATUR     LDETLELRGGS PPENDYT VSPRISE SHITTVSGGR     VVOSLDETLELRG SPENDYT VAN	1	l .	sequence	
### HABHESARLSFONTOT LWARTCHLIGHTQUETY TYVOYEDE HABHESARLSFONTOT LWARTCHLIGHTQUETY TO VUSIL HABHES LBECAPT TWIN.  WUVUELDGLEQDALDLVALVTNVVLEHTLYLVGVUVLOPGVU INSGEKCRMILRDGPLADOLDF1 TVAYNM  6807 1444 606 VGHDTVHARFTCFFKCLGFSPPVNVTVSFRSEESHTTVSGGE SVFOAGFOLQLAIALLERRGSIGAALSSRDVSGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGTLFSCLKSLSGDL EPFCGMEVISGORELESVAVOEAMA\LKFPMGAMSYCLRDS FPCGMEVISGORELESVAVOEAMA\LKFPMGAMSYCLRDS FLFRLPMGLSCPLQVQ  GVGSGASALARSRPLASSLSSRRTTRAPESGAMGLAMDLRW SRELSLYLEHQVRUGFFGSGVGLSLILGFSVAYAFYYLSSIAK PQLVTGGSSFSRFLQDHCPVVTETYYPTVWCHGGGTLLRUF ITSKPPVQYRELLKTADGGGISLDWPINDNSTCYMDASTRPT LLLDGLTGTSKESYILHMHLSELGYRCVVPNNROAGENLLLAN GKIGSKTPLMAAATFSVGNITFACSESLERPLNMLLFNYYLLTI LQSSVAKHRHWFVKQVDMPDMYMKAKSTEPKKFTSWMFGVGT DDYYTDASPSRRLKSVGIPVLCLNSVDDVSSPSHAIPTETAKC PNVALVLYTSYGGHLGPLEGIWPRQSTYMDRVFKQFVQAMVEHG BLS  6809 939 65 DYSGGTPVFFEIGHTLYTDAQTHPQGSEASTOPLAGTOTVF TDEAAQTDSQPLHPSDPTEKQQPKRLIVNNIPFRREDPLLRQW GQFKILLDVILTSYGGHLGPTLSVAYAFYALSSTOL GGRKILSVNNATAARVINKKTGNPYTNGKURVVQGVEYSV VTGFPYFTTGTAVAYRCAALLRCRGAVYNTFRAPPPP1PTY AVVYODGFYGAEI\LEATOPTDTLSPLQRRQPTATVTLESTDL GGRKILSVNNATAARVINKKTGNPYTNGKURVVQGVEYSV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TDEAAQTDSQPLHPSDPTEKQQPKRLIVNSIPFRAPDP1PP1 AVVYODGFYGAEI\LEATOPTDTLSPLQRRQPTATVTLESTDL GGRKILSVNNATAARVINKKTGNPYTNGKURVYGDEYV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TTTTPSGGRRPTALEPCTFHRFLLGP  BGRKILSVNATAARVATNKKTGNPYTNGKURVYGDEYV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TTTTTPSGGRRPTALEPCTFHRFLLGP  FSGSBEDFQDLLHGREDARAEKLINGTT GGRKILSVNATAARVATNKKTGNPYTNGKRUNTPVAGATGSPVYTTR GGRYSTPFONSVPPP1PRGSSLGFFCTREDSAFRYTTYTT TTTTPSGGRRPTALEPCTFHRFLLGP  FSGSBEDFQDLLHGREDARAEKLINGTT TDPAKTLGTPLLCPMBDVPLLEBCHLCKKTANTSTASSSDKLINLTYTT TDPAKTLGTPLLCPMBDVPLLEBPLLCKKTAHRRLTVLIPLEDC VTACCSGFTCTWGDRGKVYSPPD  GROWTFONSVPPPLATMATGGEKKRSSSSSMUNDATAAS SKRATILSLIDBRKERHERBCHKNINSHGATSKSSDK		sequence		\=possible nucleotide insertion)
### HABHESARLSFONTOT LWARTCHLIGHTQUETY TYVOYEDE HABHESARLSFONTOT LWARTCHLIGHTQUETY TO VUSIL HABHES LBECAPT TWIN.  WUVUELDGLEQDALDLVALVTNVVLEHTLYLVGVUVLOPGVU INSGEKCRMILRDGPLADOLDF1 TVAYNM  6807 1444 606 VGHDTVHARFTCFFKCLGFSPPVNVTVSFRSEESHTTVSGGE SVFOAGFOLQLAIALLERRGSIGAALSSRDVSGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGGLPVYAQSGEP RLTOAQVAAPFCENALERSSDQDTWDSLSFDVSGTLFSCLKSLSGDL EPFCGMEVISGORELESVAVOEAMA\LKFPMGAMSYCLRDS FPCGMEVISGORELESVAVOEAMA\LKFPMGAMSYCLRDS FLFRLPMGLSCPLQVQ  GVGSGASALARSRPLASSLSSRRTTRAPESGAMGLAMDLRW SRELSLYLEHQVRUGFFGSGVGLSLILGFSVAYAFYYLSSIAK PQLVTGGSSFSRFLQDHCPVVTETYYPTVWCHGGGTLLRUF ITSKPPVQYRELLKTADGGGISLDWPINDNSTCYMDASTRPT LLLDGLTGTSKESYILHMHLSELGYRCVVPNNROAGENLLLAN GKIGSKTPLMAAATFSVGNITFACSESLERPLNMLLFNYYLLTI LQSSVAKHRHWFVKQVDMPDMYMKAKSTEPKKFTSWMFGVGT DDYYTDASPSRRLKSVGIPVLCLNSVDDVSSPSHAIPTETAKC PNVALVLYTSYGGHLGPLEGIWPRQSTYMDRVFKQFVQAMVEHG BLS  6809 939 65 DYSGGTPVFFEIGHTLYTDAQTHPQGSEASTOPLAGTOTVF TDEAAQTDSQPLHPSDPTEKQQPKRLIVNNIPFRREDPLLRQW GQFKILLDVILTSYGGHLGPTLSVAYAFYALSSTOL GGRKILSVNNATAARVINKKTGNPYTNGKURVVQGVEYSV VTGFPYFTTGTAVAYRCAALLRCRGAVYNTFRAPPPP1PTY AVVYODGFYGAEI\LEATOPTDTLSPLQRRQPTATVTLESTDL GGRKILSVNNATAARVINKKTGNPYTNGKURVVQGVEYSV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TDEAAQTDSQPLHPSDPTEKQQPKRLIVNSIPFRAPDP1PP1 AVVYODGFYGAEI\LEATOPTDTLSPLQRRQPTATVTLESTDL GGRKILSVNNATAARVINKKTGNPYTNGKURVYGDEYV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TTTTPSGGRRPTALEPCTFHRFLLGP  BGRKILSVNATAARVATNKKTGNPYTNGKURVYGDEYV VTGFPYPTTGTAVAYRCAALLRCRGRAVVNTFRAPPPP1PTY TTTTTPSGGRRPTALEPCTFHRFLLGP  FSGSBEDFQDLLHGREDARAEKLINGTT GGRKILSVNATAARVATNKKTGNPYTNGKRUNTPVAGATGSPVYTTR GGRYSTPFONSVPPP1PRGSSLGFFCTREDSAFRYTTYTT TTTTPSGGRRPTALEPCTFHRFLLGP  FSGSBEDFQDLLHGREDARAEKLINGTT TDPAKTLGTPLLCPMBDVPLLEBCHLCKKTANTSTASSSDKLINLTYTT TDPAKTLGTPLLCPMBDVPLLEBPLLCKKTAHRRLTVLIPLEDC VTACCSGFTCTWGDRGKVYSPPD  GROWTFONSVPPPLATMATGGEKKRSSSSSMUNDATAAS SKRATILSLIDBRKERHERBCHKNINSHGATSKSSDK	1			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKTL
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GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASG SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKT TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDC VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIE KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	1	1		SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKT TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIPLEDCO VTACQEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDTIQGTWFLNGEELKSNEPECQVEPGALRYRIE KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEBSEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	1	l		
TDPAKTLGTPLCPRMBDVPLLEPLICKKIAHERLTVLIPLEDCO VTACOEGFICTWGRPGKVVSFNP  6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIE KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEBSEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	Į.	i i		
VTACQEGFICTWGRPGKVVSFNP  6812  4001  1682  EDAVFSLDLSTIIQGTWFINGEELKSNEPECQVEPGALRYRIE  KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI  SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL  VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP  HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	I	ļ		
6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIE KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV				
KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHI SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	6000			
SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	6812	4001	1682	EDAVFSLDLSTIIQGTWFLNGEELKSNEPECQVEPGALRYRIEQ
SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESEL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV				KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL
VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPP HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV				
HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEV	İ	1	!	
		i		
ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVT	1			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
				TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
. EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASF	1	l i		
	l .			
			•	
i i			•	VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
FFTVTVTEPPVOFLALETTPSPLCVAPGEPVVLSCELSRAGAP			•	VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA

SEQ	Predicted	Predicted end	Imino poid someth and in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<u> </u>		VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
Ì	Į	ļ	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
j	j	į.	LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
l	-	1	GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
1			CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
ļ	1	-	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
i		1	MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
****	_		LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
1		}	QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGOVYNNLHLLS
			QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
ļ			
1	ŀ		TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
			LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
		/ / /	LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
Į.		i,	CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
			TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
1	<b>i</b> :		NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGOGAMFRLPTD
			SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
]		333	DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
			POEPPNPRMKRASSLNFLNKSVEEPTOPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
	1		PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
1	1		SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
l	1		LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
1			TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
	i i		VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
[	}		GRSK
6817	172	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
	]		DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
			NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
j			IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
	1 1		LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
			TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
			ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
	l i		CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL
	į l		FLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHF
			GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
			EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
			KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
			KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
			HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
			AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
	İ		VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
	4	·	LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLONO
			SLKENOKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
			VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
			SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
			EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE
	,		QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
	Į.		QTHEEILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
			EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL
	ł	ı	
6818	2	240	ESPMKTDIFDEFFSSSALMALANDTLDLPHFDEYLFENY RGFDKVLWT/LSGAVK\CVOFSRISPDGEEGYPGELKVWVTYTL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 40.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	ł	Codon, /=possible nucleotide deletion,
1	[	sequence	
ļ	sequence		\=possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
1	}		GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
1	i		YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
	1		TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
1	ļ	İ	EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
1	ĺ		DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
ł	i	ĺ	DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
1			PNLWTDMTLVLH '
6820	1014	340	GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
1	l .	1	GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
j	J		GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
1			QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
1	Ì		VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
		i	LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
1		1	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
1		}	FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
	1	1	GOPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
		1	GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIOSPON
0022	1000	1 310	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
		-	FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1	Į.	-	
1			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
6823	654	221	GSVIEVLQRRQEGLAS
6623	854	221	PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC
	1		GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE
		1	YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLPLLLTQFGFRG
0024	838	104	ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
1	1	i	NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
		1	l .
1	1	1	LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
1	1	1	WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
6825		l	AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
0825	3	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
1		1	PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
1			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
1		1	KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
		I	GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
			IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
		1	VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
		J	TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
	L		PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
1			LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
1			NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
1		1	DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
1		1	PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
1			RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIERDKS
i			VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSÄAVNREYYRQQME
1			EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK
1			GSSSDSTAGVKE
<u> </u>	<del></del>	<del></del>	

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion) .
6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
			ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSOHPPALAPPG
,		}	HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
1	]		LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL
1	į		GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVEMLPALFPSS
6828			GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
0020	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
1			LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
			QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
			IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
1	1		HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
1	}		TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
.1			DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
1			FLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
1			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
			FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE
ł			ICALROTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
			KFKSSMHLQLTCFQAASSTMMKT
6829	1	782 .	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
į .			EQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
1			KLVLDKDMAEEGVLEEAEFYNIGPLIRIIKDRMEEKDYTVTQVP
			PKHVYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
			QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
6830	1	939	EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
	*	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
i i			RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
			CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
] .			RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
1			ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
1 1			DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
L			LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
			NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
	1		VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL
1			EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
1 1	]		SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE
] [	İ		SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK
1	1		LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS
1 1	I		NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
6832	1809	412	SEKEKDEKKKK
		****	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV
	ŀ	}	VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF
1 1			CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PPLPKYYCLISCIGCECLESVILDEVERPHONOMYTHDDAGAS
1			PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
			LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY
1			PFSWAHTYIPVVPESILATVCCPTPFMVGVQMRFQQEVMDSPME
j [			EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
			AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK
1 1			ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
I			YEEQKKQ/TETKGKNCEIRAVVNKVD
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
	ì	1	VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
LL			QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

No. mucleotide   location   corresponding   corresponding   corresponding   corresponding   corresponding   cofirst   maino acid   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   re	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No.   nuclectide   cortesponding   corresponding   to first   amino acid   residue of   amino acid   residue of   amino acid   sequence   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine,   Percline, Q-Glutamine, R-Asparagine, Percline, R-Rasparagine, Q-Rasparagine, Q-Rasparagine, percline, R-Rasparagine, percline, R-Rasparagine, R-Rasparagine, R-Rasparagine, R-Rasparagine, R-R	ID	I .	I .	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Cocresponding to first amino acid amino acid residue of amino acid amino acid residue of amino acid sequence   Scaries of amino acid sequence   Scaries of amino acid sequence   Scaries of amino acid sequence   Scaries of amino acid sequence   Scaries of amino acid sequence   Scaries of amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino acid sequence   Scaries of Amino ac	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of residue of residue of amino acid sequence sidue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen				L=Leucine, M=Methionine, N=Asparagine,
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amino acid sequence   Codon, /-possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide insertion     -possible nucleotide	1			
Sequence   \=possible nuclectide insertion	1			
NALVFYFSWKGCSSGDFCVNPCFPDPCKAFVEITNTHASVEE   GPCWILVIDEPTLCVWWCLLMYTTYPLKESALILLQTYPKQII   TRNLIKELRNVEQUEVHELHWOLAGSRIIATAHIKCEDPYS-   MEVAKTIKOVPHNIGIHATTIOPERAJSKSSVVPCELACRY   CALKQCCCTL-QAPSGKDAEKTPAVSISCLELSNNLEKKPRRT.   AENIPA\VVIEIRN\1 PINK\0 PESSL   \0 PESSL   AENIPA\VVIEIRN\1 PINK\0 PESSL   AENIPA\VVIEIRN\1 PINK\0 PESSL   AENIPA\VVIEIRN\1 PINK\0 PESSL   AENIPA\VVIEIRN\1 PINK\0 PESSL   AENIPA\VVIEIRN\1 PINK\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AENIPA\0 PESSL   AURUSTIALIAN PESSL   ANDAVEDCOLORIA PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL   AURUSTIALIAN PESSL			sequence	Codon, /=possible nucleotide deletion,
GPCWULYLDPTLCVVMVCILLYTTYPLLKSSALILLQTVPKQLI IRNILKELRNWSGVESVHERHWOLAGSRITATHAIRCEDPTS' MEVAKTIKDVPHNHGIHATTIQPEPASVGSKSSVVPCELACRTY CALKQCCGTLPQAPSGCRASRITATHAIRCEDPTS' MEVAKTIKDVPHNHGIHATTIQPEPASVGSKSSVVPCELACRTY CALKQCCGTLPQAPSGCRASRITATHAIRCEDPTS' ABRIPA\VVIEIKA\IPNK\QPESSLEDNMLEKKPRRTI' ABRIPA\VVIEIKA\IPNK\QPESSKABEAHIPINR*GA***RGGLI LCGSSASANGHH*RILMPTFSVSKABEAHIPINR*GA***RGGLI LCGSSASANGHH*RILMPTFSVSKABEAHIPINR*GA***RGGLI CSKLVLSGARGIVGTTVQVLVBAQQPLLLLFTGYWGLNLRAGEI SRAI**LIEEVTQVRDAHIGRAVVCGLSGQGVGSALKALL AAAAVRDCKEVLTVSGDKQQAEVSVPL*VRDVCBEAGCVEFGG AHGRPGLALLAKGRGGTGNEVEGQVQVDGVQKLVLSAHEGLELVAA QQDGEDQAARTHLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHI LQQVVGDALAKRGTEVEGQVQVDGVQKLVLSAHEGLELVAA QQDGEDQAARTHLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHI LQQVVGDALARE**APQTIVLLLLEDVAQRTCKKA**DLVVDVV QLLRACL AAYTCYRPDVGVVQCMS*FIAAVLLIALDTADAFTAFSNLINKPCC MAFFRVDHGLHLTVPAAFEVPFEENLPKLFAHFKKNNLTPDIY IDNIFTLYSKSLPLDLACRIBWPCFCDGEBFLFFTALGIKLF, DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMGSRNKKW QVLTALQKDSREMREGKSVPPTLRLOREFALGTINGSEMFRPLC: FRLTPGGPRRTDAL  ### MSCGRPPPTVGGMTTLKV\DNLTYRTSPDSLERVFEKYGRVCDV YIPREPHTKAPRGFAFVFRHDRDAQDAEAMIGAELOGRELIC QVARYGRRDLPRSRQGRHHAAGFEAA, RYGGRRSSGYRSSSY RSRSSTSKSSSANRSSSSYNSRSTSRSSSSSMTSSRSTSRSSSSMTSSRSTSRSSSSMTSSPRVSKKK KSRSRYBESKYGGSHYSSSGYSNSRYSSHVSSRYSSRSYSSRYSSRYSSRYSSRYSSRYSSRYSSRYSS		Sequence	<u> </u>	
TRNLIKELENVEGVEEVHELHUVOLAGSRIJATAHIRCEDPTS  MEVAKTIKOVENINGLIHATTIOPENSVGKSSVYOCELACRY CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSINNLEKKPRRTI AEMIPA\VVIEIKA\INNK\QPESSL  AGGERPAPIKULLINHPTSVSKRKAEPAHIPINR*GA*E*RGGL LCGSSASAYGHI*RLTPHSSVGKAEPAHIPINR*GA*E*RGGL LCGSSASAYGHI*RLTPHSSVGCG*HM*SKRYDTQAREVLVAGI CSKLVLSGARGIVGTVQVLUEAQOQUELLLETGYMGLNIRAGEI SRALI*LIEEVTQVRDAHLGHAVVGCAQCLSGQOGGSALAKALLL AANAVEDCKEVLTVSGKQQAEVSVAL*VPDVCVEERAGCVEFGG AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVA QQDGEDQAARTRLLQAGAHSVAHGRQGQAPCHEGKAS*DLVDVU OLLRQL  GEBADADR\EASLELIKLDISRTFPNLCIFQGGGPYHDMLHSILA AYTCYRPDUGYVQCMSFIRAVLILINLDTADAFTAFSNLINKDC MAFFROMDELMITTYAAPEVPFERLIPLIPHAFHEKKINLIPDIY IDMIPTLYSKSLPLDLAGRIMDVFCRDGEBFLPFTALGILKLFI DILTKMDFIHMAGPLTRLPEDLPAEELFASIATIQMGSRIKKM QVUTALQKDSREMREGKSVPPTLRLQREFALGTINGSPMRRELC FRLTFGQPRRTDAL  MSCGRPPPVDUGMITTLKV\DNLTYRTSPDSLRRVFEKYGRVGD YIPREHTRAPRGFAFVFFEURDAQDAEAMMGAELDGRELRF PYSSRYPESPYGGGRRHAAGPENAYHSGRSSKSGSSTS SRSASTSKSSSARRSKSSVSSRSFSSSSTSSSSTSSSSSTSSSSSTSSSSTSSSSSTSSSSSTSSSS			<u> </u>	
MEVAKTIKDVFNINGIHATIOPEPASVGSKSSVVECLACRY CALKQCCGTLPQAPSGKDAKTPAJSCLELISINNLEKKPRRT AENIPA\VVIEIKN\IPNK\QPESSL  6834  78  1151  AGGERFAFIWRLIWLFTFSVSKRAEPHIFINR*GA**RGGL LCGSSASAYGMI*RILWLFTFSVSKRAEPHIFINR*GA**RGGL CSKLVLSGARGTVGTTVQVLVBQQPLLLLFTGVWGLNLRAGEI SRAL*LIEEVTQVRDAHLGRAVVGCQCLGSQGVGSALKALLL AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVERAGCVEFGG AHGRFGLALAKGGTGNEVEGVQVDGVQKLVLSAHECHELVAG QODGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAQVSCH LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVI OLLROL  6835  1  834  GIPAADR*EASLELIKLDISRTFFPNLCTFQQGGPYHDMLHSTIL AYTCYRPDVGTVQCMSFIAAVLILALDTADAFAFSNLINKPC MAFFRVDHGLMLTYPAAFEVFFEENLPKLFAHFKKNNLTPDIY IDNIFTLYSKSLPLDLACRIBOVFCRDGERFLFKKNNLTPDIY IDNIFTLYSKSLPLDLACRIBOVFCRDGERFLFKKNNLTPDIY OVLTALQKOSERMREGKSVPPTTLRGFTGAGFAGSNKKNN OVLTALQKOSERMREGKSVPPTTLRGFTGAGFAGTNGSFMFRPLC FRITFGOPRRTDAL MSGGRPPDVDGMTTLKV\DNUTYRFTSDESLRVPFKYGKVGDV YIJPEHHTKAPPGFAFVFFEURRDAQDAEAMDGAELDGRELRY QVARYGRRDLPRSGGSVPTTRLSFFAGTINGSFMFRPLC FRITFGOPRRTDAL MSGGRPFPDVDGMTTLKV\DNUTYRFTSDESLRVPFKYGKVGDV YIJPEHHTKAPPGFAFVFFURRDAQDAEAMDGAELDGRELRY QVARYGRRDLPRSGGSVPTTLSFTSGNSSFMSSSFNSSFNSSF RSSSTSKSSSANSSSSVSNSSYSSFYSSSFYSSSFYSSRFYSRFYSR PYSRSKYRESKYGGSHYSSSGYSNSKYSKHYSKSSSSKNSSGSST SRSSTSKSSSANSSSSVSNSSYSSFYSSSFYSSSFYSSRFYSRFYSR PYSRSKYRESKYGGSHYSSSGYSNSKYSKHYSKSSSKSKSGSST SRSSTSKSSSANSSSSSVSNSSYSSKYSSSFYSSSFYSSSFYNSKFYSK KSSSRSSTSKSSSSNNSSSSSSNSRSSSMTNSSPHVSKK KSSSRSFRPSSSSSSNSSSSSSSSSSTRSSSSMTSSPHVSKK KSSSRSFRPSSSSSNDPQALVKARSSSGSSSG GHYSPGTFBDKYSAAPDSGGAGAVGSAQGAGAGASADGS GHYSPGTFBDKYSAAPDSGGAGAVGSAQGAGAGASADGS GHYSPGTFBDKYSAAPDSGGAGAVGSAQGAGAGAGASADGS GHYSPGTFBDKYSAAPDSGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				
CALKQCCGTLPQAPSGKDAEKTPAVSISCBLSNNLEKKPRT: AENIPAVYTEIKN\IPNK\QPESSI  AENIPAVYTEIKN\IPNK\QPESSI  AGGERPAFWRILWLETFSVSKAEPAHIPINR*GA*E*RGGLI LCGSSASAYGWH*RITPHSPGGS*HM*SSKAPYTQAREVLVAGI CSKLVLISGARGI (VGTTVQULVEAQOPLLLLFTGVMICHLARGE) SRAL*LIEEVTQVRDAHLGNAVVGCQCLSQGVGSALAKALL AAAAVRDCKEVLTVASDKQQAEVH.VBQVCVERGCVEFGG AHGRPGLALAKGRGTNEVECVQVDGVQKLVLSAHECHELVAR QOGGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHI LQQVVGDAL*ARE*APQIIVLLLEDVAQGRTGKRA*DLVVDVV QLLRQL  6835  1 834 GIPAADR\EASLELTKLDISRTFFNLCIFQQGGPYHDMLHSILA AYTCYRPDVGYVQGMSFLAAVLILINLDTAAPIAFSNLLINKPC WAFFRVDHGIMLTYPAAFEVFFENKRINLTPPDIV IDWIFTLYSKSLPLDLAGCHDVFCRDGESFLFRTALGILKLFI DILTKMDFHHMGPTTTRPEDLENKRLAHEKKNITPPDIV IDWIFTLYSKSLPLDLAGCHDVFCRDGESFLFFRTALGILKLFI OUTALQKUSERMREGKSVPPTLRQREFALGTNQSPMPRPLC  FRITPGOPRITDAL  6836  1 850 MSCGRPPPDVDGMTTLRVDLDLAKRAHEKKNITPDSLRRVFKKW QVALTALQKUSERMREGKSVPPTLRQREFALGTNQSPMPRPLC VARYGRRDLPRSRGGRHAAGGFAVAYGRRSRSFGKRSSRSF RRHRSSRSGRSGSGSRSRSRSRYSRGSFSFSRSVGKSRSFFSRSFSFSRSFSFSRSFSFSFSFSFSFSFSFSFSF		ļ	1	
AENIPA\VVIEIKN\1PRK\0PESSI AGQERPAPIWRLLMLPTPSVSRKAEPAHIPINR*GA*E*RGGL LCGSSASATGMI*RLTPPSVSRKAEPAHIPINR*GA*E*RGGL CSKLVLSGARGIVGTTVQVLVEAQOPLLLLPTGVWGLMLRAGE SRAL*L1EEVTQVDAHLGANVACAQCLSQGQVGSALAKALL AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFG AHGRPGLALAKGRGTNSVEEQVGGVGVKLVLSARIECHELVAA QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHI LQQVVGDAL*ARE*APQITVLLLLEDVAGGRTGKKA*DLVVDVI QLURQL GBSS  1 834 GIPAADR\ESSLELTKLDISRTFFNLCIFQQGGPYHDMLHSILA AYTCYRPDVGYVQGMSFIAAVLLINLDTDADAFIAFSNLINRQC MAFFRUDHGLMLTYPAAPEVFPEENLEKLEHAFKKNNITPDIYI IDMI\$TTLYSKSJEDLDLACRIHOVFGGEFFJERTALGILKLFI DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKWM QVUTALQKDSREWRBGKSVPFTLRLGREFALGTNGSPMPRLC GRUNDFITTHGOPRITDAL VIPREPHTVAPKSJEDLACRIHOVADAEAAMGABLLORELRY QVARYGRRDLPRSGCSRRAGAGDAEAAMGABLLORELRY QVARYGRRDLPRSGCSRRAGAGSVSRYSRYSRSSSKYRSSP RRHRSSRGPSGSRSSSSYRXGSSYSRSSYRSHSSSSSKSSSSF RSSASTSKSSSARRSKSSSVSRSSRSRSSSSTRSPSSSVSRSS SRSASTSKSSSARRSKSSVSRSKSRSRSSSSTRSPPRVSRRYSR PYSRSRYPESRYGGSHYSSGYSNSRYSRYHSSSSSKASG PYSRSRYPESRYGGSHYSSGYSNSRYSRYHSSPSSSSKASG SRSASTSKSSSARRSKSSSVSRSSSSSFTRSPPRVSRRYSR PSSRSKRPFKSPEEGQMSS  6837 1 1369 TDGAAVAGNGSDYPFGGTAP/GGPRTRRP\SGTSSSGKASG GNYSPGTPFDKYSAAPDSGGAPGVSPGQQASGAAVGGSSAGE RGAPTPHEKALTSPSWGKGAELLLGQPDLIGSLDGGAKGDSS GNYGEFASDEVSTSVANDEDVSSSSDNPQALVKASRSPLVTGSI KLPPRGVGAGERGPKAPPPAGGLIHNDESTSTDSVGGGGGGG GHVSPGTFFDKYSAAPBGGGAPGVSPGQQASGAAVGGSSAGE RGAPTPHEKALTSPSWGKGAELLLGQPDLIGSLDGGAKGDSS KLPPRGVGAGERGPKAPPPAGGLIHNDESTSTDSVGGGGGGG GFUSPGTFGLGQVRTTISTSSGAPPBGLGSCSCSEAVKSAMST DLDSLMAEHSAAWMPADKALUQCLQQVDLIG LQQQFSIL SLHBDLSNRFGTFVAALT  6838 16 499 LTDTPPPRHTHHHSISDYKATLRCWALGFYPMEITLTWQQDEI DQTRDMELVETTPAGGGTFQWAAVVORDSEB/Q/RYMCHVQHU GLEPPLTLRWEGSGPTTPIVGTGSBPPQVKRLDALLSEPIDING GLEPPLTLRWEGSGPTTPIVGTGSBPPQVKRLDALLSEPIDING GLEPPLTLRWEGSGPTTPIVGTGSBPPQVKRLDALLSEPIDING GRAGGGPPBEALSAFFGRUNGSGSPOVERLDALLSEPIDING GRAGGSPPEALSAFFGRUNGSGSPOVERLDALLSEPIDING GRAGGSPPEALGARDALRSAFFGULTGARVVLACLLDFLDAG SRAKTYPLTLKEARAGGTYDFACKLYCTDSDRSLISLSKSGKNVEH HPSSGLGYKUDLDVRRMDLRSEASFGLTKAVVLACLLDFLDAG SRAKTYPLTLKEARAYQKLVXVCTDSDRSLISLSKSGKNVEH				
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PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSI KLPPRGVGAGEHGPKAPPPALGIGIMSNSTSTPDSYGGGGPGIP PGTPGLEQVRTPTSSGAPPPDEIIPLEIIQAQIQLQRQQFSIS EDQPLGLKGGKKGECAVGASGAQNGDSELGSCCSEAVKSAMST: DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPMS KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWI SLHSDISNRFGTFVAALT  6838 16 499 LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEI DQTRDMELVETRPAGDGTFQKWAAVVVPSGEB/Q/RYMCHVQHI GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVW RKKNSDRVSYSEAASSDHAQGSDVSLTACKV  6839 1 1195 AAPAGGGPDEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIH RGMFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVI HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGT SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELI	]			GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
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RGNFPTLSVQPRQIRAGGPQHPGGAG\IHV!RVRLHGSAASHVI HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAG SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVBLH	6930			
HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAG\ SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK	6839	<u> </u>	1195	
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	1			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
	]			PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
				AARRYACLVTLHRVVNESTVCLMNHERROTLDLIAALALQALAE
	]			QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
CN				
	6840	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNV	L	L		FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEQ	Predicted	Predicted end	l Deci-
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
Į	location	corresponding	H=H1Stidine, I=Isoleucine K=Lysine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine.
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	1-4.0	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<del>                                     </del>	TDIPVAMEHOPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
		İ	TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
- [		İ	EMKDDSDSEKQQQIHHIKNLYAFNLFCOKRFDESMOVFAKIGTD
[			PTHVMGLYPDLLPTDYRKOLOYPNPLPVI.SGAELEKAHLALTDY
1		1	LTQKRSQLVKKLNDSDHOSSTSPLMEGTPTIKSKKKILOTIDTT
1			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKVSFT.TT
ĺ	1		LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
ı			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
1	1		SFPAGKTPVPAGEEGELGEYRQKLLMFLEISSYYDPGRLICDF
			PFDGLLEERALLLGRMGKHEOALFIYVHILKDTRMAREYCHKHY
			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLONA
i		ľ	LQVLELHHSKLDTTKALNLLPANTOINDIRIFIEKULFENDOKY
ł			RFNQVLKNLLHAEFLRV\OEERILHOOVKCITTEEKVCMVCKKK
6841	1	3206	IGNSAFARYPNGVVVHYFCS\KEVNPADT TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
			REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
i			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
1	J		VDEGADLLGEFSGMGKEVGNLLLENSOLLRTKNAL NAVKNDLTA
i			KVDQLSGEQEVLRGELEAAKOAKVKLENRIKELEEELKPVKSEA
1			IIARREPKEEAEDVSSYLCTESDKIPMAORRETRVEMARVI MR
ŀ	. 1		RNOYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
ł			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
1	}		SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
'	f .		AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
			PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANOPGTVAD
			QFTVCNAHVLCISSIPAASDSDYPPGFMFLDSDVNDFDDGADGV
J	ŀ		LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
1			NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
			AONGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSTRCMAUZVDPVWCG
			YKNKVHVIQPKTMQIEKSFDAHPRRESOVROLAWIGDGUMUSIB
1 1			LUSTLKLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRTTAI
1 1	. [		LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
1			TSGEG\ARPGG\IHVYG\DDSSDRAARSFIPYCSMAQAQLCFH GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
1 1			KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
6842			ERSHIIVWQVSYTPE
0042	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
	1		RKLFQSVKLHCPKCHLLOEVPHEGDIDITFODGATKTPDVKLON
	ļ		TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAFFLIQGTVHHYGC KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
			LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMPC
F-6043			PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPVECSE
		l	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRESSLLOHOP
			VHTRERPYECSECGKSFSLRSNLIHHORVHTGERHECGOCGKSF
	ſ	·	SKKSSLI IHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
	1	ĺ	RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
			LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPLSLVTTIFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
			QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
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NO:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Cortesponding to first   Selection   Selection   Helicidine, I-Isoleucine, Kelysine, Leleucine, Kelysine, Corresponding to first   Selection, Kelysine, Leleucine, Mambethionine, NaBaparagine, seldue of amino acid   Sequence   Seserine, T-Threonine, V-Valine, Seserine, T-Threonine, V-Valine, Sequence   Sequence   Seserine, T-Threonine, V-Valine, V-Valine, V-Valine, Sequence   Seserine, T-Threonine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V	ID	beginning		(A=Alanine, C=Cvateine D=Aspartic Acid R=
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VVFGCTGFFVTRAGVTPDPUCLSGISKVSVGGIFYGNKLNFSF SEBSVTVEVTRAGOPHAPHLARELMPSQSRLSILDGHKVSFPRS AGRIQMSPPKLPGSSSSEPPGRTFDVRDPLGSPLMVTLGSSSP TESLTUDDASFPSGTGASETSLGPSLMFRLHPPLLGTLLACHSP PAARLSGKVHAAMDEFKAPCL  (17FLKTIK-LNRLAEHP*TENEKLTKLRNTIMEQTTRTEESARG ITFIKTRGSAYALSQM'TISNEKFABCVSKAHHLIGAGHSSEFKP MTONEOKSVISKFRTGKINLLIATTVAEGGLDIKEKRKVTRYTEE VTREIAMVQARGRARADESTVULVAHSGSGVIEHETVUDFREEM MYKAJHCVQNMKPBEYAHKILELOMOSIMEKKMKYKRNIAKHYK NNSSLITPLCKNCSVLAGGEDIHVIENSGGVIEHETVUDFREEM MYKAJHCVQNMKPBEYAHKILELOMOSIMEKKMKYKKRNIAKHYK NNSSLITPLCKNCSVLAGGEDIHVIENSGCUFSBED  6847  1450  348  SMCWNSDRIEMPLIDLALILTYPSSVPYTGHISDBSLSRKYCLT RENKTLQKKCADVQINGEIICKCQAMGTMMYHKGIDLPCLKTR NFVVVFKNNSTKKQYKKWLEPITFPNISCCUFSBED  FYFOFELAKKVLQBEPWLDDSYSEVLQRENGVALRCP PGAVRSLDALGWERGPLALVKLLLAKHYPOGKAVVGAVLESDP YFGFELAKKLQBEPWLDDSYSEVLQRENGVALRCP PGAVRSLDALGWERGPLALVKLLLAKPUGAKVPGAVLESDP YFGFELAKKLQBEPWLDSYSEVLQRIKGPHKCALIFADNSG IDIILGVFFFYRELLLROTEVILACNSGPALMOVTHSESIIVAG RIAGMPPVVHSARREELLLVOTGSVSLOSDLICHDALDSND  LKVIIISAGDLAVKSLLAKPUGAKVAVLSUDSDLICHDALDSND  LKVIIISAGDLAVSENGRAVHTYHHAALRCSSKIKLAVIKNAWLAERIG GRAFSVIFKYEVPAE  6848  19  16  AMMINSLOSIENTVLSNPKKRNTLSLAMLKSLOSDLIHDADSND LKVIIISAGPVFSSGHDLKEITERGGROVHAEVFOTCSKYMMH IRRHPVPVIAMVNGLATAAGCGUVASCDIAVASDKSSFATTGVN VGLFCSTFOVALLARAVPKVALEKEPISAGDENGVEVSHEPV-VER VGLFSTOVALARAVPKVALEKEPISAGDENGVEVSHEPV-VER  6849  70  821  SLGVGGSCLEGGSBAPEPOTTTSP PYGNNATOGEDLYHGSYEC VCULFASVADKSKINDVINKISFNNERLRVCLANGIIGHKWYVERP VFRISCUSERIKTIGSTYMAATGLNATSGODAQODAERSCSHLCTM VEPAVALGSKLDVINKISFNNERLRVCLANGEISAPVENKMI GLESKBELRHLKILHVKSNLTKUPSNTTDHPHITKLVIINDGT KLLIVUNSKKOGQLCTYFLANDLTRTGPPSATLG  RGCHMEENTFFEKKGRUFSKANQOKGELHLIFMLSGVPDAVFDLTD LOVIKLELIPPAKTIGHNINGVINTIPPSITHVKRILESL VFRINKLESLEDAVAYFSKIRANGOKGELHIFENISHINIGIDLISK NNIRTIEEIISFORLIKKHYSTDATSHINIH TEISININGELDLIKK NNIRTIEEIISFORLIKKHYSTDATSHINIH TEISININGELDLIKK NNIRTIEEIISFORLIKKHYSTDATSHINIH TEISININGELDLIKK NNIRTIEEIISFORLIKKHYSTDATSHINIH TEISININGELDLIKK NNIRTIEEIISFORLIKKHYSTDATSHINIH TEISININGELDLIKS NNIRTIEEIISFORLICHLIKKHYTUNGHETSINNIH GLESK		ļ		
SEBSYTVEYTARAGPWAPHLEAELWPSOGRISLLICHKVSFPPS AGRIOMSPPKLPGSSSSEPFCRTFDVRDPLOSPLWTLGSSSP TESLTUDPASP'SGTGASETSLGPSLWPRLHPPLLGTLLACHPS PARLEGKVHAMWPEFKAPCL  LYFLKTIK'LNRICHEPP'YENEKLTKLRNTIMEGYTRTEESARG IIFTKTROSAYALSGWITEMEKPACVGWKAHLLIGAGHSSEFKP MICNEGKEVISKFRTGKINLLIATTVAEGGIJIKECKIVITKYGL VTMEIAMVQARGRARADESTVUVAHSGSGVIEHETVNDPREKM MYKAILKVONMKPEFYAHKILELGNGTMEKMHYKNILACHKY NNPSLTTFLCKRCSVLACSGGDLHVIEKMHYWNTPEFKELTV RENKTLCKKCADVGINGEITCKCGAMTMWHKGLDLPCLKTR NFWVVEKNISTKKQVKKWVGHFITFDNLDYSECCLFSDED SCHMISDRIEMBELIDLALILTYPPYYGHLSDDSLSRKYCLT WFEDALINGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKICOTTRQ PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVCRERGVALRCF PGVVRSLDALGWEERGLALVKGLLAGNVEDWGAKAVSAVLESDP YFOFEEAKRKLQERPWLVDSYSBWLQRLKGPPHKCALIFADNSG IDIILGVPFFVRELLLGRTEVILAGFSLKLAVIKMALAERLG GRIFSVIFKYEVPAE  6848  19 16 AMWINDLOTINIVLSNPKKRNTLSLAMLKSLGSDILHDADSND LKVIIISABGPVFSSGHDLKELTEEGGRDYHAEVFCCSKVWHH IRNHPUVVIAMVNGLATAAGCQLVASCODIAVASDKSSFATPGVN VOLFCSTROVALARRVPRKVALEMLFTGEPISAGCALLGLIKK VVPEABLOEETMRIAKRIASLSRPVVSLGKATFYKQLPQOLGTA YHISGAMVDHLALBACGGGITAFKKPFWSHEPV*VEH  6849 70 821 SLEVDGSCLEGGSPAPRPOTOTSP*PVGNRMTYGQEDLYHGSYSC VCLFRSAVDVBLEKGRENGLIKGRILHDEILGKF PKPSGVEKIKTIGSTYMAATGLARTGQDAQDAERSCSHLGTM VEFAVALGSKLDVIKNISFNRFRLARTGQEDLYHGSYSC VCLFRSATUPSSNTHMSTGRILDGRICHLINEILDFBLLSK PKPSGVEKIKTIGSTYMAATGLARTGQDAQDAERSCSHLGTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VEFAVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VERVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VERVALGSKLDVIKNISFNRFRLARTGGENDADAERCSCHLTM VERVALGSKLDVIKNISHVERTERLEDHADAERCHLTMSHNINTHTEITGL		,		
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PARALSGKVHAAMPERKAPCL  6846  213  1258  LYFLKTIK LINICAEHP *VENEKLTKLENTIMEGYTRTEESARG LIFTKTRGSAYALSGWITENEKFAEUGVKAHHLIGAGHSSEPKP MITONEGKEVISKFRTGKINLLIATIVAEEGDILKECNIVIRYGL VTNEIBAWQARGARADESTYUVAHSGSGVIEBETVINDPREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKHKTKRILAKHYK NNPSLITFLCKNCSVLACSGEDIVIEBETVINDPREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKHKTKRILAKHYK NNPSLITFLCKNCSVLACVAGEDIVIEBETMINTPEREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKHKTKRILAKHYK NNPSLITFLCKNCSVLACVAGEDIVIEBETMINTPEREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKHKTKRILAKHYK NNPSLITFLCKNCSVLACVAGEDIVIEBEMKHKTKRILAKHYK NPSVLYVENNSTIKKOYKKWEUPIPPINLDYSECCLPSDED  6847  1450  348  SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT WFEDDALNGVL*REAPLIDVSYCRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP PFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFPPDYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVFDWGAKAVSAVLESDP FFAYGTLTVRSLIDTTEHCLAFTENDPYSKYRCHALACT ERGADLVVLEGMGRAVHTNYHAALKCESLKLAVIKNAWLAERLG GRLFSVIFFXEVPAB  6848  19 16  AMMWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVILISABGPVFSSCHOLKELTEQGROWHAEVFOTCSKVMMH VOEFASLOFENTHIARKTASLSPVSLGKATETYKQLAPGLOFTSTWAM VVEFASLOFENTHIARKTASLSPVSLGKATETYKQLAPGLOFTSTWAM VVEFASLOFENTHIARKTASLSPVSLGKATETYKQLAPGLOFTSTWAM VVEFASLOFENTHIARKTASLSPVSLGKATETYKQLAPGLOFTSTWAM VVEFASLOFTSTWAMATCHANTSGOODOLATHASTYCLOPGLAYNOTYCYSG VVLKASVADSKATETYTHATTYTTATATATATATATATATATATATATATATAT	1	i		AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
1256		1		TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
I ITTKTRGSAYALSOW TENEKHAEVGUVANHILIGAGHSSEFEP MTONECKEUYISKERTGKINLLIATIVABEGIDI KECNIVIRYGL VTNE IAMVQARGARADESTYUVAHSGSGVI EBETVINDFREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKMKTKRIN IAKHYK NNPSLITFILCKOSVILAGGEDIUSEKKMKTKRIN IAKHYK NNPSLITFILCKOSVILAGGEDIUSEKCHAEVGUVIRGELIPTOREM MYKAIHCVONMKPEEYAHKILELOMOSIMEKKMKTKRIN IAKHYK NNPSLITFILCKOSVILAGGEDIUSEKCHAEVGUVIRGELIPTORELDSECLESDED  6847 1450 348 SMCWNSDRIEMFILDLAILIYPPSVPYTGHLSDSISKRYCLT WFEDALNGVI*REALIPTORUNSTKKQYKKWWELPITFPILDSSICSRYCLT WFEDALNGVI*REALIPTORUNSCHEROKYKWINLCTIRGO PFAYGTITVRSLIDITEHCLEFEPPPDYSKVKYCRENGVALROP PFAYGTITVRSLIDITEHCLEFEPPPDYSKVKYCRENGVALROP PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEARRALGERWILDVSSEMLQRIKGPPHKCALIFADNSG IDIILGVPFFVRELLIKGTEVILLOTGSSSFCLDLSRLDKGLAALVR RIAGMDPVVHSALREERILLUQTGSSSFCLDLSRLDKGLAALVR RIAGMDPVVHSALREERILLUQTGSSSFCLDLSRLDKGLAALVR RIAGMDPVVHSALREERILLUQTGSSSFCLDLSRLDKGLAALVR RIAGMDPVVHSALREERILLUQTGSSSFCLDLSRLDKGLAALVR RIAGMDPVVHSALREERILLUQTGSSSFCLDLSRLDKGLAALVR GRIFSVIFFYEVPAE  AMMINSLOGIRNIVLSNPKKRNTISLAMLKSLQSDILHDADSND LKVI ILSAEGPVFSSGHDLKELITEQGRONHABVFCTGCSKVMMH IRNHPVPVI AMVNGLATAAGCQLVASCDLAVASDKSSFATFGVN VGLFCSTFQVALAALROGGETIALFTGTGPISAGPALLHGILINK VVPEABLGETMRIARKLASLSRPVVSLGKATFYKQLPODLGTA YYLTSQAMVONLALROGGETIALKYGUKPEVPV*EH VVPEABLGETMRIARKLASLSRPVVSLGKATFYKQLPODLGTA YYLTSQAMVONLALROGGGTTALKKPUWHSPEPV*VEH VEFAVALGSKLDVINKHSFINFRILRVGLINIGFVVAGVIGAQKPQ VDLWGATTVAVASRMSSTGVLGKUTSEQDAQDERSCSHLIGTM VEFAVALGSKLDVINKHSFINFRILRVGLINIGFVVAGVIGAQKPQ VDLWGATTVAVASRMSSTGVLGKUTSETAMAJGLGGYTCYSRG VIKVKGKGGLCTYFINTDLTTRIPPSATLG  6850 2 1235 ARGINIEMTFERKIRCHISRNAQDKQELHLEMLGCPAKVEQTAFFIL ROHLRCLHVKFTDVAETPANVYLLKNILREFLYLIGNINSSNINKH GLESLERHHLKILHVKSNITTVIQEDKTLCHCPAKVEQTAFFIL ROHLRCLHVKFTDVAETPANVYLLKNILREFLYLIGNINSSNINKH GLESLERHHLKILHVKSNITTVIQESTTHVANLESL NINTTIEETISPQHLKRULHVSNITTNIDAPHTIKILVININGT KLLUMSLKKMMNVABLELQNCELERIPHAIPSLSNILQELDLKS NINTTIEETISPQHLKRULHVSNITTNIQGOKTTSLPEKVGGLSQ LTQLELKGRICLDRIPAGGCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINTPPANGI  VSAQVSAREGEROLGWILLBASSGEYKSLEEAEDCYPPFSLLTLD L	ł	ì		PAARLSGKVHAAWPEFKAFCL
IITTKTRGSAYALSGMITENEKFAEVGVARHHLLGAGHSSEPKP MTONEGKEVISKPTCKINLLIVADEGGIJ KECNIVITRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM MYKAIHCVQNMKPEEYAKKILELGMQSIMEKKMKTKRIN LAKHYK NNSSLITFLCKNGVIAGGGDIHVIEKMHVINKTEPKELYIV RENKTLQKKGDYQINGBIICKCGQAMSTMWVHKGLDIPCLKTR NFVVVYEKNISTKKOVYKKWEUPIPTDLDYSECLEPSDED  6847 1450 348 SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT WFEDALNGVI-RAEAIQPHCVNAGDRMEKRGKYVMKLCLTBODD PFAYGTITVTSLLDTEHCLEMFPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERGLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKKKLQERPWLDVSYSCHOLKGRIKVGRENGVALRCF PGVVRSLDALGWEERGLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKKKLQERPWLDVSYSCHOLKSRLWKHKALIFADNSG IDIILGWFPFVRELLLRGTEVILAGNSPBALNDVTHSESLIVAE RIAGMDVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHAALREERLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHAALREERLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHAALREERLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVVHAALREERLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDVHAALREGGGDIAGNEKKPWHSPFOTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDLAVSDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEHLFTGBEISAQEALLHGLLNK VVPEABLQEETHRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLAALROGGGGIAPCKKPVWMSHEPV-VEH 6849 70 821 SLGYDGSCLEGGSPAPRPOTDTSP PVGNNATQGEDLYHGSYBC VCVLFASVPDFKEFYSESNINHEGLERLINEI IADFDELLSK VPERSGVEKIKTIGSTYMAATGLANTSGQDAQQDAERSCSHLGTM VERVALGSKLDVINKHSFNWFRRRUCLINEGVVAGVIGAQKPQ VDIMGNTVHVASRMESTSGVLGKUTSETAWAJGLGYTYSRG VIKVKKKGQLCTYFLINTDLTRIGPPSATLG 6850 2 1235 ARGINHEWTFEKKRCHINTSGPDASCSHLGTM VERVALGSKLDVINKHSFNWFRRRUCLINEGVVAGVIGAQKPQ VIKVKKKGGLCTYFLINTDLTRIGPPSATLG CLESLERHHLKILHVKNDTLYKVPSNTTDVAPHITKILVINNOT KLLVINSLKKMMNVAELBLORCELER PHAIPSLSNLQSLDLKS NNIRTIEBIISPQHLKRHTCLKLWHNKIVTIPPSITHVKNLESL VFSNNKLESLEVAVFSLQKERCLDVSNNISMIPIETIGLGLDLKS NNIRTIEBIISPQHLKRHTCLLKLWHNKIVTIPPSITHVKNLESL VFSNNKLESLEVAVFSLCKRECLDVSNNISMIPIETIGLGLDLKS NNIRTIEBIISPQHLKRHTCLLKLWHNKIVTIPPSITHVKNLESL VFSNNKLESLEVAVFSLCKRECLDVSNNISMIPIETIGLGUPLOH HLHITTONVOLIPPANGI LTOLEKKGLCORLERATERNGL	6846	213	1258	
### MTQNEGKEVISKFRTGKINLLIATTVAEGLDIKECNIVIRYGL VTWE IAMVQARGRARADESTVLVABIGGGCV 12 HEBTVNDF REKM MYKAIHCVQNMKPEYAHKILELQMQSIMEKKMKTKRNIAKHYK NNFSLITFLCKNCSVLACGGEDIHVIEKMHYNMTPEFKELMIV RENKTLQKKCADVQINGEI ICKGQAMGTMWHKGLDLPCLKIR RENKTLQKKCADVQINGEI ICKGQAMGTMWHKGLDLPCLKIR NFVVVERNSTKKQYKKWVELPITFPNLDYSECCLFSDED SMCMNSDRLEMPLIDLAILIYPSYVPYTGHISDDSLSKRYCLTI WFEDALNGVL*RAEAIQPHCVNAGDRMEKERQKYNMKLQTLRQQ PFAYGTLTVRSLLDTREHCLNEFPPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERQLAUVKGLLAGNVEDWGAKAVSAVLESDP YFGFEEAKKKLQERPHLVDSYSEMLQRLKGPPHKCALTFADNSG IDIILGVFPFYERLLLRGTEVLLGNSGPALNDVTHSESLIVAE RIAGMDPVHSALREERLLUVQTGSSSFCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAMLAERLG GRLFSVIFKVEVPAB  16 AMWINSLDGIRRIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSCHDLKELTERGGRDYHAEVFQTCSKVMMH IRNHPVPUIAMVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVLEMETGEPISAQPALHEGLINK VVPABALQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDCGGGITAFLOKKRVWSHEPV-VVEH CHAPALGSKLDVINKISKNRTLESLALLEILADFDELLSK VVPASCLEGGSPAPRFQTDTSPFPVGNWATQGEDLYNGSVEC VCVLFASVDPFKEFYSESNINHEGLECLELLEILAILDTDELLSK VPESVGVEIKITIGSTMAATGQDAQOADERSCSHLGTM VEFAVALGSKLDVINKISKNRFLRGUENGEPVAGVIGAQKPQ VDIWGRTVNIVASRMESTGYLGKICVTEETAMALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG  6850 2 1235 ARGINNEWTFEKLRGHISKNAQDKQELHLFMLSGVPDAVFDLTD LDVIKLELIPEAKIPAKISGNATUGEHLFANLSGVPDAVFDLTD LDVIKLELIPEAKIPAKISGNATUGEHLFANLYGINLSENNIMMI GLESLEELHILKILHVKSNITUCEHLICHPAKVCGTAFFFL RDHLRCLHVKFTDVABIPAWVYLKNIRELYLIGKILNSENNIMMI GLESLEELHRILLILHVKSNITUCEHLICHPAKVCGTAFFFL RDHLRCLHVKFTDVABIPAWVYLKNIRELYLIGKILNSENNIMMI GLESLEELHRILLILHVKSNITUCEHLICHPAKVCGTAFFFFL RDHLRCLHVKFTDVABIPAWVYLKNIRELYLIGKILNSENNIMMI GLESLEELHRILLILHVKSNITUCEHLICHPAKVCGTAFFFFL RDHLRCLHVKFTDVABIPAWVYLKNIRELYLIGKLUNGSNIMMI GLESLEBLERLILLILHVKSNITUCEHLICHPAKVCGTAFFFFL RDHLRCLHVKPTDVABIPAWVYLKNIRELYLIGKLUNGSNIMMI GLESLEBLERLILLUCELLERINGCCTHLKKSGLUVEDHLFDTLPLLEVL YFSNINLESLIPVAVFSLGKLECLDWSYNISHPIFICICLONLQ HLHITONKVDILPFQGFLLSCPKAGTGLUWARAGLMUGAGA LKQLFRQVSAREGENCLGWNLADSAGRAREVGWMAAGLMIGAGA	[	}		
### VTNEIAWQARGRARADESTYULVAHSGSOV IEHETVNDPREKM MYKAIHCVQMMKPEYAHKILELQQGSIMEKKMKTKRNIAKHYK MYKAIHCVQMMKPEYAHKILELQQQSIMEKKMKTKRNIAKHYK NNPSLTTPLCKNCSVLACSGEDIHVIEKMHHVMMTPEFRELYIV REMKTLQKKCADVQINGEIICKCQQAMGTMYHKGLDLPCLKIR NPVVVFRNNSTKQYKKWEVEPITFPNLDYSECLFSDED  6847 1450 348 SMCMNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT WFEDALMGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ PFAYGTLTVRSLLDTREHCLNEFNPFDPYSKVKQRENGVALRCP PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRILQREPMIJDSESWLQRKKGPPHKCALIFADNSG IDIILGYPFVRELLLRGTEVILACNSGPALMDVTHSESLIVAE RIAGMDPVWBALAREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVWBALAREERLLLVQTGSSSPCLDLSRLDKGLAALVR RAGADLVVIEGMGRAVHTWHAALRCESKLAVIKNAWLAERLG GRIFSVIFKXEVPAE  684B 19 16 AMWWNSLDGIFRIVULSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAGGPVFSSGHDLKELTEEGGRDYHAEVFOTCSKVMMH IRNHPVPUIAMVNGLAFTAGCUASCDILVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEABLQEETMRIAKKIASLSRFVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRGCQGSITAFLOKRRWHSEPV*VEH  6849 70 821 SLGYDGSCLEGGSBAPFPOTDTSP*PVGNWATQGEDLYHGSVEC VCULFASVPDPKFPYSESNINHESLECLRLINEILADFDELLSK PKPSGVEKIKTIGSTYMAATGLNATGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRWGAVGVGAQKPQ YDLWGTVNVASKRESTGVIGKTQVTEETWAALQSIGAYCYSRG VIKVKKGGQLCTYFLNTDLTRTGPPSATLG  6850 2 1235 ARGLINHEWTFEKLRQHISRNAQDKQELHLFWLSGVPDAVFDLTD LDVIKLELIPEAKIPAKISQNTNLQELHLGCPAKVEQTAFSFL RDHLRCLHVKPTDVABIPAWVYLKNLRELYLIGKINSENNKMI GLESLRELRHLKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHLKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHLKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHLKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHRIKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHRIKILHVKSNILVSNINTLELYLIGKINSENNKMI GLESLRELRHRIKILHVKSNILVSNINTNINTENIPEIGLLQNLQ HILHITENKVDILPKQIFKCIKKRGLVVSNINSNIPIEIGLLQNLQ HILHITENKVDILPKQIFKCIKKRGLVVSNINSNIPIEIGLLQNLQ HLHITONKVDILPKQIFKCIKKRGLVVSNINSNIPIEIGLLQNLQ VSAQVSAREGENCLGWNLADSSQESYKSLEAEDCYPPSLLTLD LRDLFKQVEQGFLLSCPKAGTDLSMRAREVGWMAAGLMIGAGA	1	ł		
MYKAIHCVOMMKPEEYAHKILELOMGSINEKKMKTKRNIAKHYK NNPSLITFICKNCSVLACSGEDIHVIEKMHVNMTPEFKELYIV REBKTLOKKCADYQINGBIICKCGQAWGTMWHKGLDLPCLKIR NPVVVERNSTKKQYKKWVELPITFINLDYSECCLFSDED  SMCMNSDRLEBMFLIDLALIVPSYVPYTGHILSDGSLSKRYCLT WFEDALMGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ PFAYGTLTVRSLLDTBEHCLINEFNIPDYSKVCKGRNGVALRCF PGVVRSLDALGWEERQLALVKGLIACNVEPWGCKAKVSAVLESDP YFGFEEAKRKLQERPMLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGWPPFVERELLLRGETLLACNSGPALADVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRIFSVIFKXVPAE  6848  19 16 AMWINSLDGIRNIVLSNPKKRNYLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRRHPVPUIAMVMGLATAAGCQLVASCDIAVASDKSSFATFGVN VUFFASLQEETHRIARKIASPVVSLCKARTYKQLPQDLGTA YYLTSQAMVDNLALRIOGEGITAFLQKRRPVWSHEPV*VEH  6849 70 821 SLGVDGSCLEQGSPAPRQTTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLELIMEILADFILLSK PKPSGVEKIKTIGSTYMAATGLNATSGQDAQDARRSCSHLGTM VEFAVALGSKLUVINHSHSTRLRVGLMHEPVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKQGLCTYFLNTDLTRTGPPSATLG  6850 2 1235 ARGINEWTERKIRGHISRNAQDKGELHLFMLSGUPDAVFDLTD LDUIKLELIPEAKIPAKISGMTNLQELHLCHCPALVEQTAPSFL RDHLRCLHVKFTDVAEIFPAWYLLKNIKEVTLIPSTTHVKRMI GLESLRELRHLKILHVKNPSNITDVAPHLTKLVHNDGT KLLVLNSLKKMMNVABLELQNCCLERIPHAIFSLSNLQELDLKS NNIRTIEETISFQHLKRILCHNINKIVTIPSTTHVKRMLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HHHITGNKVDILPKQLFKCIKLRITLNLGQNCTTSIPEKVGQLSQ LTQLEKKRCLDRIPADAGCQKMLKKSGLVVEDHLFDTI-PLEVK EALNQDINTPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMRARGVWMAAGLMIGAGA				
NNSSLTYPLCKNCSVLACSGEDIHVIEMMHHVNMYPEEKELYIV RENKTLQKKCADYQINGEIICKCQAWGTMWYHKGLDLPCLKIR NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED  348 SMCWNSDRLEMPLIDLALILVPPSYVPYTGHLSDSLSEKYCLT WFEDALNGVL*RARAIQPHCVNAGDRMBKFRQKYMNKLQTLRQQ PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPMLVDEYSEMLQRIKKGPPHKCALIFADNSG IDIILGWPFVRELLLRGTEVILAGNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTSSSFCLDLSRLDKCLAALVR ERGADLVVIGMGRAVHTNYHAALRCESLKLAVIKNAWILAERLG GRIFSVIFKYEVPAE  4 AMWNSLDGIRNIVLSNFKKRNTLSLAMLKSLQSDLHDADSND LKVIIISAGGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKYMMH IRNHPVEVIAMVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVVRALEMLFTGEPISQDEALHGLINK VVPPAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGTTAFLQKKEVWSTEPV*VEH  6849 70 821 SLGVDGSCLERGGSPAPRFOTDTS*P*PVGNWATQQEDLYHGSYEC VCULFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKPSGVEKIKTIGSTYMAATGLNATSQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNFRLRVGLNHGPVVAGVTGAKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAMALQSIGYTCYSRG VIVKKKGQUCTYFLNTDTTTGPPSATLG  6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVILKLELIPEAKIPARISQMTNLQELHLCHCPAKVEQTAPSFL RDMHLRCLHVKFTDVAETBAVLLKHINEILYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELLERIPHAIPSISNLQELDLKS NNIKTIEEIISFQHLKRICLKLMHNKIVTPPSITHVKNLESL YFSNNKLESLPVAPFSLQKLRCLDVSYNNISMIPIEIGLGLONLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCTITSLPEKVGQLSQ LTQLEKKGNCLDRLPAQLGGCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINTPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEERAEDCYPPSLLTLD LRDLFRQVEGGPLLSCPKAGTDLSMGRAREVGWNAAGLMIGAGA	1	1		
RENKTLOKKCADYQINGEIICKCGQAWGTMYUHKGLDLPCLKIR NFVVVFKNNSTKKQYKKWELPITFPNLDYSECCLFSDED  8447  1450  348  SMCWNSDRLEMPLIDLALILVPPSYVPYTGHISDDSLSRKYCLT WFEDALNGVL*RABAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ PFAYGTLTVRSLLDTREINEFNPPDPYSYVKQRENGVALRCP PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWLVDSYSEVHLQRLKGPPHKCALIFADNSG IDIILGVFPFYPRELLIKGTEVILACNSGPALNOTHRSELIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAAUVR ERGADLVVI EGMGRAVHTNYHAAIRCESLKLAVIKNAWLAERLG GRLFSVIFKVEVPAE  6848  19  16  AMMWNSLDGIRNIVLSNPKKNITLSLAMLKSLQSDILHDADSND LKVIIISAGGVFSSGHDLKELTEQGGRDVHAEVPOTCSKVMMH IRNHPVDVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALENLFTGEPISAGEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPOLGTA YYIISQAMVDNIALRDGGGITAFLOKKKPWSHEPV*VEH  6849  70  821  SLGYDGSCLEGGSBAPRPOTFISPP VGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRRLINE I LADFDELLSK PKRSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISPRILRVGLHINGFVVAGVTGAOKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKKKGQLCTYFLNTDLTRTGPPSATLG  6850  2  1235  ARGLINEWTFEKLRQHTSRNAQDKQELHLFMLSGVPDAVFDLTD LDVIKLELIPEAXIPAKISQMTNLQELHLCHCPAKVECTAPSFL RDHLRCLHVKFTDVAEIPAWVLLKNILELYLIGNINSENNKMI GLESLRELRHIKILHVKSNLTKVPSNLTDVAPHHTKLVIHNDGT KLLVLNSLKKMMNVAELELONCELERT PHATFSSNLQELDLKS NNIKTIEEI ISFQHLKRICLKLMHNK UTTPPSITHVKNIESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKYDILPKQLFKCIKLRTLINLGQNCITSPERVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVDHLHFDLIPLEVK EALNQDIN IPFANGI  VSAQVSAREGENCLGWNLADSSQESYKSLEERAEDCYPPSLLTLD LRDLFRQVEGGPLLSCPKAGTDLSWGRARREVGWAAAGLMIGAGA		ŧ		
NPVVVFKNNSTKKQVKKWVELPLTFPNLDYSECCLFSDED	1 .			
6847  1450  348  SMCWINSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT WFEDALMGVL*RAEAIQPHCVMAGDRMEKERGKYWNKLTLRQQ PFAYGTLTVRSLLDTREHCLINERNFPPPYSKVKQRENGVALRCF PGVVRSLDALGWERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPKCALIFADNSG IDIILGYPFVRELLLRGTEVILLAGSGPALNDVTHSESLIVAE RIAGMDPVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAULAERLG GRLFSVIFKYEVPAE  6848  19  16  AMWINSLDGIRNIVLSNPKKRWTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVEVIANVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEMLFTGPPISAQEALLHGLINK VVPPAELQEETMRIARKIASLSRFVVSLGKATFYKQLPQDLGTA YVLTSQAMVDNLALRDGOGITAFICKRKPVWSHEPV*VEH  6849  70  821  SLGVDGSCLEGGSPAPRPOTDTSP*PVGNHATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHIGPVVAGVIGAQKPQ YDIWGMTYNVASRMESTGVIGKIQVTEETAWALGSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG  6850  2  1235  ARGLINEWTFEKLRGHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVIKLELIPPAKIPANTGLRUKHINEUTLCHCPAKVEQTAPSFL RDHLRCLHVKPTDVASIFDAWTYLLKNLRELYLLGNLNSENNKMI GLESLRELRHLKILHVKSNLTKYPSNITDVAPHLTKLVIHNDGT KLLVLNSLLEMMNVAELELQNCELERIPHAIPSLSNLQELDLKS NNIRTIEEIISFQHLKKRITCKLMINKIVTTPPSTTHVKNLESL YFSNNKLESLPVAVFSLQKLRCLIDVSYNNISMTPIEIGGLLQNLQ HLHITGRKVDILPRGVIKLRTLNLGQNCITSLPPEKVGQLSQ LTQLEKKNCLDRLPAQLGQCCMLKKSGLVVEDHLFPDTLPLEVK EALNQDINIPPANGI  6851  1765  660  VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFRQVEGGPPLLSCPRAGTDLSMGRAREVGWMAAGLMIGAGA				
WFEDALNGVL*RAEAIQHCVRAGDEMEKERQKYWNKLQTLRQQ PFAYGTLTVRSLLDTREHCLINEFNFPDPYSKVKQRENGVALRCF PGGVRSLDALGWEERQLALVKGLIAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPKKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVMSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVAE  6848  19 16 AMMWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTBEQGRDVHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLETGEPISAQCALLHGLINK VVPEABILQEETMRIARKIASLSRPVVSLGKATFYKQLPODLGTA YYLTSQAMVDNIALARGGITAPLOKREVWSHEPV*VEH  6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDPKEFYSESNINHEGLECLRILINEIIADFDELLSK PKPEGVEKIKTIGSTYMAATGLNATSGQDAQODABERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNGFBVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWAQSLGYTCYSRG VIKVKGKGQLCTYFINTDLTRTGPPSATLG  6850 2 1235 ARGINHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLGELHLCHCPAKVEGTAFSFL RDHLRCLHVKFTDVAEIPAWVILKNILELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMNVAELELQNCLGRETPHAIFSLSNLQEDLKS NNIRTIEEIISFQHLKKRITCIKLHINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLCLLDVSYNNISMTPIEIGLLQNLQ HLHITGNKVDILPKGLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLEKKGNCLDRLPAQLGQCCMLKKKSGLVVEDHLFDTLPLEVK EALNQDINIPPANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEGGPPLLSCPRAGTDLSMGRAREVGWMAAGLMIGAGA	6947	1450		
PFAYGTLTVRSILDTREHCLNEFNFPDPYSKVKQRENGVALRCP PGVVRSLDALGWERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWIVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKANLAERLG GRIFSVIFKYEVPAE  6848  19 16 AMWINSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILLHDADSND LKVIIISAGEPVFSSCHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATTYKQLPQOLGTA YYLTSQAMVDNLALRDGGGGITAFLQKKRFVWSHEPV*VEH  6849 70 821 SLGVUGSCLERGSPAPRPGTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKPSGVEKIKTIGSTWMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLINGFVVAGVIGAQKPQ YDJWGNTVNVASRMESTGVLGKIQVTEETMAMQSLGYTCYSRG VIEWKGKGQLCTYFLNTDLTRTGPPSATLG  6850 2 1235 ARGLNHEWTFEKLRCHISRNAQDKQELHLHFULSGVPDAVFDLTD LDVILKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAPSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNINSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTTKLVIHNDGT KLLJVINSLLIPEAKIPAKISQMTNLQELGERIPHAIPSISNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNISMIPIEIGLLQNLQ HLHITGRKVOTLPKQLOFKCIKLRTLNLGQNCTTSLPEKVGGLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPPANGI  6851 1765 660 VSAQVSAREGENCLGRNLADSSQESYKSLEEAEDCYPPSILITLD LRRDLFNQVEGGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1 004/	1450	348	
PGGVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDII LGVPPFVREILLRGTEVILACNSGPALNDVTHSESILVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRIFSVIFKYEVPAE  6848  19 16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKYMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRGQGGITAFLQKKRPVWSHEPV*VEH  6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHGSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEILADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VBFAVALGSKLDVIKKHSFNNFERLVGLINGPVAGVLGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGINHENTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBAKIPAKISQNTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEITPAWVYLLKNLRELYLIGRINSENNKMI GLESLREIRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISPQHLKRLTCLKLMINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HHHITGNKVDILPPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGERCLGWNLADSSQESYKSLEEAEDCYPPSILITLD LRDLFNQVEQEPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
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RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTYHAALRCESLKLAVIKNAWLAERLG GRIPSVIFKYEVPAE  16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDLLHDADSND LKVIIISABGPVFSSGHDLKELTEEQGRDVHAEVPQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTBGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQANVDNLALRDGGGGITAFLOKRRPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQGYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLMHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVINSLKKMMNVAELELQNCELERIPHAIPSLSNLQELDLKS NNIRTIEEIISFQHLKRITCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLCDVSYNNISMIPPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	ı			
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GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIPSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
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KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1			GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1			1
HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI  6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
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6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				
LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6851	1765	CCA	L (
		.,os	Uaa	· ·
CV(TIVI DIADOCONI DESARROLIDADO DE CONTRES	[			1
				CYCVYKLTIGRDDSEKLEREGEEEWDDDQELDEEEPDIWFDFET

SEQ	Predicted	Predicted end	I hmino
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W-Trumbonhan V Towner
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
J	sequence .	1-1-1-00	\=possible nucleotide insertion)
ļ ——			MARPWIEDGDWIEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE
į.	İ	ĺ	HKNTMENONCYMCEGUI DI CHOLDENDEGGKANRAHPIKQRPFPYE
1	1		HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
1	i		INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
i		1	YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK
Į.			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL FIRNGNREILLETPAP
6852	1	407	
1	_	107	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
İ	į.		GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
ŀ	1		IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
6853	3	469	KTD
	1	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
1			KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
ì			ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
6854	1148	505	VDNPTFEEDETPNQETAVREIKS
1	1140	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEPSTQAK
ł			PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
1		 	IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
Ĭ	<b>i</b> 1		LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
6855	1913	1148	LFGIESKSSDS
	""	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
-			EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
Ì.			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
1			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
6856	1617	. 997	LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
	101,	991	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR
1	1		TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
1 1			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
1 .		•	RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
6857	1	617	HWALFGASERGFDPKDTRHQRKNKSKAISGC
	- 1	617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
1			KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF
1 1			DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT
1 1			TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858		669	REDGIVED TO SEE THE PART OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
1 1	- 1	000	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
1 1	Į.		LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM
1	İ		SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
1 1			IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR
1 1	ľ		KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN
6859	1 -	1150	
1	-	4130	GETMPKKAKTKAKKKPRKRSDSSGGYNLSDI1QSPSSTGLLKSG
	ļ	ł	KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
, i			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
l l			SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
1	· 1		VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
1 1	1		AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
} I	i i		SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
[ ]	1	ł	VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
6860	1889	1516	YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
		1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
1 1	1	ļ	DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
6861	1889		MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
	2009	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
<u> </u>			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

Deginning corresponding to first amin acid corresponding to first amin acid residue of amin acid residue of amin acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequences sequence sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide   location   corresponding   to first   damino acid   residue of   samino acid   residue of   samino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seque				
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Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences sequences seque	NO.		ļ	
to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence s				
amino acid residue of amino acid sequence solve of amino acid sequence code, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleotide deletion, y-possible nucleo				
residue of amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence sequence sequence  sequence  sequence  sequence  sequen	İ			
amino acid sequence    Codon, /=possible nucleotide deletion,  -possible nucleotide insertion	ì			
Sequence			4	1
MSSFULDGOQHMSIRPAGPMSIMGAMNANGHOGHIYM   EEIDREFINIKLIKAEDKLEEGGEVEYNOEDGGSSVOTONSIGNA	1	i e	sequence	1
6862 2 471 EEIDREFINKLKEKDKLEKQEKPYNOEDKGJSGVOTONSEGNA DEEDLGJANGVYDKKISFINI SCONDREBER TYAREERLARET FG IPLEPPROREGGYEGGGGEGEGGGGGGGGGGGGGGGGGGGGGGGGG		sequence	[	
DEDDELGENCYTOXTKSFFDNISCODDRERREPTHARERRIARET FGIPLRPBRERGGYSRGSGEGFFGGRGRGCGFFTAPAGFER GFRGGGGGFFFADFEYRTTAFGP FGEPALKSEESFOVASTIT PLUF DEPNTCKNNOPCKGVCSTVGGS ALGSCF BCYALMADGVSCEDQDBCLMSAHDCSRQFCVTHIGSF YCVMIETVILADGY LINAIRKVCNI NECVTULAITCSRGEBCVNTIL GSPHCVKALITCSPGYALMCGECDVDBSCLMSTHTCODGFCLONT KGSPYCOARGROUPFILDERGNVCUDINGCTTUCKSEDCCONTIL GSPHCVKALITCSPGYALMCGECDVDBSCAMSTHTCODGFCLONT KGSPYCOARGROUPFILCARGYBASDGFTCVDINGCTGSEPCPGPSCI NTVGSYTCOARDILCARGYBASDGFTCVDINGCTGSEPCPGPSCI OVCHNIPGSYNCCCAGGGGDAFGGGCLONPAGGGCLONPAGGGC GVCHNIPGSYNCCCAGGGGDAFGGGCLONPAGGGCLONPAGGGC GVCHNIPGSYNCCCAGGGGDAFGGGCLONPAGGGGCLONPAGGGC GCOVGCAGGGACAGGGGCAANT GCOCCAGGGACAGGGCCONTIDECAGGGGLONPAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCONFAGGGCCCONFAGGGCCCONFAGGGCCCCCCCCCO	6063	<del> </del>	471	
FGIPLRPRRGGGTRGRGGLGFRGGGRGGTFTAPGGFRG GFRGGGGGFEADFETRITATAGE  6863  2216  487  FGRPALKSEPSQUASHTIPLDLPQPHTCKDNGPCKQCSTYGGS FGREGGGGFALKSEPSQUASHTIPLDLPQPHTCKDNGPCKQCSTYGGS VCWHIPVLCADGY LIMAHRKCYDLDRCYTDLHTCSRGERCYNTL, GSPHCYKALTCEBCYALKOGECEDVDECKGMATHTCOPGFLCONT KGSPYCQARQRCMDGFLQDPESMCYDLHTCSSEPCKRGFRGFXCTI, GSPHCYKALTCEBCYALKOGECEDVDECKGMATHTCOPGFLCONT KGSPYCQARQRCMDGFLQDPESMCYDLHRCTSLSEPCRRGFRXT ROYCHNALGGYCCKGCGGAGGGGAGGCCLDVNECHAGFGRCOHT CENTLGSYRCCKASGFLAADGKRCEDVNECEAGCAGAIY GSYCCKGCGYGLAEGGITTCDLDRCAGAGAILCTFRCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS VQCACPEGGTTMTAMGRSCKDVDECLAGTHRCSBAGTCHTPCLANPGS PFOLINGARAVEQGTAMGRAFTGDTLALNI IKIGNEEPGTTBCNDTGAGT PFOLINGARAVEQGTAMGRAFTGDTLALNI IKIGNEEPGTTBCAGHTFTCLATHTCAGA PFOLINGARTCHTPCLANPAGAGTCHTTCAGAGTAGAGAGAGAGTTTAGAGAGAGAGAGAGAGAGA	6062	1 2	1 4/1	
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AB7   PREPALKSEPSQUASHTIPLELDPATCKINGPCKQUSTYGGS     AIGSCPGYARMDGWGEDDDRELMGAHDGSRRQPCVNTLGSF     YCWHTVLICADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL     GSHCYKALTCEPGYARMDGWGEDDDRELMGAHTHTCDPFLCONT     KGSHCYKALTCEPGYARLDGEEGDDRELMGATHTCDPFLCONT     KGSHCYKALTCEPGYARLDGEEGDDRELMGATHTCDPFLCONT     KGSHCYKALTCEPGYARLDGEEGDDRECMGHTHTCDPFLCONT     KGSHCYKALTCEPGYARLDGEEGDDRECMGHTHCTGPFLCONT     KGSHCYKALTCEPGYARLDGEEGDDRECMGHTHCTGPFLCONT     KGSHCYCKRGCHDGEGDDRECMGHTHCGAGATLCTFRCLNVPGS     GVCVCRGCGYGLAEDGHTCTDIDECAGGAGILCTFRCLNVPGS     GVCVCRGCGYGLAEDGHTCTDIDECAGGAGILCTFRCLNVPGS     GVCVCRGCGYGLAEDGHTCTDIDECAGGAGILCTFRCLNVPGS     GVCVCRGCGYGLAEDGHTCTDIDECAGGAGILCTFRCLNVPGS     GVCVCRGCGYGLAEDGHTCTDIDECAGGAGILCTFRCLNVPGS     GVCCRGCGYTWTANGRSCKDVDECAGTHCSBASTCHTQGA     FCCLRFECPPHYQVGKKTCKGTCTDTLECAGGAILCTFRCLNVPGS     GVCLRGAATCYMGAGALGHTCTGAGAGILCTTRCLNVPGS     GVCLRGAGATCYMGAVLFQCALTAGAGILLATIKGSPGTTRLN     AYTGVVYLGARALGPATLECAGAGILCTHAGAGILCTTRLN     AYTGVYLGARALGPATLECAGAGILCTHAGAGILCTTRLN     AYTGVYLGARALGPATLECAGAGILCTHAGAGILCTTRLN     AYTGVYLGARALGPATLECAGAGILCTHAGAGILCTTRLN     AYTGVYLGARALGPATLAGAGILCTHAGAGILCTTRLN     AYTGVYLGARALGPATLAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGILCTHAGAGIL	l	1	Į.	
AICSCPGYAIMADGYGCEDDESCHIGAHDCSRROPCVNTLGSF YCVNHTVLCADGYILMAIRCVDINSCYTHCTSGREECOVTL GSPHCYKALTCEPGYAIKOGECEDVDECAMSTHITCGPGLONT KGSPYCORROPILLCARGYHASDDGTKCVDUNECETGYBECGPGPGCI NTYGSYTCORNPLICARGYHASDDGTKCVDUNECETGYBURGCEG GVCHNLPGSYRCCXAGFOLABGGHCCHASPGRLOOH CENTIGSYRCCXAGFILAADGKRCEDVNECEAQRCGOECANIY GSYCCYCRGYOLABGGHTCTDIDRCAGGAGILCTFRCINYGS YCACPGGGTYMTANARGSKROVDECLAFTHCSABATCHNIQGS FRCLRFECPRYVQVSKTKCRTTCIDFLECQNSPARTHOLOAN FONGLIVPAHITFIGEPAPAFTGDTIALAII IKSNEEGYFGTRRIAN AYTGVYLQRAVLEPRDPALDVERKLWRGSVTTFLAKHHIFFT FALI  AYTGVYLQRAVLEPRDPALDVERKLWRGSVTTFLAKHHIFFT FALI  AYTGVYLQRAVLEPRDPALDVERKLWRGSVTTFLAKHHIFFT FALI  LADSSPSNLQIITKELLSMHHQDPDALTKEFDYLPPVDSRSSG FYCURNGGATCYMNAVPQOLTMQGLPESLSVDDDTDNNPDDSV FYOVGSLFCHLMESKLQYYVPENNFKLIFKMANKELYYRGODAY EPFTSLIDDMDEYLKKRGARDQIFKNTFGIDSKICCCOPHRY EREBAPMAINIGVTSCQSLEISLDGFVRGEVLGSNAYYCEKCK EKKHITVKRTCIKSLPSVLYHILMFFGFGDAKGKWKYFADTVIE EREBAPMAINIGVTSCQSLEISLDGFVRGEVLGSNAYYCEKCK EKKHITVKRTCIKSLPSVLYHILMFFGFGBRSIKYNDGCICCCPHRY EREBAPMAINIGVTSCQSLEISLDGFVRGEVLGSNAYYCEKCK EKKHITVKRTCIKSLPSVLYHILMFFGFGBRSIKYNDGCICCPHRY ERFELMDETLEYECGGGFYRPKVYDOTNPYTOVRRYWANYHLFY ORVSDONSDVLJKKKSRWYWRGAERDLISASPSFISTSDSTCHFF WILMBEYTVSGMARGDSSSEVGENGRSVDGGGGGGSFKKVALT ENYELWGUTVISGGALAGHYYSFIKORASPSFISTYDGNICK MYNEDDVYSSDVJSKVSINGATKKHFYYSFIKORASPSFISTYDGNICK PHRYNIDRIS.ILTKLWKGEKKGLFYEKMPRI IYOWYDERILKF MYNEDDVYSSDYSFVSILASIANATKKHFYCAKKYGANYDFIENALF HRYNIDRIS.ILTKLWKKGEKKGLFYEKMPRI IYOWYDERILKF MYNEDDVYSSDYSFVSILASIANATKKHFYCAKAYFOLAGHI LIKHALRHISFILLGASRONNO HRYNSSAPFICHBETGFTFRILL VIAHDWSSGRVAFFIRENTSSLALIEMVYVCCFCNERFSFTMILM SEGKPYLLEVMPALREITGSLALIEMVYVCCFCNERFSFTMILM FIKNQLETAPHELKNTFQCSNNONTSTRGTFCFTGTTSAQDTLA YATALLNEKEGSGSSNGSSSSANSSSSPANGODHHLQQSSSPMMIGEL FIKNQLETAPHELKNTFQCSNNONTSTRGTFCFTGTSTATGDFTGRTSADDFLA TATHLUREKEGSGSSNGSSSSSSSSSSSSSSSSSPMMIGDRHCOLA CSCRGFSEVENDAMFNINGSNSCTGCVFFLVTAACKPARAKFKENSHM WSNAVONLOKKOSHYMTLGSNNONTSTRGTFCFTGTSTATGFTGTTGRTSADDFLA TIEMBERAGSVALBELVEKKORFPSGUYYVISDNIKTGNSSR PGGSSVOTIOPKRD  DEFERMILLSKVTFGGRPAGDFTGGTGLHERPMADLVALLG SLYDSSOVILTSGR			<u> </u>	,
YCUNHTVICADOY ILNAHRKCUIDECAMSTITICOPOFICONY KGSPYCOAROROMOFIODPEGNOTOTINECTSLISEPCRPGSCI NTVGSYTCORROFIODPEGNOTOTINECTSLISEPCRPGSCI NTVGSYTCORROFILOARGYHASDDETKOVDWECETGYBYRCGEG QVCHNLPGSYRCDCKAGFGROAFGRGCIDVNECNASPGRICOHT CENTILSYYRCSCAGFGROAFGRGCIDVNECNASPGRICOHT CENTILSYYRCSCAGFGROAFGRGCIDVNECNASPGRICOHT CENTILSYYRCSCAGFGROAFGRGCIDVNECNASPGRICOHT CENTILSYYRCSCAGFGROAFGRGCIDVNECNASPGRICOHT CENTILSYYRCSCAGFGROAFGRGCIDVNECNASPGRICHT GSYQCXCRGGYOLAEDDGHTCTDIDECAGAGGILCTFRCLAVPGS YQCACPEGGYTMTANGRSCKDVDECALGTHNICGSEATCCHNICGS FRCLRFEEPPSYVQVSIKTKCERTICHDFLECOMSPARITHYOLM FOYGLLVPAHIFR IGPAPAFTGDTIALNIIKGREEGYFGTRRIAN AYTGVYJCARAUEPPFALDVEMKLEGSVFGTRRIAN AYTGVYJCARAUEPFALDVEMKLEGSVFGTRRIAN AYTGVYJCARAUEPFALDVEMKLEGSVFGTRRIAN AYTGVYJCARAUEPFALDVEMKLEGSVFGTRRIAN AYTGVYJCARAUEPFALDVEMKLEGSVGSVTFLAKMHIFFT TFAL  LADSSPSNLOIIKECHMESKLOYYYPENSKYLERSMAYYCEKCK PROMATAURLOTTSCOLEISLDOPFUSSVLESSNAYYCEKCK EKRITVKRTCIKSLFSVLVIHLMRPGFDRBSGRSIKYDDOITENDDSY POWGSLCHMESKLOFYTGSVLESSNAYYCEKCK EKRITVKRTCIKSLFSVLVIHLMRPGFDRBSGRSIKYDDOITEND MINIMEPYTVSGMARQUSSSEVGERGRSVDOGGSPKKXVALT EFFOLNDETLEYECTGGEYRPKVYDQTRPGTVRGSCKGKWKFRDTVIE EFFOLNDETLEYECTGGEYRPKVYDQTRPGTVRRWANYHLFY QRVSDONSPVLPKKSRVAVYRQEABLALSASSFSEISPGSSPR PHRRNDRGSILTKLVKKGEKKGLFVERMPARIYOWRDEBLIKF MKRNDVYSSDYFSFVLJASLANIKLKHPYYPCMAKVSLOLAIQ FLCTYLRTKKKLRVDTEEMIATIEALLSKSFDACOMLUEYFI SEGRELIK IF FLLECNVREVYNAVATILSASPFDACOMLUEYFI SEGRELIK IF FLLECNVREVYNAVATILSASPFDACOMLUEYFI SEGRELIK IF FLLECNVREVYNAVATILSASPDACOMLUEYFI SEGRELIK IF FLLECNVREVYNAVATILSASPFDACOMLUEYFI SEGRELIK IF FLLECNVREVYNAVATILSASPFDACOMLUEYFI LUCHABAGGNAGAGGSSNONGTRENAORAFGCHLINTVALL VLHSDVSSORNVAPGIFKORPPISTAPSFOLOPKKKSL HOLLEVLLALLIDKDVPROKENCROCYFFIFTOMYCCFCNEHEFFTMLH PIKNQLETAPPHELKNTFOLLHSILVIEDDIOVERKFVFFTSTMIH SEGRPYLLEMPAARSELUTGSLLALEVGYCCFCHEFFTMLH WSNAVQWLQKRMSEHYWTLQSNVSNETSTGKTFGRTSAGGGSSP CSCRGGSVEDCKMYGVSSVHLHFFYEGAVPFILLECUGGGEFLV LLOGRADDYNQALGTCRLAGTALCVAAGVILLAICLFWAMTGHLSQ DFREFTLYTTGGRTSTAVFTPOLUFEETITYNAIHLDLEEFRNSG VEKKIPDTKEETIHLIMIYFPSLSIHGIEGAFFTKTVI PGNV TICKSTIKLOPHNVSAVEKOR	6863	2216	487	
GSFHCKKALTCEPGYALKGGECEUDDECAMGTHICOPGFLCONT KGSFYCOAROROMGENGDEMCVDINECTSLISECPEGPGSCI NTVGSYTCQRNPLICARGYHASDDETKCVDVMECESTGVHRGGEG QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECNASPGRLCOHT CENTLSSYRCSCASGFILAADGKREEDVNECRAGFGRCANTY GSVQCVCRGGVQLAEDGHTCTDIDECAQAGGILGTRICTPRCLNVPGG YQCACPEGQTYMTANGREGKODVBECALGTRICSEARTCHNIQGS FRCLRFECPPNYVQVSKTKCERTTCHDFLECOMSPARITHYQLAN FOTGLLVPHATHFRIGAPAFTGGTILAINIKGREGVYBETRIN AYTGVYYLORAVLERRDFALDVEMKLMRQGSVTTFLAKMHIFFT TFAL  6864  2 2933 LADSSPSNLOJIIKELLSMHHODDFALTKEEPLYDPUSGRSSG FVGLRRGGATCYMNAVYOQLYMPOCLAPSLLSVUDDDTDNDDSV FYQVQSLFGHLMESKLQYTVPENFWKLFKMMKKLYVREQODAY EFFTSLIDQMDSYLKKMGRDJIFKNTFOGITSDKICKOCPHRY REREAFMALNIGVTSCQSLEISLDQFVGRGSVLEGNAYYCKCK EKRITVKRTCIKSLPSVLVIHLMRRGFDWESGKSIKYDGLTRF MILMBEYTVSGMARQDSSEVGUERGVOGGGGSPRKWADLT ENVELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWKFNDTVIE EFFDLNDETLLEYECFGGTSPRKVVQTOTVORRYWNAVMLFY QRVSDONSPVLJKKSRVSVVRGEAEDLSLASPSSPEISFGSSPR HRENNDRISLITKLVKKGEKKGLEVMARTIVORRYWNAVMLFY QRVSDONSPVLJKKKSRVSVVRGEAEDLSLASPSSPEISFGSSPR HRENDRISLITKLVKGEKKGLEVMARTIVORRYWNAVMLFY GRVSDONSPVLJKKKSRVSVVRGEAEDLSLASPSSPEISFGSSPR HRENDRISLITKLVKGEKKGLEVMARTIVORRYWNAVMLFY GRVSDONSPVLJKKSRVSVVRGEAEDLSLASPSSPEISFGSSPR HRENDRISLITKLVKGEKKGLEVMARTIVORRYWNAVMLFY GRVSDONSPVLJKKSRVSVVRGAEDLSLASPSSPEISFGSSPR HRENDRISLITKLVKGEKKGLEVMARTIVORRYWNAVMLFY GRVSDONSPVLJKKSRVSVVRGAEDLSLASPSDEDGSSPMKOVLYFIS  SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQVFFFINTYVQCGTRADGLL LRHSALRHISFLLGSASGONNQTRRWSAGAREFGRLINTVALL VLHSDVSSGRNVAPGIFKQRPPISLAPSSPLEHEEVERLEFFMLH FIKNQLETAPPHELKNTFGLLHSILVIBDFQVCGCSSEPMGCRS GLALMMHSHNSHDDSSRCQCVKFFLVLAQKCPAAKEYFFRENSHH WSMAVQMLQKKMSEHYWTLQSNVSNETSTGKTTGTTISAQDTLA ATATLLKEKRQGSGSSNGSSSPARRNGDRHLQQSSEPMMIGEL RSDLDDVDP  6865 1820 1242 DPERWKHLSKVTPPGSSVSTFPVOVUTLOFFGGSGSMPSCRRS CSCSRGFSVEDCKMYGVSYLHLLFYEGYAVPPKLEGIGEGEFLV LDQRADYNQALGTCRLAGTALCVAAGVILLAICLFMANTGMLSG DFRETYTLYGGTRATCHREDLDWANINAVSAFKALEQDLDVNIKF 1IEGMERAGSVALEELVERGEKDEPFSGDJYTVTSDHLHTEGRTF PFGGSSVOTIOPKRDS VEKFLPDTKEETLMHLWRYPSLSHIBLEADFEGTTVTBOLL GRSTIRLVPHNNSAVERCYNTERE	1		t .	•
KGSPYCOARORCMDGFLODPEGNUTUNECTGYBURGEG NTYGSYTCORPULCAGRYHASDDGTKCUDWECTGYBURGEG QVCHNLPGSYRCDCKAGFYRADGTGCUDWECHASPGRLCOHT CENTIGSYRCSCASGFLLAADGKRCEDVNECAGAGGILCTFRCLAVPGG SYQCACPEQGYTMTANGRSCKDVDECALSTINCSERTCHNIQGS FRCLRFECPPWIYQUSKTKCERTICHDFLECOMSPARITHYOLM FOTGLLVPAHIFRIGPAPAFTGGTIALNIKGREEGYFGTRILM AYTGVYLQRAVLEPRDFALDVEMKLWRQGSVTFLAKMHIFFT TFAL  LADSSPNLQIIIKELLSMHQPDPALTWEFDVLPSUSSSG FFTSLIIDDMEYLKKMGROQIFKTHEFDVLPSUSSSGSWFYQGLRGGGAGILCTFRCLAWHIFFT TFAL  LADSSPNLQIIIKELLSHHQPDPALTWEFDVLPSUSSSGS FYGURRGGATCYMMAVPQQLYMQPGLPSSLLSVDDDTDNPDDSV FYQVQSLEGHLMMESKLQYYPPENFKKIFKHMNKELYVEQQDAY EFFTSLIDDMEYLKKMGRQQIFKHFMSFGSUSLOCCHRY EREAFMALNIGVTSCQSLEISLDOFVRGSVLEGGANAYCCKCK KERITVKRTCIKSLPSVLVIHLMRPGBGSIKVDGLOFHRY EREAFMALNIGVTSCQSLEISLDOFVRGSVLEGGASMAYVCSKCK KERITVKRTCIKSLPSVLVIHLMRPGBGSIKVDGLOFHRY ERNELBYGVUNGGAGAGHYSFIKDREGGSKLWWKRMDVYSDVYSDVYSFVLSKGRKGVDVGGGSPRKWALTI ENYELWGVIJNGGQAHAGHYSFIKDREGGSKLWWKRMDVYSDVYSDVYSFVLSLASLANTKLKHPYYPCMAVSLQLALI ENYELWGVIJNGGGAHAGHYSFIKDRAWSTALDKSSPDACWMLWFYIS SEGREILKIFLLECNVERWKWAVATILEKTLDSALFYODKLKSL HERDHNDRISILTRILVKKGEKKGLEVERMFARIYOMVEFTIS SEGREILKIFLLECNVERWKWAVATILEKTLDSALFYODKLKSL HERDHNDRISILTRILVKKGEKKGLEVERMFARIYOMVEFTIS SEGREILKIFLLECNVERWKWAVATILEKTLDSALFYODKLKSL LRHSALRHHISFLLGASRONNOIRRWSSAOARSFGRILHNTVALL UNLSDVSGORNVAPGIFKORPOFTSTFOVGKGTRAGGLL VILHDUSGORNVAPGIFKORPOFTSTFOVGKGTRAGGLL VILHDUSGORNVAPGIFKORPOFTSTFOVGKGTRAGGLL VILHDUSGORNVAPGIFKORPOFTSTFOVGKGTRAGGLL VILHDUSGORNVAPGIFKORPOFTSTORTSAQDTLA SEGRYLLEWMBALBELTGSLLALIEMWYCCFCHBHFSFTMLH FIKNQLETAPHELKNTFQLLHEILVIEDPIOVERVEWSELLHHE SEGRYLLEWMSALGSSESPANNEGDRHLQGSSSFMMGCNRS CSCSRGBSVEDCKWWGVRSYLHLFYEGVAVPFKLEGIGEGEFLW LDQRAADYNOALGTCRAGSESPANNGSENGRHLQGSSSFMMGENRS CSCSRGBSVEDCKWWGVRSYLHLFYEGVAVPFKLEGIGEGEFLW LDQRAADYNOALGTCRAGSSESPANNGDRHLQGSSSFMMGENRS CSCSRGBSVEDCKWWGVRSYLHLFYEGVAVPFKLEGIGEGEFLW LDQRAADYNOALGTCRAGSSESPANCHURGHLYGLLICLHWAMIGHLSO DTKAEPLDDEARSHVEVERGDEPGGTLTALLCLHWAMIGHLSO DTKAEPLDDEARSHVEVERGDEPGGTLTALLCLHWAMIGHLSO DTKAEPLDDEARSHVEVERGEBEFTTYKAIHLDLEETRISAG VEKLFBTTYKKEILWHYFSLLIHGLHED	Į.		l	
NTYGSYTCORMPLICARGYHASDDGTKCUDVBECRGYNGGGG QVCHNLDGYYCCCKGGFORDAFGGGCTDVNECMASPGGLOHP CEWTLGSYRCSCASGFILAADGKRCEDVNRCMASPGGACOMT GSYQCYCKGGTQLAEDGHTCTDIDECAGGGILCTFRCLNVPGS YQCACPEGGYTWTANGRSCKOVDECALGTRINGSEAFTCHNICGS FRCLRFECPPNYVOVSKTKCEKTTCHDFLECONSPARITHYOLM PGYGLLVPHAHIFRIGPAPAFTGGTIALNILKGREGYFGTREIN AYTGVYLCRAVLEPROFALDUEMKLMRQGSVTTFLAKMHIFFT FIAL  6864  2 2933 LADSSPSNLQIIIKELLSMHHQDDPALTKEFDYLDPVDSRSSG FYGLRNGGATCYMNAVOQLYMPOGLPSELLSVDDDTDNDDSV PYQVGSLGCHTLMESKLQYYVPENFWKIFKMMNKELYVRGQDAY EFFTSLLIDQMDBYLKKMRDQIFSULSVDDDTNDDDSV PYQVGSLGCHHLMESKLQYYVPENFWKIFKMMNKELYVRGQDAY EFFTSLLIDQMDBYLKKMRDQIFSULSVDDDTNDDDSV PYQVGSLGCHTLMRRGFOMEGGRIKVTQGTFF MINIMEDFYTYSGMARGDJFSNLTGSUSDCKTCKCCHRY EREAPMAINLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLESVLVIHLMRRGFOMEGGRIKVTQGTFF MINIMEDFYTSGMARGDSSSEVUEGGGGGSPKKVALT ENYELVGVIVHSGQAHAGHYSFIKDRRGCGKGKWKFNDTVIE EFFDLNDETLEVECFGGFFRFNVYDQTNTVVRRRWNAYNLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLSAPSSPEISPGSSPR PHRPNNDRISLITKLVKKGEKKGLFFNFNTVVRRRWNAYNLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLSAPSSPEISPGSSPR PHRPNNDRISLITKLVKKGEKKGLFFNFNTVVRRRWNAYNLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLSAPSSPEISPGSSPR PHRPNNDRISLITKLVFLGFGKTRAFTYTVGRRTWANYLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLSAPSSPEISPGSSPR PHRPNNDRISLITKLVTLAFTENTIVGRTWANYLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLASPSSPEISPGSSPS PHRPNNDRISLITKTLUFTENTIVGRTWANYLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLASPSSPEISPGSSPS PHRPNNDRISLITKTLUFTENTIVGRTWANYLFY ORVSDONSPVLJKKSRVSVVRGEABDLSLASPSSPEISPGSSPS PHRPNNDRISLITKTLUFTENTIVGRTWANYLFY ORVSDONSPVLJKKSRVSVRVRYSPFTVVRRRTWANYLFY ORVSDONSPVLJKKRRVSVRVRYSPSPTSTAPSPULDELBELFT  HELDEVLANDARGERSPRANGGRANGTRAVSSPACHTURYLFY ORVSDONSPVLJKKRRVSVRVRSSPARSPRANGGRHLHVTQLLL ULHDAVSGRNVAPGIFKGRPFSTSARSPRILDERFYTLL FIKNQLETAPPHELKNTTGSLLALIEMVYCCCNCHEFFFTMLH FIKNQLETAPPHELKNTTGSLLALIEMVYCCCNCHEFFFTMLH HUSHAWAVQULGKRWSENYTLLSVRYPPGSSVSTTPVVVRILGGSGGSMMSCCRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPFKLEGIGEGEFLV LDGRADYNQALGTCRLAGTALCVAAGVILLAICLFMANTGHLS PFFGSSVOTIOPKRDS  ORPERFYTLYGGRAFGGGLAWHQOSESSPMIGGEL SLUDSGGHILVPGLYBGSTFGGGLAHPANGLVALL SLUDSGGHI	1	1	1	· <b>I</b>
QVCHNILPGSYRCCGCAGFQRDAFGRGCIDVRECMARGEGCANTY CEMTLGSYRCCGAGFLLANDRIGEDWECKAGRGECANTY GSYQCYCRQGYQLAEDGHTCTDIDECAQGGILCTFRCLNYPGS YQCACEPGCYTHTANGRSCKUVDECALGTHNCSEASTCHNIQGS FRCLRFECFPNYVQVSKTKCERTICHFLECONSFARITHYQLM FQTGLLVPAHIFRIGPAPATGDTIALNILKGNEGYFGTRRIN AYTGVYVLQRAVLERPDFALDVERKLWRQGSVTFILARMHIFFIT TFAL  LADSSPSNLQIIIKELLSMHHOPDPALTKEFDYLPPVDSRSSG PVGLRNGGATCYMNNVFQOLYMQPGLPESLLSVDDDTDNPDDGV PYQVQSLFGHLMESKLQYYVPENFWKIFRGWIKELYVREQQDAY EFFTSLIDOMDBYLKKMGRQQIFKNTFQGIJSDOKICKDCPHRY ERSEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLSPVLVIHLMFRGCGGKGKWKFNDTVIE EFFLINDETLEYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGKGKWKFNDTVIE EFFLINDETLEYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGKGKWKFNDTVIE EFFLINDETLSYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGKGKWKFNDTVIE EFFLINDETLSYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGKGKWKFNDTVIE EFFLINDETLSYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGGKGWKFNDTVIE EFFLINDETLSYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKSRVSVVQERBCGGGKGWKFNDTVIE EFFLINDETLSYSCFGGEVRPKVVDQTNPYTDVRRYWMAYMLFY QRYSDOMSPVLPKKRNSVVVQUERBCGGKGKWFFDTVS HRYNDRLSILTKLUKKGEKGLFYSKMPARIYQDKLKSL HOLLEVULALLDEDVPERCKACQFFTSFTGVTQGGTRAGDLI. LRHSALBHHISFILGASRONNQIRRWSSAQAREFORLINTVALL VHSDVSSGRNVAPGFTKQRPFISSPSLLPHEEVBALFFMLH SEGRPYLLEWMPALRELTGSLLALEWYVCCFCNEHSFFTMLH PIKNQLSTAPHBELKNTFOLHEILVIEDPIOVERKYFFTENH SEGRPYLLEWMPALRELTGSLLALIEWYVCCFCNEHSFFTMLH PIKNGLSTAPHBELKNTFOLHEILVIEDPIOVERKYFFFENH WSWAVQNICKMSEHWATLGSNVSNETSTGKTGRTISAQOTLA SCERFFTLYGGTKAPATLALIELEFTGAPFDPPCHAMIGNISG CCSRGPSVEDGKWYGVRSVLHLEYEGYAPPRLEGIGGEFLV LDQRAADYNQALGTCALGTALAGALACAGALLAICLFWAMIGNISG DTKREPLDPBADSHVEVFGDBPQQLSPIFRNASGGWFSPPAS PFGGSSVQTIQFRNS PFGGSSVQTIQFRNS PFGGSSVQTIQFRNS PFGGSSVQTIGFRNS VEKLFPTKESLIMHJMYPSLSLTGGAFFGGILLEPMALVYLYIGNKYNTL GLHRWIANIDDTGYLAAKRAIRTTVFGTEPDRIDLVALLG GLHRWIANIDDTGYLAAKRAIRTTVFGTEPDRIDLVALLG GLHRWIANIDDTGYLAAKRAIRTTVFGTERDRIVTGTFLXMF	ì		i	
CENTLGSYRCSCASGFLLAADGRCEDVRECEAGRCSGECANTY GYQCYCRGGYQLAEDGHTCTDDECAGGGILTCFRCLNYPGS YQCACPEGGYTMTANGRSCKDVDECALGTHNCSEAETCHNIGGS FRCLRFECPFNVVQVSKTKCERTTCHDIEGCONSFARITHYQLN FOYGLLVPAHIFRICPAPAFTGDITALNIKGNEEGFGTRILN AYTGVYYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT TFAL  6864  2 2933  LADSSPSNLDITIKELLSMHHQPDPALTKEPDYLPPVDSRSSGG FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV FYQVQSLFCHLMESKLQYYVEDRWKLFKMMKKELYVEEQQDAY EFFTSLIDQMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDQIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDGIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDGIFKNTFQGITSDOKICKDCPHRY EFFTSLIDDMDBYLKKMGRDGIFKNTFQTVICKGRSWYKNDTFUTS  GRYBLICUTURTKKKLRVUTEEGRYPKVYDQTNLYTDVRRYNAYMLFY QRVSDONSPVLPKKSRVSVVNQEAEDLSLGABSPEISFGSSSFFISPGSSFF PHRRNNDRLSILTKLVKKGEKGLFYSKMFANIYADAWLFY GRYSDONSPVLPKKSRVSVVNQEAEDLSLGABSPEISFGSSFFISPGSSFF PHRRNNDRLSILTKLVKKGEKGLFYSKMFANIYADAWLFYIS SEGRELKIFLLEGVNTREVRAVALLEKTPYYDCKKKSL HOLLEVLLALLDKDVPENCKACAQYFFLPNTFVQOKLKSL HOLLEVLLALLDKDVPENCKACAQYFFLPNTFVQOKLGTRADLI LIRKALRHMISFLLGASRQNNQIRKNSAQAREFCNLINTVALL VLHSDVSSQNNAPGIFKQRPPISTATGKTFQRFISADDTLA VATALLMEKSQSGSSNGSSSPANENGDRHLQQGSSSPMMGEL SEGREPYLLEWMFALRELIGSLALIEMVYVCCTCREHEFSFTMLH WSWAVQHLOKKMSEHYWTLOGNUTSTTGKTFQRFISADDTLA VATALLMEKSQSGSSSNGSSSPANENGDRHLQQGSSSPMMGEL RDDLDDVDP  6865  1820  1820  1820  1842  DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMFSCNRS CSGRGSVEDGKWYGVRSYLHLEFYEGYAVPFLEGIGEGEFLV LDQRAADYNQALGTCHAAGVILDAILTHYGTKELPMGLIVSOK DTKAEPLDPBADSHVEVFGDDFSGTFGGILHEPMALDVALLG SLVDSSGHILVPGITNSAVFWCRDDDFHSGFFGGILHEPMALDVALLG SLVDSSGHILVPGITNSAVFWCRDDDFHSGFFGGILHEPMALDVALLG SLVDSSGHILV	1	t	1	
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YQCACPEGGYTMTANGRSCKOUDECALGTHNCSEAETCHNIQGS FRCLRFECPPNYVQVSKTKCERTTCHDLECONSPARITHYQLM FQTGLLVPAHIFRIGPARAFTGDTIALNIIKGNEEGYFGTRIN AYTGVYLQRAVLEPREDFALDVEMKLMRQGSVTFTLAKMHIFFT TFAL  6864 2 2933 LADSSPSNLQIIIKELLSHHHQDPALITKEFDYLPPUDSRSSSG FVGLRNGGATCYMNAVPQQLYMQPGLPSSLGSVDDDTONPDDSV FVQVGSLFGILMESKLQYYVPENFWKIFRMNKELYVREQODAY EFFTSLIDQMDEYLKKMGRQQIFKMTFQGIYSDQKICKDCPHRY EREEAFMALMIGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLPSVLVIHLMRRGFDWBGGSFRKXVBLT ENYSLVGVIVHSGQAHAGHYSFIKDRRGCKGKWYKFNDTVLE EFDLINDETLEYECFGGEYPRYVDQTNPYTDVRRYNNAVMLP QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR PHRPNNDRLSILTKLVKKGKRGLVFURFARIYGMYRDENLKF MKNRBVYSSGYPFSVLSLASLANTKLKHPYYFCHAKVSLQLAIQ FLPQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQMLVEYFIS SEGRELKIFILKENVREVENATIEATLSKSFDACQMLVEYFIS SEGRELKIFILKENVREVENATIEATLSKSFDACQMLVEYFIS LRHSALHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGLVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCKGVFFRRNSGAGREFGNLHNTVALL LRHSALHHMITSFLUGSRCHVATUGCFCNEHFSTMLH SEGRFYLLEWMFALRELITGSLALALEMVVCCFCNEHFSTMLH SEGRFYLLEWMFALRELITGSLALALEMVVCCFCNEHFSTMLH WSNAVQWLOKKMESHYMTLOSNVSNETSGKTFGRTISAQDTLA YATALLAEKEGSGSNGSESSPANENGDRHLQCGSESPMMIGEL RSDLDDVDP GESWKILLSKUTPPGSSVSTTFVQVVRLQSFQSGSMMFSCNRS CSCSGGSSVEDGKMYGWRSYLHLFYEGXAVPFKLEGIGEGEFLV LDQRAADYNQALGTCRLGATAL-CVAAGVLLALCIPMANIGMLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGGSSVOTTOBYRDS  6866 1571 495 DCPRFYTLYGLRATCMRDLDWANNAVSAFKALEQDLPVNIKF IIECMERGSVALEBLUFKKKDRFFSGVLYVIVISDNILIGGRKF VEKEIFDTKEELITHLMRYPSLSIHGIEGAFFLDFTKEVINGRV VEKEIFDTKEELITHLMRYPSLSIHGIEGAFFLDFTKEVINGRV VEKEIFDTKEELITHLMRYPSLSIHGIEGAFFDFGTKTVIGGRV VEKEIFDTKEELITHLMRYPSLSIHGIEGAFFDFGTKTVIGGRV IGKPSIRLVPHMNSAVEKOVTPHLEDUFSRNSSRNAVVSMTL GLHPWIANIDDTGYLAARARRTVFGTEPDDNIRDGSTIPIAAMF  GEHWKSVVLIPPLGAVDDGEHSGRGERGFGTKNVBNYIEGTKLPAAPFI  GEHWKSVVLIPPLGAVDDGEHSGRGFGTENGRTNIEGRTIPIAMM	1	1		1
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AYTOVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT TFAL  LADSSFSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSG FVGLRNGGATCYMNAVPQQLYMQPGLPSLLSVDDDTDNPDDSV FYQVQSLFGHLMESKLQYVYPENFWKIFKWMKELYYREQDDAY EPFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDCKICKDCPHRY EREEAFMALNLGVTSCQSLEISLDGPVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRPP WMLMMEPYTVSGMARQDSSSEVGENGRSVDQGGGSBRKKVALIT ENYBLVGGIVHGSQAHAGHYSFIKDRRGGCKGWYKFNTDVIE EFDLINDETLEYECFGGEYRPKVYDQTMPYTDVRRYWNAVMLFY QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR HRRNNRRLSILTKLVKKGEKKGLFVERWPARIYQMVREDNLKF MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLOLAIQ FLFQTYLRTKKKLRVDTEEWHATTEALLSKSPACQMLVEYFIS SEGRELIKIFLLECNVREVRNAVATILEKTLDSALFYQDKLKSIL HQLLEVLLALLDKDVPENCKAQYFFLFNTYQKQGIRAGDLI LRHSALHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VIHSDVSSQRNVAPGIFKQRPFISIAPSSPLEHHEEVEALLFW SEGRFYLLEVMFALRELTGSALLIEMVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVTCCFCNEHFSFTMLH FIKNGLETAPPHELKNTFQLLHEILVTEDPIQVERVKFVFETEN GLALMHHSHNIVDSSCCYCKFUNTLAQKCPAAKEFYKENSHH MSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLMEKEQSGSSNGSESSPANENCDRHLQCSESSPMHIGEI CSCSRGPSVEDFGWYGVEKVETUTAQKCPAAKEFYKENSHH MSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLMEKEQSGSSNGSESSPANENCDRHLQCSESSPMBGCNRS CSCSRGPSVEDFGWYGVEKVETUTAQKOPAAKEFYKENSHH MSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLMEKEQSGSSNGSESSPANENCDRHLQCSESSPMBGCNRS CSCSRGPSVEDFGWYGVEKYLDLFYEGYAVPPKLEGIGGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDBFEQQLSPIFRNASGGSWFSPPAS PFGGSSVGTIOPKNS  TIEGMERAGSVALEELVEKEKDRFFSSCUTYUTSIDNUMISQRKP AITTGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKKFLFDTKEEILHHLNRYFSLHGHIEGAPEPGTKTVTJGRV TIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSRNSSNKNVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDNIRDGSTIPIAKMF OEIVHKSVVLITPLGAVDDGEHSQREKINRWYIEGTHLFAAFFI	į.	}		FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
TFAL  LADSSPSNIQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSG  FVGLRNGGATCYMNAVPQQLYMQPGLPESLLSVDDDTDNPDDSV FYQVQSLFGHLMESKLQYYPPENFWKLFMMNKELYREQODAY EPFTSLTDQMDBYLKKMGRDQIFKNTFQGTYSDOKICKDCPHRY EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKVDGIFFF MMLMMEPYTVGSMARQDSSEVGENGRSVDQGGGSBFKKVALT ENYELVGGIVHSGQAHAGHYYSFIKDRGCGKGKWKFNDTVIE EFDLINDETLEYECFGGERYRVVDQTBPYTDVRRYWNAVMLFY QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR PHRPNNDRLSILTKLVKKGEKKGLFVEKMFARIYQWRDENLKF MKNRDVYSSDYFSFVLSLASAMKKLHFYYPCMAKVSLOLAIQ FLPGTYLRTKKKLRVDTEWIATLEALLSKSFDACQMLVEFFIS SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVDENCKNCAQYFFLFNTFVQKQGIRGGDL LRHSALRHMISFLLGASRQNNQIRMSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISLAPSSPLLPHHEEVEALLFM SEGRPYLLEVMFALRELTGSLLALIEMVVCCFCNEHFSFTMLM FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFFETEN GLLALMHHSNIVDSSCCYQCKFLVTLAQKCPAAKEYFKENSHH WSNAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA VATALLNEKEGSGSNGSESSPANENGDRHLQQGSESPMMJGEL RSDLDDVDP  6865 1820 1242 DPERWKHLSKVTPPGSSVSTTPVQVVVRLQSFQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRADYNQALGTCRLAGTALCVAAGVLALICLFWAMIGMLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGGSSVQTIQPKRDS  6866 1571 495 DCPRRYYTLYGIRATCMEDLDWAWINAVSAFKALEQDLPVNIKF ILEEMERGSVALEELUEKEKDRFFSGUDTIVISDNIWISGKKP ALTYGTRGNSYFMVEVKCRQDDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYYGLVFLIEEEINTYKAIHLDLEEYRNSGS VEKKFLFDTKEEILHHLBKYYPSLSIHGIEGAFDEFGTKTVJFGRV VEKKFLFDTKEEILHHLBKYYPSLSIHGIEGAFDEFGTKTVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRV VEKKFLFDTKEEILHHLBKYPSLSIHGIEGAFDEFGTRVJFGRW VEKKFLDHINNVSAVEKQUTRHLEDUFSKRNSNKWVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGETPDNIRGSSTIPIAKMF		1		FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSGG FVGLRNGSATCYMNAVFQQLYMQLPESLLGSVDDTYDNPDDSV FYGLRNGSATCYMNAVFQQLYMQLPESLLGSVDDTYDNPDDSV FYGVQSLFGHLMESKLQYTYPENFWKIFKMWKELYVREQQDAY EFFTSLIDQMDEYLKKMGRDQIFKMFYGGIYSDOKICKDCPHRY EREAFMALNIGVTSCQSLEISLDQFVRGSVLEGSNAYYCEKCK EKRITVKKTCIKSLPSVLVHHLMRRGFDWESGRSIKYDEQIRFP MMLMMEPYTVSGMARQDSSSEVGERGRSVDQGGGSBPKKVALT ENYSLVGUIVISGQAHAGHYYSFIKDRRGGGKKWKYKFNDTVIE EFDLNDETLEYECFGGEYRPKVVDQTNPYTDVRRRYWNAVMLFY QRVSDQNSPUPKKSVEVVRQEABDLSLSAPSSFBISPGSSRR PHRPNNDRLSILITKLVKKGEKGLFVEKWPARIYQWRDENLKK MKNRDVYSSDYFSFVLSLASLMATKLKHPYYPCMAKVSLQLAIQ FLFQTYLRTKKKLRVDTBEWIATIEALLSKSFDACQWLUVEYFIS SEGRELIKIFLLECNVREWRVAVATILEKTLDSALFYQDKLASL HQLLEVLLALLDKDVPENCKNCAQYFFLENTFVQKQGIRAGDLL LRHSALRHMISFLLGASRONQIRRNSSAQAREFGRILHTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMH FIKNQLETRAPPHELNNTFQLHEILVIEDPIQVERVKFVETEM GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLMBKEGSGSSNGESSSPANENGDHLLQGSSESPMIGEL RSDLDDVDP  6865 1820 1242 DPERKHLSKVTPPGSSVSTTPVQVVRLOSPQSGGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADVNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAPFLDDEADSHVEYGDEPPQQLSFIFRNASGGSWFSPPAS PFGQSSVOTIQPKRDS  6866 1571 495 DCPRRFYTLYGGRATCMEDLDWAWINAVSAFKALEQDLPVNIKF IIECMEEAGSVALEELLVEKEKDRFFSGVDYIVISDMLWISQRKY AITYGTRGNSYMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLIEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTKTVTHGRW VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTKTVTHGRW VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTKTVTHGRW VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTKTVTHGRW VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTKTVTHGRW VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTRTVTHGRSR VEKFLFDTKEEILMHLWRYPSLSIHGLEGAFDEPGTRTVTHGRG UFKFSIRLVPHMVSAVEKQVTHHLEDVPSKRNSSNRWVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGGEDDNIRDGSTIPTAKMF GEHWHANIDDTQYLAAKRAIRTVFGGEDDNIRDGSTIPTAKMF GEHWHANIDDTQYLAAKRAIRTVFGGEDDNIRDGSTIPTAKMF		1	ŧ	AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
FVGLRNGGATCYMINJFQQLYMOPGLPESLLSVDDDTDNPDDDSV FYQVQSLFGHLMESKLQYYVPENPIKLTKMMNKELYVREQQDAY EFFTSLIDQMEYLKKMGRQQTFKNTFQGIYSDQKICKDCPHRY EREAFMALNIGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK EKRITVKRICIKSPSULVIHLMRGFGPMESGRSIKYDEQIRFP WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPKKVALT ENYELVGVIVHSQGAHACHYYSFITURRGCGKGKWKFNDTVIE EFDLNDETILEVECFGGEVRPKVVDQTNPYTDVRRRYWNAYMLFY QRVSDQNSPULPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR HRPNNDRLSILTKLUKKGEKKGLFVEKMPRIYQMVRDENLKF MKNRDVYSSDYFSFVLISASLMATKLKHPYYPCMAKVSLQLAIQ FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQMUEYFIS SEGRELIKIFLLECNVRVAVANTILEKTLDSALFYDOKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKOGIRAGDLI, LRHSALRHMISFLIGASRQNNQIRRWSSAQAREFGNLHNTVALL VUHSDVSSGGRNAPPGIFKQRPPISIAPSSPLEPLHEEVEALLFM SEGRPYLLEVMFALRETGSLAALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLHEILVIPDFIQVERVKFVETERN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSMAVQWLQKKMSEHYWTLQSNVYSETSTGKTTQRTISAQDTLA YATALLNEKEGGSSNGSESSPANENGDRHLQCGSESPMIGEL BEDDLDDVDP  6865 1820 1242 DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDCKWYGVSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADVNQALGTCRLAGTALCVAAGVLLAICLFWMMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGGSSVQTIQPKRDS  6866 1571 495 DCFRFRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF ILEMBEAGSVALEELLVEKEKDRFFSGVDYIVISDNIMISQRKY AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEBINTYKAIHLDLEEYRNSSR VEKKFLFDTVKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRV VEKKFLFDTVKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRW VEKKFLFUKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRW VEKKFLFUKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPYSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGLEGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGLGAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGEAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGEAFDEPGTKTVTPGRY VEKKFLFUKEEILMHLIMKPSLSIHGEAFDEPGTKTVTPGRY VEKKFLFUKEEILMHMINGLGGAFLEPALFAFL	1	i	1	TFAL
PYQVQSLPGHLMESKLQYYVPENFMKIFKMMKELYVREQQDAY EFFTSLIDQMDYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY EREAFMALNIGVTSCQSLEISLDQFVRGEVLEGSMAYYCEKCK EKRITVKRTCIKSLPSVLVIHLMRFGFDMESGRSIKYDEGIRFP WMLMMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPKKVALT ENYELVGVIVHSQQAHAGHYYSFIKDRRGCKGKWYKFNDTVIE EFFDLNDETLEYECFGGEVRPKVVDQTNPYTDVRRRWMAYMLFY QRVSDQNSBPVLPKKSRVSVRQBABLISLSAPSSPEISPGSPS PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF MKNRDVYSSDYFSFVLSLASLARATIKKHPYYPCMAKVSLQLAIQ FLFQTYLRTKKKLRVDTERIATIEALLEKSFDACQWLVEYFIS SEGRELIKIFLLECKVREWRVAVATILEKTLDSALFYODKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDIL LRHSALRHMISFLLGASRQNNOIRRMSSAQAREFGRLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISTAPSSPLLEHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYVCCFCNEFFSFTMLM FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSSCYQCVKFUTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP 6865 1820 1242 DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGUSQ DTKAEPLDPEADSHVEYFGDREPQQLSPIFRNASGGSWFSPPAS PFGGSSVQTIQPKRDS  6866 1571 495 DCPRFFYTLYGLRATCMRDLDWAMINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDILWISQRKY AITYGTRGNSYFMVEVKCRDOPHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTKTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTRTVTPGRV VEKFLFDTKEEILMHLMRYPSLSIHGIEGAFDEPGTRTVTPGRT JGKFSIRLVPHMVSAVERQVTVHLEDVPSKRNSSNRMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDNIRDGSTIPTLAKMF GEIVHKSVVVLIPLGAVDDGEHSQNEKINRWYIEGTKLFAAFFI	6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY EREBAFMALNIGVTSCQSLEISLDQFVNGEVLGGSNAYYCEKCK EKRITVKRTCIKSLPSUVIHLMRFGFDWESGRSIKYDEQIRFP WMLMMEPYTVSGMARQDSSEVGENGRSVDQGGGSPRKVALT ENYBLVGVIVHBGQAHAGHYYSFIKDRRGCKKKWKFNDTVIE EFFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRYWNAYMLFY QRVSDQNSPVLPKKSRVSVVNGAEDLJSLSAPSSPEISPQSSPR PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLOLAIQ FLFQTYLRTKKKLRVDTEEMIATIEALLSKSFDACQWLUEYFIS SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFIFNTFVQKQGIRRGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHHTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGRYYLLEVMPALRELTGSLLALIEMVVYCCFCKEHFSFTMLH FIKNQLETAPPHELKNTFQLLHAILVAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP  6865 1820 1242 DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQSMMPSCNRS CSCSRGPSVEDGKWYGVSVLHLFYEGYAVPPKLEGIGEGEFLV LDQRRADVAQALGTCRLAGTALCVAAGVLJALCHAMMIGNLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGGSSVOTIOPKRDS OTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGGSSVOTIOPKRDS OTREPSTLYGLRATCMCDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGRSYEMVEVKCRDQDFHSGTFGGILHEEPMADLVALLG SLVDSSGHILVPGHYDEVPLTEEBINTYKATHLDLEYENNSS VEKTLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMWVSAVEKQVTRHLEDDVFSKRNSSNKWVSMTL GLHPMIANIDDTQYLAKKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF GLHPMIANIDDTQYLAKRAIRTVVEGTEPDDNITRGSTIPIAKMF	1	j		FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
EREAFMALNLGVTSCQSLEISLOFVRGEVLGGSNAYVCEKCK EKRITVKRTCIKSLPSVLVIHLMRFGFDWBGGRSIKYDEQIRFP WMLMMEPYTVSGMARQDSSSEVGENGRSVDQGGGSPRKKVALIT ENYBLVGVIVHSGQAHAGHYYSFIKDRGCCKGKWYKFNDTVIE EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY QRVSDQNSPVLPKKSKUSVVRQEAEDLSLSAPSSFEISPQSSFR PHRPNNDRLSILITKLVKKGEKKGLFVEMPARIYQWVRDENLKF MKNRDVYSSDYFSFVLSLASLMATKLKHFYYPCMAKVSLOLAIQ FLFQTYLRTKKKLRVDTEWIATIEALLSKSFDACQWLVEYFIS SEGRELIKIFLLECNVREWRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPFJSIAPSSPLLPHLEEVERALLFM SEGRFYLLEWPMALRELTGSLLALIEMVVYCCFCHEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVSLPDIQVERVKFVFETEN GLLALMHHISHNHDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP 6865 1820 1242 DPERWKHLSKVTPPGSSVSTTPVQVVRLQSFQSQGSMMPSCNRS CSCSRGPSVEDGKWYGGNSYLHLFYEGTAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEYFGDEPEQQLSFIFRNASGGSWFSPPAS PFGQSSVQTIQPKRDS 6866 1571 495 DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGDYJVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMWVSAVEKQVTRHLEDUFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAKKRAIRTVFGTEPDDNIRGSTIPIAKMF GLEHWIANIDDTQYLAKRAIRTVFGTEPDDNIRGSTIPIAKMF GLEHWIANIDDTQYLAKRAIRTVFGTEPDDNIRGSTIPIAKMF GLEHWIANIDDTQYLAKRAIRTVFGTEPDDNIRGSTIPIAKMF GETVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL	l	1	i	FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
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AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL	1 0800	15/1	495	
SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL				
VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL	1		1	
IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL	1	1		
GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL	1			
QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL		1		
	1			
EMAQLH	1			QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL
	1	}		EMAQLH

0~~	I was a second		
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, F=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1 .	1	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i .	amino acid	sequence	Codon, /=possible nucleotide deletion.
6867	sequence		\=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPOESRSPORSP
1		i i	LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
		1	YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILOAP
1 1		[	KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKOL
			LPGAEGYVGGHRTSKIMRFVDKITKSKYFOKATETEFIKKKIEF.
1			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HSAMDPRSTSCLLKDPPVEAADQP
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
[ [			KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1			KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
1 1			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
1 1		,	NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
			LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
l			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENOLNKFLONLLSDER
	i		LCQSEALYAFLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEOMLVYYINIF.
1			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLOSI.
į			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
6070			HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
ļ			DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
j	i		GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEOLLPELLKKAG
i			YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
ŀ	1		NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRO
1	1		ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
- 1	- 1		IGKILELLQDLHVADNTFVFFTSDNGAALISAPEOGGSNGPFLC
-			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
ŀ	Į.		AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
1	- 1		QHKAHFWTWINSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
			IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
6871	209	1100	QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
	203	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTS1ASEDPLQNLCLAS
1	}		QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
!		!	KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
ľ		l	EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
- 1			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNOTNKTFTDF
ł	1		RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
6872	990		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
00/2	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
1	1		KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
I	[		LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
6873	1000		PTSRPPPR
00/3	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
i	•	l	IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSOKEK
ļ	İ	(	DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
1			DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
ł		1	CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
1		1	QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
	ļ.	.	DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 740;	location	corresponding	1 " "
]		to first	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	
<b>!</b>	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł		sequence	Codon, /=possible nucleotide deletion,
- 6000	sequence	ļ	\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
		1	GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
			SCPDLPSQTDKKCS
6875	1688	349	VIGTGERGNSÄSEKWEIMFNEELGDPFIIIHSISLLNAEEHSTA
ł			TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
<b>[</b>		<u> </u>	LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
1			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
(		[	VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
1			PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
1		]	CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
1		l	IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
1	}		QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
1	1	l	KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
	l	<u>L</u>	KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
1	<b>!</b>	i	LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
1		ì	DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
1	1		RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
1		į.	VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
1	1	j	EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
1		1	PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
1		1	EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
1		į.	PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
i	ł		AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
J	1		QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
1		Į.	PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
1	1	Ī	EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
į.		i	IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
ł	i	Į.	LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
ı			EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
1		ŀ	TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
			VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
1			II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
l	1		KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
1	1		FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
1			FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
1			NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
1		1	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE
1			CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
1			MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
1	1		NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
[			VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
1	1		KPOVPEYAPROERIRDLSGNLWERSSGDGEELERLTKPKSDESD
1			EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
1		2233	QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
1 3302	*	030	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
1	]		TNAVHKCRVHGLEIEGRDCGEATAOWITSFLKSOPYRLVHFEPH
1	1		MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK
<u> </u>	<del></del>	<u> </u>	SWELVEL UNITED TO LOCK TO THE WASHINGTON TO SERVICE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
I	amino acid	amino acid	P=Proline, Q=Glutamine, R≈Arginine,
l l	1	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<b></b>	sequence		\=possible nucleotide insertion)
1		ì	KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
ļ			LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
6883	2794	2256	VLENPGTIKVGDPVYLLGQ
0003	2/39	2256	NSKLKLNQNLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
1		†	ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
		1	DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
Ì	1	1	NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
6884	2	99	ANC
6885	297		BFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
0000	231	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
1	l.		TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
	ł	{	YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
		1	LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
1	1	{	GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
1			MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
		[	DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
1			LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA IMNLDNISYADCLKOLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
****	_	7247	
			QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
ŀ			GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
1			LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
1			QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
Į į			VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
			DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
•			GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
			KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1			GQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
1			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
1			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
[ ]	ļ		LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
			SL
6888	1.	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
1 1	,		NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
			IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
1			LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
			EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
1 1	1		LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
	į		AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
ļ			LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
1 1	}		AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
j ĺ			ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
}	. 1		ICEKHILWLKDYKNSSNWKLFKECNKQGQPAVVSGVHKKMNISL
			WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
} . [	1		KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
j !	i		EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
1 1	1	İ	EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
{	ţ	ĺ	DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR
L			DQSWYVNKKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
			NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
j	}	1	NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
	1	007	TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
1	1		AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
i	l		ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
1	1	i	LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
1			V DINDEFF V V DOGNE F DATABLE F V SDRAKAEQQ V NQDAMPPAS V K
6891	1980	1262	
1	1	1202	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
1	l		AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
1			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
1	1	1	LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
1	1		VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
1	1	1	FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
	ł		QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
	l .		NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
1	1		TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
	ì		SQAHLHLKHARSFHKTVPVKAFPAFLOTVSLEDFLKKIORVDFD
ł		1	IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
1	1	1	RTVTIKLKNVNFEVKTRASTVSSVVSTABEIFAIAKELLKTEID
	ļ.		ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
}	1	j	ATECTLEKTOKOKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
ì			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
	1		NVPASSLCEKODYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
1	1	ł	DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
1			VFNPW
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLOSTSEDKEOOYTSOT
Į.	Ì	ĺ	TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
1	1	1	VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
1			EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
ì	1		AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
1	l		EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
1			QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
1	1	l	SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
i	1		MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
1	1	)	SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
1	1	1	PPPRGRGRGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
I			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
1	Į.	]	PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
			KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
ł	1		FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
1	1		SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
1	1		SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
L			DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
1			AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
i			SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
1	İ		YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
	I		DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

SEQ	Predicted	1 5 2 2 2 2 2 2 2	
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Ì	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	4		(=possible nucleotide insertion)
1			LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
6898	919	346	LMVSEAVQQQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
1	1	320	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW
1		ł	LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFIMGILNPA
i	1	j	QGFLLSLAFYGWTGCSLGFQSPRKEIQWESLTTSAAEGAHPSPL
1	1		MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC NKNEGDPALPTHGDL
6899	120	827	
1		""	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
1	Ī		LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
ŀ	į.		TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
1	[	ĺ	NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
İ	į		EIDKATEHKHTLEERQRTEERHRTETGTPWKTKYFIKEGDGWVY
6900	3	451	HKPLWKIIPTTQPAE
	. •	331	TEVLGSKGIHELRSSTSALHHALEESASLLTMFWRAALPSTHIP
			VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQQKES
			MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
6901	1	201	LADLVGDSWPALRFQEK
	_	201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
6902	2	267	SFPKAARQFLLKWSFYRYHLGFS
1	_	207	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
6903	1	149	SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
1	_	119	RINQVYRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI HIILK
6904	464	2092	
1 1		2032	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
			VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
1 1			DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
1 1	1		SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
!!!			AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
j			VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
1 1			TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
			CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
1 1	Í		RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
1 1			ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
			IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
1 1			FRKDFEPYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
<u> </u>	İ	- <del>-</del>	VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
6906	3	611	SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI
j [	1	•	ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET
	]		TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
1 }	į		PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
L	İ		SFAPDIDGDEDLPGPPVRYYFSHDTD
6907	2	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS
1	Ì	1 1	SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
	į		DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
		i	GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS
		ļ	SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
1		i	SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ
!!!	,		TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL
		ļ	FRRIENTA PERCENTA PERCENTA PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PROCESS PRO
	1		ERRLEALAAEFSSNWQKEAMRLERLELRQGAFGQGGGGLSHED
	1		TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE
ĺ			DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE
			DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFFA WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS
			"TOW THROUGH VOID OKER MOAD DRELESKILTHVAE MOCKS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	
	to first	amino acid	L=beucine, M=Methionine, N=Asparagine,
ł	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W≈Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Į	<b>[</b>	1	AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA
1	Ì	į	DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
ļ	ł	ĺ	nstissapkdfaifgfdedlogegtllgkftydodgepiotphf
			QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
ł		1	PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
	1		QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
l .		ł	GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
Į	1		AFILPSGGKISSALHFCRAVCRRAERRVVPLVOMGETDANVAKF
	1		LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
1			SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
1			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
l	ł		LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
		ł	LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
j	1		LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
1	ł	ł	LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
1			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
		1.	NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
Į		}	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKOIRK
1	1	ſ	KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
	1201	1 300	PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	· -	044	SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
1	ĺ	Ī	GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
		ł	YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
	İ	1	
	ł		DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
	l	į.	SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS NPETLDLYRDIPELQGF
6913	1643	. 1558	
6914	1251	615	KKSHEESHKEELSYGAQASLPLPCSDFR
1 0,14	1237	012	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSATRSQHSGVDI
I		İ	CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
l	İ	l	ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
1	1		QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
6915	254	<u> </u>	CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
1 0313	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
ŀ			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
<del></del>			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
Į.			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
		L	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
į			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	<u></u>		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
i			DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
1			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
•			LGRHCPTVSFVLRAODDAFVHTPALLAHLRALPPASARSLYLGE
			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
		i	
<b>!</b>			LLRAAARVAPFPFEDVYTGLCIRALGLVPOAHPGFLTAWPANRT
			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT ADHCAFRNLLLVRPLGPOASIRLWKOLODPRLOC

SEQ	I Decati		
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid r-
1 70:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
İ		corresponding	H=Histidine, I=Isoleucine, K=Lycine
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine.
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
6919			\=possible nucleotide insertion)
0313	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
Ì	1		ELDKLHKEVSTVRAANSERVAKLVFORLNEDFVRKPDVALSSVG
1	l	1	ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEDHVFDG
1		,	NCWAFEGDQGQVVIQLPGRVQLSDITLOHPPPSVEHTGGANSAP
			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSETOTPHI
1			QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
-6020	<u> </u>		AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
ł			PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
ı	l i		QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
i	ì		SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
1			NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
i			YIRLPLDPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
ŀ	! !		SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1	<b>)</b>		HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
l .	j [		IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
			EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
ľ	1		FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
i			SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
L			YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVRDREREREREREREKFPLDSTGSELKQNIHSIT
Į l			GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
[			VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
1			KGAQERLPTVPLSGMYNKSGGKVRLTFKLEODOLWIGTKFPTFK
i i	1		LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
6923			VDAIKDTVLGKWQYF
6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
1 1	l f		LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAOSGILSDPFV
1 1	1		VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINFFOOVESPWCY
1	1		SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYOVNIOTIEVEKK
1	I		QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATI.KCP
1			DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
6924	i		EIIFYT
6924	2210	1235	PEERVICEVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
ľ	j		KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEOVSHHPP
i			ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMTCEGVLD1.LE
	1		HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGVSATVIR
1	- 1		HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTVNNG
į	ı	į	ETKVIDTTTLPVYPKKIRPLEKOGPMESRNLWREVTRYLRI.GDT
ı	į		DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
			SPLESTLMGLEVQSFPV
6925	2	1653	RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLUESMCAL
ĺ			SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYOKEKDLCTKVF
i	•		DQWSESDQVEFVEHLISRMCHYOHGHINSYLKPMLORDFTTALD
l l			EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
[		}	ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
- 1	1	ł	IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
l	Ī		LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
1		1	TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
I	· 1	.	WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
]	·	j	STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
[	ĺ	ĺ	GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
}	ļ	Ī	RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL
		ł	NVPPSAQNETRSPSRTYTYISR
6926	1	733	SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL
		L	TOTAL TENEFRINGEN I KUCQSIGAPPL

SEQ	Predicted	Predicted end	12-3
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *sston
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1		1	DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
1		İ	YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
İ			PGAGGGRGFQMQPQHQHQHQHQHHPPGPGQPTPPPEALPCRDGT
1	!	ì	DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
6927	2	1484	SHGAISSVVSDASSAVYYCNYPDV
	}	2404	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
	1		CQGFAWATDLSTDLESQLSVSCKCYEAANEILQFRDLKSQNPEH YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
1			KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
1			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
	1	ļ	WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
	]		VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
	!		VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS
1			NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
			ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
1			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGOLAA
6928	1000		GSAASSNAVQ
0 9 2 8	1086	777	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
į	]		IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
6929	1749	607	ETEMKALGERVSIL
	,	007	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
1			NLHQHDPQDLRHNGNVVAGRPSCSRGPRRAIQKPQPAGGRRSG RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
			QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
			ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
1			KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
6020			QDAMLVDIEDLTRHAESQQKHMAEKMPAK
6930	131	545	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
			SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTOR
	ļ		RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
6931	2	<u> </u>	HSSLKQ
	_	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
			PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL
			LIPSCPGALTDLASSGSLARILQHFHSESKPICAVGHGVAALCC
	]		ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
6932	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
			SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
Į l	1		QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
	1		QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELQGKALKVFEA
	ļ		EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNI.WACI.
	j		HTSFAWLLKACGSRLTEKLLEGAPTEDTLVOMEKLADLEERSES
[	l	!	WDNSEAEEEEKAPVLPESTEGRELTOGPAESSSLSGCGSWOPRK
	Ì	.	LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
6933	1423		KTLQEVTDSLLGGWLMAQGVGGII
0233	1431	890	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
<b> </b>	ĺ		SDDDCPSASKVYKASDSAEAIEAFOLTPOOOHLIREDCONOKT.W
1	1		DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
	ļ		DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
6934	3030	2500	SKGR
		2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
		j	CWTPFFFVQMWSVWDANAPKBASAPIIVMLLASLNSCCNPWIYM
1		1	LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS HRSSSQRSCSQPSTA
		<del></del>	

SEO	Predicted	Day 32 - 1 - 3 - 1 - 1	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
j	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6935	886		\=possible nucleotide insertion)
1 0333	000	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
	i		VAMDGWLYAVGENDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
6936	1747		VGVAVLELLNFPPPSSPTLSVSSTSL
0330	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
1	1		TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
1			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
ļ.	l		NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
			AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
			DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVOOEPONGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTROA
ŀ			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMOYLREG
1			YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
			TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
1			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
1			ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
1	i ,		GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
i l			TGLORRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
			EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
}			LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
i l			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
			EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
			VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
	•		LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
1 1			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
1 1	· •		KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
			EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
1 1			VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
) [			HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVOLOGSG
1	1		RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
<b> </b>			AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
L l			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
L	i		QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKOP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
]	ļ		HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
	ļ		VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
l l			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
j /	İ		TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
1			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
<u> </u>			
}			LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
			FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYO
	. 1	ł	
]	1		SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
] [	1		VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL LNV
<u> </u>		1	ARTY.

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V≈Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
6945	sequence	ļ	\=possible nucleotide insertion)
0,45	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
İ		j	HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
1		1	IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY
ļ		1	RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
1			HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
1		1	LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
		1	AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
1		]	CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM
1	i		G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
1			LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
j	}	i	FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
1			GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
1		i	NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD
L			YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLP
}	1		NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
			NF/EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVOD\OD\LE
			AIRKODL\VEL\YLTN\CEKLSAKSLOTLRSFSHTLGVP+AFFC
			C\TNILLLRKENPGGL/CEDEYLFNPTCOVLVKDFTFEGFSRIR
1			F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIOTSDAA\FLTO
Ì			WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
1			YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
l			EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
1			IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
}			RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
			QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
1			VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
			NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
			RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
			WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ
1			GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
6000			ATARQETKEMARKVIEHCSNFKEENMDTSR
6947	2	1682	TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRGLKMLNVP
1			SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG
			LKGRLIEVTEEELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
	ŀ		DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
1 .	]		DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
] [	1		/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
1 1	]		MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
i i	l.		IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
1			HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
1	İ		IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLLA
] [	ĺ		AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE KLAPKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK
	ł		SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
6948	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSR
1 1	j	_	CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
[			AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
[ [		ľ	DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDQI
]			APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
[ [		ĺ	TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
<u> </u>			QETVE
6949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
			QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ	Predicted	I Due 33 - 1 3	
1D	beginning	Predicted end	The sequent containing signal manera-
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cvsteine, D=Aspartic Acid B
	location	-	Glutamic Acid, F=Phenylalanine G-Glucino
1	corresponding	corresponding	H=H1Stidine, I=Isoleucine K=Tyeine
	to first	to first	L=beucine, M=Methionine, N=Asparagine
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	II .	S=Serine, T=Threonine, V=Valine,
- 1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- !	sequence	sequence	Codon, /=possible nucleotide deletion
<b> </b>	Sequence	<del></del>	\=possible nucleotide insertion)
1	1		SCSTDTSEVPRWPENKEDHLVYADEESSNITDGPITPEDAVENT
i	1	· ·	BEPSTISTAST YPDVLTRVSLYRSHI NFSMI FSDAI UCODSTE
1			SAFPIGSSGFSLVKEIKDSTSOHDDDNISTTSGFSSDACDVDIT
	1		VSKNISLPPLWSPEAERSHSLSOHTATSSKKPAFNISAFCTICD
· I	i	1	SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVPOSKI.DNTDVOA
- 1		1	PVKKQMKAKQLSAQSYGVTSSTARRTIASI.FKMGGDIADAUDID
		Í	SIVSSPLNSPLDRSGIDITDFOAKREKVDSOYPPVORIMTDKDV
[	1		SIATNESVYPERPSLTPSGEFRETNORIDEKCSTGVFENMTPGON
į.	i	ł	REQRESGESYPHESLPAANGLSSGVGGGGGKMRRERHAEVACVD
ļ	1	1	LEEBEMEGPVLPKISLPITSSSLPTFNFSSPETTTSSDSDTMCC
	1	Į ·	QALINKVQMTSPSSTGSPMFKFSSPIVKSTEANVI.ppscicppp
		1	SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKVTDDEDG
1	1		EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAOPTATCDURV
- [	1		TRPAISSESSGIGEGESLKAGSSWOCDTCLLONKUTDNKCIAC
	j		QAAKLSPROTAKQTGIETPNKSGKTTLSASGTGFGDKFVDVICT
1	1		WDCDTCLVQNKPEAIKCVACETPKPGTCVKRAI,TLTVAKSESAET
1	]		MIASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAFDNVC
1	1 1		VSCMSEKPGSSVPTSSSSTVPVSLPSGGSIGLEKEKKDEGIMDG
ı			ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAACC
1		•	SFRFGVSSSSSGPSQTLTSTGNFKFGDOGGFKTGVSSDSGVIND
	1		MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGT.epgt.
1	1		SNPVFLTPFQFGVSNLGOEEKKEELLKSSCAGEPEGTGVINGTD
	1 1		VPANTIVTSENKSSFNLGTIETKSVSVAPI,KCOTSFAKKEEMDA
ł	1 1		TRUGGESFUNVEPASLPSASVEVLGRTEEKOOEDVTSTSLVEGEG
1	1		ALIMAEPAC\QPVFSFGEFOROTKDENSSKSTFSFSMTVDGPVP
1	] [		SEQPARATEAEGAQTNTTADOGAARPDLSYLNNSSSSSSTDATE
[	1		AGGG \ 1FGSSTSSSNPPVATFVFGOSSNPGSSS \ AFGNTAFGCT
į	1	i	SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTGGPGPG
		į	ATTISSSAGSSFVFGTGPSAPSASPAFGANOTPTFGGGGGASOR
1			NPPGFGS1SSSTALFPTGSOPAPPTFGTVSSSSOPPVFGOODEO
1		j	SAFGSGTTPNSSSAFOFGSSTTNFNFTNNSDSGVETECANSCED
	1		AASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
6950	2585		IAVRRK
	2383	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS
		1	DVPEQRDSKCKVKWTHEEDEOLRALVROFGOODWKFLACHPDND
1 1	1	ł	TDQQCQYRWLRVLNPDLVKGPWTKEEDOKVIELVKKYGTKOWTI
1 1		į	TAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDDTTCERHYD
1 !			LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
<b>!</b> !		j	APPVILLELEDKDGLQSAQPTEGOGSLLTNWPSVPPTIKEEEN
) 1	1	i	SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDOFGSDB
]		f	ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDDDAWCDLSKE (
1 1		1	DLPEEPSAEDSINNSLVQLOASHOOOVLPPROPSA\1.VPCVTPV
]		1	RELIGHTISDLSRSSRGELIPISPSTEVGGGGTGTDDGVLVDODV
] [	1	1	RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTI.PFSPSOFINE
j í			WARQUILELESPSLTSTPVCSOKVVVTTPI,HRDKTPI,HOVUAAR
1 1	ĺ	i	VIPUQKISMUNTPHTPTPFKNALEKYGPLKPLDOTPHT PEDL VP
1	1	. 1	VLKSEAGIELIIEDDIRPEKOKRKPGLRRSPIKKVPKSI.AI.DIV
]	1	1 -	DEDMKLMMSTLPKSLSLPTTAPSNSSSITT.SCIKEDNSII NOCE
[	ĺ	<b>.</b>	LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACCGTPDOLEMOR
6951	1940		KARQLLGRLKPSHTSRTLILS !
	1940	239	AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
ļ		j (	QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSOAAADMA
•	}	1 7	TPTPRAEGHPPT\TPSPPSLRO*PPPTIKAD/SSTCDADARMAT
		1 7	TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTPDDDDDD
1	1	1 1	PGSSRKGAGNSSRPVPPAPGGHSRSKEGORGPNDSSTDLGOVDD
		1	LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEQ	Predicted	Predicted end	I amino paid account in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the co
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
l l	1		TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
	· ·		SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
1	1		THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
			STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S
1	1		WPSACPSPP\LCPADGVLHEEEEEDRQPGEQPEAYGNNTHHPGT
}	1		TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
ļ			C C C C C C C C C C C C C C C C C C C
6952	658	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
1		-41	PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
Ì			ASPONDERI DI CU TERMENDENCOSE EQSASPEQUEGRDASALWI
6953	1512	349	ASRQARGELRLCLTTAVRGTSPSVSPVCQSS  NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
1	]	- = -	FSPUEDCKMCCINI\ KI EVELDAMBODYGOVECH
1			FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC
1			GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
1	]		EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA
i			YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
1			ETPEEREVRRMRDREAKRLQRMQETDEQRARRLQRDREAMRLKR
	]		AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
			ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
İ		_	*PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRLP
1			PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR
1			*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS
1			DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
			AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGGAPPNQVGSS
			VMQAMSTGI
6955	1968	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
			WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
			GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
	i 1		ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
1			LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
			/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
1 !			LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQLW
			KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY
1 1		!	GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
<b></b>			F
6956	8605	3839	QTSTS1FASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
1			DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS
1 1			PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV
]			TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGLT
1 1			ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWOGETW
) ]	j		YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF
1	ļ		EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV
			PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
} l	<b>,</b>		AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKKS
1 1	1		KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
] }	İ		KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRVP
			GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLOEGL
!	i		LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
1 1	ļ	l	PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
[ 1	ı	1	LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
; ;	İ		VLAKRIGRSEVEMEGPEECLGRRRSSRIMEVISGMEEEEEESI
			AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
1 I	İ		SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVIK
			KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
[	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
<b>[</b>	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
)	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Ston
ł	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
ļ			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
1	,		LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
ł			LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
ļ			SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
	İ	ĺ	PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
1	1		GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
j			SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
1	j		REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
1	Ī		AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIG
1	}		YEITPRIRVWRQTLERCRSAAQVCLCLGOLERSIAWEKSVNKVT
			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
i			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
1			GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
			SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
1			SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
L I	•		YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV RYNPDF
6957	82	3514	HLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
1			ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
i i			EDLSEKPTINGSRKWMDLASKAGKHLOLKETFERHSRVYTFEMO
1			IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
1 !			SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPOVDVWELLKN
1			TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDD
1 1			VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
1 1			CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
1	į –		EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
]			PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
1			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
			LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMNSRGDKAIMEG
1 1	i		SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASTK
	ŀ		VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIF
1 1	i		RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\I
1 1			GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
			GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
}		ļ	IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
		ļ	GAELDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
			TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
1			GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
		'	MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTODI.
	l	1	VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
6958	274	1000	NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
	~	1663	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLSL
	j	Ĭ	DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
	İ	1	HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC
1		ļ	WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRELQK
1			LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM
1		ſ	LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
1		!	LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
1	ļ	1	CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
ļ			RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLONTCEYNAFEDS
6959			SSSDPKVLTLFMAV\LPVVLGFS
	1	1469	SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	_	\=possible nucleotide insertion)
<b>——</b>			LOPOTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT
1			WTELEDROGRVYPHPODLLAALPLALVLLAMRLAFERFIGLPLS
1			RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGL
1	ŀ		TLOOTORWFRRRRNODRPOLTKKFCEASWRFLFYLSSFVGGLSV
1	<b>j</b>	İ	
1		•	LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWYLLELG
1		ł	FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH
1	i	ĺ	HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMQ
· ·		1	YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFF
İ		1	GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV
1	ſ	•	EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
		1	RHTTAT
6960	387	2068	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
			HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT
	į	1	PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHP
1	1	1	KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGK
1			TRKKPVVKKOAPGKASVSRKOAREESEESEAEPVQRTAKKVEGN
1	ļ	1	
1		t	KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWK
ł	<b>!</b>		PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG
1		1	DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA
į.			KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
1	1	<b>f</b>	SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
ı			ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
i			ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGB
į.			LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
6961	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
	1		NOESFOLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
	1	i	SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
1	ł	1	ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
	1		NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
	1	l .	TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
1		1	
1	1	İ	PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
1			LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6962	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
ì		l	NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
1		1	LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
1	1		SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
I	1	1	ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
1	1	Į.	NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
I	<u> </u>	1	TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
I	i	1	PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
1	1		LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
1	1		LYRAOAELOHVLGRAREAODLGPEPQLYALL\LGQQEGDRTKEQ
6063	<del> </del>	<del> </del>	1 7 7
6963	374	2618	RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
Į.		1	EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
J	1	1	LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS
1	1	1	PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
	i	1	LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
1		1	TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
1	1		RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
1		1	STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
i			ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
ı	1		EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
-1	1	I	
- (		1	RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR
L	<u></u>	1	QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid seguence Predicted end nucleotide location (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine, D=Aspartic Acid (A=Alanine, C=Cysteine,	d, E= ine, =Stop  ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequence location corresponding to first amino acid residue of amino acid sequence STASGQGEKKPYECTLCNKTFTAKQNYVKHFVHTGEK	=Stop  ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
location corresponding to first amino acid residue of amino acid sequence  location corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence  corresponding to first L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \_=possible nucleotide insertion)  PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPL STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	≃Stop  ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid sequence Serine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, M=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *Codon, /=possible nucleotide deletion, \	=Stop  ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
to first amino acid residue of amino acid residue of amino acid sequence  Tesperature  amino acid sequence  Tesperature  p=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \_=possible nucleotide insertion)  PFLFSLPQPLAGQOTQFVTVSQPGLSTFTAQLPAPQPL STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	=Stop  ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
amino acid residue of residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \ =possible nucleotide insertion)  PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPL STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPL STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
amino acid sequence Codon, /=possible nucleotide deletion,   -possible nucleotide insertion	ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
sequence   \=possible nucleotide insertion)   PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPL   STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	ASSAGH PHQCSI SLNVHM PAGTPP MHVSDG
PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPL STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	PHQCSI SLNVHM PAGTPP MHVSDG
STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEK	PHQCSI SLNVHM PAGTPP MHVSDG
	SLNVHM PAGTPP MHVSDG
	PAGTPP MHVSDG
RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTP	MHVSDG
GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMR	
6964 1 178 SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSI	CUTTIF
QIFIG\NCSMFVLVI	GKILL
6965 757 208 NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALE	1100000
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SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKD PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\C	
PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGST	LALKRY
FQESISTLE 6966 820 1867 IITALGVRGMPGCPCPGCGMAGPRILIFITALALELLGR	10000-
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KICLLPDQKNSKOTGVKRKTOKPVFERNTTE IP PILAGARTILL LTVVDPDKSSRCULGVSVPLCEVDLINGGHWKALI PSSONE VELGELLISLNYLPSAGRLNUTNI TRAKQLLQTTOVGOSDPPKKI OLVHGIKLIVKTKTS PIKAPST PVPKPSSFSKVPGGELENISLV PTVFGIRMKSSNDEIGRIVIG\QYSGP\SEPNHWRRMLNYTHT AVEQHNSLRSRAECDRVS PASLEVT  6971 37 3702 ACFVVFGSRSFKLIFREIGHENMGKESGKLPSGVSAKLKRWKKGHS SDSNPAICRHRQAARSRFSSPSGSGDLTVDAVKLHBLQGSGL RLGKSEAPETHBEEAELUTLEKSSGTFLSGLSDCTNVTPSKVO RFWESNSAAHKEICAVLAAVTEVIRSGGGKFTETEYFALTKRA AQMGVCSVLKGSEPMEKAPHIPAAISTAKFCIQSIEKSGGSK EATTTLHMITLLKDLLPCFPBGLVKSCSETLLRWTLSHLVDTVA CAMQAFISI,FHARPGLSTLASELNAQIITALYDVVPSENDLQPL LAMLKVMEKAHINLVKLQMDIGLGLHLPRFFGTAVTCLSPHSQV LITAATGSLKEILKECVAPHADIGSVTSASGPAQSVARMFRAV EGISTYKEHAAMSSVLQLLCVFFEACGRQAHPWRKCLQSLCDL RLSSHPHFHAALDQAVCAAVTSMPEVVJPLEIDGSSETLD FRSMLLPVIRDHVOGTRLGFFTTYFLFLANTLKSKAMDLAQAG STVESKIYNTLQMOMMTLLPGFCTRFTDVAPLEIDGSSETLD FPRSMLLPVIRDHVOGTRLGFFTTYFLFLANTLKSKAMDLAQAG STVESKIYNTLQMOMMTLLPGFCTRFTDVAPLDINSLLERASG VLDPASSIPFTLISVLDLVVALAPCADEAAISKLYSTIRPYLESK AHGYQKKAYNTLEEVCASPGGGALPVQCINSLLELASKTDVA KSALGFIKRVAVTWOQALATLITRYLCIPLUNSLLELASKTDVA KSALGFIKRVAVTWOVALHARHVQLWSLAIKSSDENDEN CARKNAFALLVEMHAPRIFGSNQEBALCCYLVLLYBGLVGAV WSCSILALITILLPEFEGIMGTSTVEQLLERVCLLLASKTRDVV KSALGFIKRVAVTWOVAHLARHVQLWBALIKKSJDMRRHFRMK LRHEFT\KFTRK\KQCQAASMAKSGGDFLNFLDFKVAQRVLA TQGGFGGGRKDHISFRVSADGRLITREADCANREBEEGAKGED EEERSGKGKGRKLARGRGSRAMLKGGGGBEPINFLDFKVAQRVLA TQGGFGGRGKDHISFRVSADGRLITREADCANREBEEGAKGED EEERSGKGKGGRANLARGGGGGSPLFINFLDFKVAQRVLA TQGGFGGRGKDHISFRVSADGRLITREADCANREBEEGAKGED EEERSGKGKGGRGVGHNRFRVSADGRLITREEADCANREBEEGAKGED EEERSGKGKGGRGVGHNRFRVSADGRLITREEADCANREBEEGAKGED EEERSGKGKGGRGVGHNSTRYGDFLNSLLING RXCMKLQGGGFGLVHAAGGSGCUCHNRRHCORGF PTRACKHYLDFLAGTBFPPPPPTATTERPGPATVPGGAGGGGARSAAGGGGRANAAATEDFNCKAGGGGGARGAGGGGARSAAGGGGAGGAGGGAGGGAGGGAG	ł	Į.		LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM			
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FVNBEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH PTERCFVF  6973 1 1964 LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA SPRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFVEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	1		1				
6973 1 1964 LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA SPRROEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	1			1 "			
6973 1 1964 LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	1			1			
SPRROBILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSBFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	6055	ļ	ļ				
KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY RMLSRPE/SGREHSVFTGVAIVHCSSKDHQLDTRVSBFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	6973	1	1964	_ ~			
RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSBFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	1	1					
KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL	1	1		_			
	1	1					
NVVGFPLNHFCKOLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL							
	L	1	<u> </u>	NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-)	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ı			SDVEGGGSEPTORDAGSRDEKAEAGEAGQATAEAECHRTRETLP
1	· ·	ļ	PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS
1			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
1			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNQHHRALGKKAEDLF
1	j	•	QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
1	ĺ		GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ
1	<u>j</u>		IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
j	1		KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
			QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
Ì	]		LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
1	1		SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
ľ			TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
1	1 '		LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
1	[		STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT
			PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
1	1		KELLOTEL SCELDWELMI + DEEDL WEDDEN + KODING
			KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPQAQKDVDAVDKVMK
	j		ELDENGDGEVDFQEYVVLVAALTVACNNFFWENS
6976	1216	970	GCOLANAVCTTENGRUMERALIPAGENTACIONETWENS
	1		GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
1 .			MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTERAVDQDKW
			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
	j i		PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKAFCKGK
1	j		ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
1 i			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
1 1	1		VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
1 .			ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
1 1	1		KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
			CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
L l			FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
į į			AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE
j l			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
]		ļ	AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
]			NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
] ;			DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
! Ì	}		DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
	1		VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
	İ		GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
[ ]	ł	]	DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
i i		į	GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
j	į		GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
	ļ	j	NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
1			RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
}		İ	EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
!		)	PPEKRFDNRGGGGFRGRGGGGGFORYENRGPPGGNRGGFONRGG
	[	·	GSGGGGNYPGGFNPSGGGGYGONPUGNPUGNPUGNPUGNPUGNPUGNPUGNPUGNPUGNPUG
J		İ	GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
1	]	j	PQQQPPPQQPPPPQQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTUSSYGPPOGPGTPPGTPARTER
ļ			PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
1	1		GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
6980	1	420	NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
	<del></del>		GTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT

SEO	Predicted	I needs and and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
(	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
1			CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
· I	1		GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
6981	10		SEKCSCCA
0301	}	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
1			APRLLEPQGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT RQSLRKLKQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
1			ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLO
I			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
1			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
<u></u>	<u></u>		PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVAWLAPP
			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
1			GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
			PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
1			YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
	<b>,</b>		KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPP
1		i	SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
1		·	LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
l			AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
1		İ	CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
1		ļ	IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
1		ľ	GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI
6004			KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
		ĺ	KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
1	İ	}	DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
1		,	GSLIVAFEGCPV
6985	1887	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	l		WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
1			YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
1			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
			LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
1	!	j	VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
	j		ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
			LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
	l		AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
	1		FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
1			DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
		•	KEIAEIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQEENC
1			RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
1			KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
1	1		VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
1			GOYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
1	ĺ		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
6988	3	689	ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
	,	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
1			FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
1			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL
	·	<u> </u>	TODAM AT VOID

SEQ	Predicted	Predicted end	l Amino and a
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
1 .	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			RPEKNFDSLESLISAIQGDIEEAKKRLELPEHLKIKEDNFFOVS
6989	2	1118	KSKIMNGH
1	_	1110	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
-	·		KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
j			ALVOVIEDKLKGEMMOLQHGSLFLRTPKIVSGKDYNVTANSKLV
1			IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV
i			SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
	į i		EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
1	<b>}</b>		RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
L			EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
J	j		KNLGGKSSGRRQGIKKMEGHYVHAGNIIATORHFRWHPGAHVGV
			GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
6991			KTFVHVVPAKPEGTFKLVAML
0991	169	451	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
Į			SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
6992	944		CGRHVH
1	341	510	ROAPGCSSLALROVROVYCGLVRAPQVQTRPLSSRFVERRGALY
ł			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY
İ			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLWDMLT
6993	1	374	
		3	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
	)		VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
1 1	1	•	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
			SSQVLWAISSAISVAFFALSGIAAOLLNALGLAGDVLAOGLKLS
	}		PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVTF
]			LAGFVALMRSVPDPSTRALLLLLALLILYALLSRLTGSRASGAOL.
6995	144		EAKVRGLERQVEELRWRQRRAAKGARSVEEE
3,55	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
1			LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
1 1			BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
			EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
1			GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
1	1		RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFTWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
	j		SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
1	j.		GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
			KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
1	1		MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLOKIR
1	•		EESRAVFLQRKSRELLDNEELONLWFLLDKHOTPPMTGERAMTN
ŀ	İ	į	YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMOFFNY
l			VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTI.POL
ļ			DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIODILACSFLDD
ŀ	1		LLELRDEELSKESQETNWFSAPSALRVYGOYLNLDKDHNGMI.SK
1			EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
[		·	RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIOELMKTHGOD
	i		PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
6997	370	1104	NGFWTYENREALVANDSENSADLDDT
į.	=	1104	AMELTIFILRLAIYILTPPLYLLNFLGLWSWICKKWFPYFLVRF
		Ĭ	TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
	<u>-</u>		YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	<del></del>	<u> </u>	QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
	1		VAAECSTWNYFWOOVLDPAWHLLFDGCNLTRESWKALERASFSK
1	1	•	LKLQHIQAPLSWELVRPHIYGYAVK
6998	<del> </del>	616	FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
0938	1	010	SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
ļ	1	1	APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
1		i	
	1	i	LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
			FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
1			ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
			YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
l		1	LARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
			LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
1	1	1	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
ł	į.		KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
1	[	1	OCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
l .	1	1	TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
1	)	1	NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
	1	1	GOIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
Į.	1	ł	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	2	827	GPGVVFLELMESEGPPESERSEFFSQREEENEEEAQEPEETGP
7000	1 2	827	
1	1		KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN
1			LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
1	l .	1	ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
	1	1	RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
1		Į.	ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
			DQKRSQDDTSN
7001	2056	844	RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
1	į.		FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
	1		TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI
i	l .	J	VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN
1		1	APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
		i	HYFIDRDGOMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFOL
			QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK
1	1	1	SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ
1	1		VLERLOORGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
1			RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
1	1043	1 470	TPCSRHOSRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
!			SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTOWSSV
1	1		
[	1 '		PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
	<del> </del>		RGAEVC
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
1	}		GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
Ī			GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
1			LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
1			FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM
1			GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
1			G\PKRTLKTOLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE
1			GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
1			GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
			QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
			VDPEFADMITVQEFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL
1		1	EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE
			I BEVEEDEINENDENDENCEVRINNIIVAUCIEVEVANDIEERE
1	ł		VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

,	020	TR-17-	· - · · · ·	
	SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
- [	NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ı	110.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
J		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
-		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [		amino acid	sequence	Codon, /=possible nucleotide deletion,
-1		sequence	_	\=possible nucleotide insertion)
ſ				QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
. 1			i	LRTCMDVLRENQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
- [			ļ	VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
- 1				YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
1				IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMO
ı				GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED
-				KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
-				ERRVAAKQLEMONKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
ŀ	7005	63		DREKVTQRSVSPSPVPVSYL
- 1	7005	6.3	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
- 1				WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
- 1				ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
-1			·	FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
1				GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
1				LWRSSG
r	7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
1				VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
				LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
1				SKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
- [			•	DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
1				VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
F	7007			DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
	7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
1	ľ			YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
ı	ļ			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
1	į			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
	ĺ			QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
1	1			VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
1				MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ PGQFFGDQTCSCRLFGIRFGDIILL
r	7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
ŀ	ľ		77.7	SPPPLAGPGQKMVQKKPAELQGPHRSFKGQNPFELAFSLDQPDH
Į		j		GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
				RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKI1EKQPGH
		1		IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
1				SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
	1	İ		NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
	1	Ĭ		AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPPVG
	į	ł		RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
1	ļ	1		KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
F	7009	1		WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
1	1	<b>-</b>	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
	1			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
	- 1			LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
	1			WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
Г	7010	79	571	GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
	1			GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
l	1	į.		VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
L	1		ł	HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
Γ	7011	3	994	RIQTLPNQNQSQTQPLLXTPPAVLQPIAPQTTFGVQTQPQPQSL
1	1	ĺ		LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
	- 1	1		ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRSRERSPQ
1	j	· 1		RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
L				ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
<b></b>			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
1	i .		AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
1			DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
	i *	2001	
	Į į		AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
	į		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
1	<b>\$</b>		TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
	1		NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
	İ		DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
İ			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
l	1	<u> </u>	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
i			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
J	]		LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1			VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
1			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
l	1		YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
	ļ		FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
ĺ	j ·		LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
	!		PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
1			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
Į			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
į			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7013	1	2661	H
1 7013	_	2001	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
Į.	į		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
ļ	J.		TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
			NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
l			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
	1		TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
	1		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1	}		VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1			YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
[			FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
1	1		LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1		_	PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
		-	FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
i			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
}			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP AQQSPSM
7014	3	3950	1
'***	'	3330	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
ŀ			ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
I			CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
[			PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
<b> </b>			HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
]			SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
			PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
1			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
			PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
j i			SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
L		L	RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN

	1 200 12 12 13	· · · · · · · · · · · · · · · · · · ·	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
1.			ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
-			IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
1		]	LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
	f		VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
ł	1		YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
			LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
1			ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
ı	ł		TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
<b>,</b>			DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
1			QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE
1	i		ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
	·		DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
			TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
			DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
İ			SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
			CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
			NOKLKILEFKOVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
1			GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
· F			SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
1			KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
1	J		QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
1			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
			FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
1			EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
i	į		LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
			KLTK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
1			AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
1			LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM
.			PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
			TATPQTQLQLQQVAAAAAATARSSSSSRRRYSSSSSSNSKQ
		•	FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQQQHLIKLHHQNQQ QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQALQAQPPIQQP
	ļ.		PMQQPQPPPSQALPQOLOOMHTTOHHOPPPOPOOPPVAONOPSO
			LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
			QVQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
			QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF
1	1		\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
1			LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
			SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
1			LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
			RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
			KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
7017	1	1705	HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
''''	- 1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
1 '	]		FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS
]	, [		DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
			YSLEYMSCPDCSQSPSIODGGLMOASVPGPSEEPVVYNPTTAAF
1			ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPOKPG
	[		GETTPSVTDLLNYPLAPEILTGDNQYYCENCASLQNAEKTMQIT
L			EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS
		·	

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·			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Coden / manifel and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
	sequence	Bequence	Codon, /=possible nucleotide deletion,
	Bequence		\=possible nucleotide insertion)
1	j	1	FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
•		1	SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ
1	ì		SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK
I	1	į.	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
	1	1	LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
L	)	l,	PGSCGPTGGGGGGFNTVGRLVF
7018	484	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGTERIRAPEIIFQ
1			PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP
ţ	1	1	CMVADMENEL I EMB DEDECEOUGLA CADAL DAMES DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE LA CARREST DE
{	ĺ	1	GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHL
ŀ	l	1	DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
7019	1040		QASSKGSAAGGGGAGEQA
1 ,019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
ŀ		1	RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
	1	[	SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
1	1	}	GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
			SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
L	1	İ	ARESASAKIKEEEAAKD
7020	1	2154	FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
ſ	1	i	NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
	1		DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
	ļ		NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFOF
1		1	
1	1		NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
ł	į.	Į.	MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
1	}	1	ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
	1	1	FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
	Ì	ļ	FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
J	i	i	VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTT
ł			INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
}	1	İ	PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
<u> </u>	1		MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS
	i		LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
-			TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG
	<b>{</b>		TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
'	<u>I</u>		PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
	<b>}</b>		ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
	[		CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	
	"	0.50	VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN
			DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKELVNNLAEIY
			GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
	j l		DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG
			EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
			VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
			ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
			WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
	1		TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
			VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
			EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
7024	1207	100	ILGQAYAFARHPQKPAPHAVHPTGTKAL
,,,,	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
j	j		SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
ĺ	1		QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
ı			RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
ľ			FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
			VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL

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Michelide   Cotation   Cortesponding   Cotation   Cortesponding   Cotation   Cortesponding   Cotation   Cottesponding   Cotation   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottesponding   Cottespon	ID	beginning		(A=Alanine, C=Cysteine, D=Assertic Acid, P
Corresponding to first and corresponding to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to first and continued to	NO:	nucleotide	location	Glutamic Acid. F=Phenylalanine G-Glyging
Leucine, Membelhoine, Na-Asparagine, samino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque	-		corresponding	H=Histidine, I=Isoleucine, K=Lysine
amino acid amino acid amino acid amino acid amino acid asequence  sequence  sequence  7025  232  832  832  832  832  833  ENRYFORDERSHYNTYMORE PREDODYTYMBIATYLLINPE LPTYYGRERSHOTOLIGE INSERTION  TESTKOVAGASHENYRYTYMORE PREDODYTYMBIATYLLINPE LPTYYGRERSHOTOLIGE INSERTION  7026  328  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146  1146	j		to first	L=Leucine, M=Methionine, N=Asparagine
residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1			P=Proline, Q=Glutamine, R=Arginine.
amino acid sequence    Codon,	j			S=Serine, T=Threonine, V=Valine,
Codon, /=possible nuclectide deletion, /-possible nuclectide dissertion	l			Watryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Yatryptophan, Ya
TGSPTKOVAQASHSYRVITMOSPKDEIQOYTODHISTATYLLINPDG LPTDYYGARSASICISUSVRHHAARRSVLIS  832 BANSPIGNIEND'R KYHSILDCERGGWEGNTOSOTIQDNQEECF KQVIRTCEKRPTFNQHTVENLIGRIANTGUKINEFKELIKAPISG SHIPTINIESKPGGWEGNTOFFUNDEVLYOTUTURITY ECKSCOKSISILSSLIGHKRIHTGEKPFKCKDOGKAFFEHSQLS VIKKRIHTGEKSYECKECKGKAFSICG  7026 328 1146 NENESIGDIKDIKKAAKSHLDPAHKSHFHPVTESLVPLCFIFDG LIQALISVOKSKSHITVONENBERGTTPASRFKOMPRIFILEK SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMASIGLIS HOESSADLLISONARSSINGHISPHWYGEMFTIGDFSEPJIKL LEKSS'LIPRKHR*OPINAVRHFLDQCMGGSIARRAIVSEIPVFE EKKNOS-KOLGHIF*WAGKTHPHYWGAVTHSINSCKLIG ODEOPHIFG GRILOQOGPPEDABEGGKKRGAGWEGGYPETVKENKLEH YYOSLKTVPEGEMGORMDLREFLPATHITGYKSHAKELHICL KNKYFKLELBLEMGKGKVEVOPLISWYPEELHVISNSCKLIG ODEOPHIFG GRILOQOGPPEDABEGARGGKRGAGWEGGYPETVKENKLEH YYOSLKTVPEGEMGORMDLREFLPATHITGYKSHAKELHICL KNKYFKLELBLEMGKGKVEVOPLISWYPEELHVISNSCKLIG ODEOPHIFG GRILOQOGPPEDABEGARGGGKRGAGWEGGYPETVKENKLEH YYOSLKTVPEGEMGORMDLREFLPATHITGYKSHAKELHICL KNKYFKLELBLEMGKGKVEVOPLISWYPEELHVISNSCKLIG ODEOPHIFG GRILOQOGPPEDABEGARGGGKRGAGWEGGYPETVKENKLEH OAKALSSPCINVINHBASSIPRIOLIDVGKREILFYDRILCDVP CSGGTMRKINTUNFPEGEVINNEVENTLISKLIKTERADOL OAKALSSPCINVINHBASSIPRIOLIDVGKREILFYDRILCDVP CSGGTMRKINTUNFPEGEVINNEVENTLISKLIKTERADOL OAKALSSPCINVINHBASSIPRIOLIDVGKREILFYDRILCDVP CSGGTMRKINTUNFPEGEVINNEVENTLISKLIPATHICKTOR OAKALSSPCINVINHBASSIPRIOLIDVGKREILFYDRILCDVP CSGGTMRKINTUNFPEGEVINNEVENTLISKLIPATHICKTOR OAKALSSPCINVINHBASSIPRIOLIDVGKREILFYDRILCDVP CSGGTMRKINTUNFPEGEVINNEVENTLISKLIPATHICKTOR KNOSMYSMLSPTYKORMEDERKLIPATHICKTOR KNOSMYSMLSPTYKORMEDERKLIPATHICKTOR CKGGFRSTPTTHAGATTH PETPEGSIP PROGRESSOPPAL FULLYBAKKGMSCKYSTMERTINGVPRAGGRESSOPPAL FULLYBAKKGMSCKYSTMERPENTLAGATTH PETPEGSIP PROGRESSOPPAL PELLPEATT*HSAGTHT PETPEGSIP PROGRESSOPPAL FULLYBAKKGMSCKYSTMERPENTLAGATHTH PETPEGSIP PROGRESSOPPAL AAROKRGHREA OGGEVVARGCGEGRESSOPPAL FULLYBAGGGGGKGRAGGERSOPPALLAGGGRENGPAN PERLPEATATYPPSGGGGGKRROWSPALLARFRUNGEN AAROKRGHREA OGGEVVARGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ŀ		sequence	Codon, /=possible nucleotide deletion.
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7033 689 815 RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGF*APPGPSSA	-7075			
	7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
1		1 '	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i	\=possible nucleotide insertion)
			LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
	1	}	GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
	ŀ		AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
	i	ì	WDWRRPPLOVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
	i .	l .	
	1	i	SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
	<u> </u>	<u> </u>	NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
	ŀ		KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	ł	1	TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
l	ı		1 7 7
J	I	1	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
}	j	1	FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
	1	1	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
l	I	1	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
	i	1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
l	l .	i.	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
1	1	1	GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
}	1	1	
Į.	1	1	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
]			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1	1	ļ	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1		1	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
	1 .	•	. ( K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	1		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
	1 '	1	
1	i	1	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1	l .	1	FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
ì		i	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
l			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW-
	i		YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
İ	i		TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
l	i		· ·
			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
l	l .	ł	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
	1	1	FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKFQ
1			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
	1	I	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1			K
7036	442	761	CLAPLFSCFOIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	1 446	1 /31	7
I		1	RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
	<u> </u>		PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	1	1	RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1	1	1	PPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1 ,330	1 1,3	1 391	
1		J	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
1	1		LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1	1	1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
J		1	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
1	1		LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEOLRRRDRLQRQAFEEIIL
1 .333	1 ***	991	
1	1	1	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
Ī			LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
Į.			QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	1		LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
ŀ			LQEAASPAAERACRSSKGTSTSRTG
	1	<del></del>	
7040	34	790	KITODODDODOCCCUCCOMCCVI CCCI.DDAMCKTAI.EVUCCCCC
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

ID   beginning   nucleotide   location   corresponding to first   location   corresponding to first   location   corresponding to first   maino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid amino acid acid amino acid acid amino acid acid amino acid acid amino acid acid amino acid acid amino acid acid amino acid acid acid acid acid acid acid acid	SEQ	Dwo dd ab a d		
No: mucleotide location corresponding to first amino acid corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		Predicted	Predicted end	Amino acid segment containing signal peptide
coration   corresponding   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst				[A=Alanine, C=Cvsteine, D=Aspartic Acid E.
corresponding to first amino acid amino acid amino acid amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequ	1			Glucamic Acid, F=Phenylalanine G=Glycine
to first amino acid residue of residue of residue of residue of residue of amino acid amino acid amino acid asequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	-	(		H=H1Stidine, I=Isoleucine, K=Tysine
amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	- 1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence    Sequence	ļ			P=Proline, Q=Glutamine, R=Arginine
amino acid sequence  Codon, /-possible nuclectide deletion,	· I			S=Serine, T=Threonine, V=Valine,
Sequence    Codon, /-possible nuclectide deletion,    -possible nuclectide dissertion    PGSGRRALIPALSLDTSSFV8RPPNSTGVRRVDGFLRSSFRGIG   EFFFIKYVSIDDVERLORRGGASKEAMCFNACKILLEHROGNI     APVRAKYEMLMKELEATKGYLMLDPNKKLSEPDLEQWELDSLE     VLEALECVERLESSWPPCAKHLMITCFDI    TO41	· I			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
POSQRRAILPALS.DTSSPVRKPPNSTOVRNUDGFLRSSPRGLG EFFELKVISIDDVERLQRRKGGASKRAMCNAKLKILEHQGRI ARVRAKYEMIMBELEATKGYLMLDPRIKLESEPDLEQWELDSLE TLEALECVTERLESRVIPCKAHLMMITCFDIT TO41  1 567 SGRVAMGRRAPAGGGIGRAMHRIOTOSSEPPLEQWELDSLE NGSYDMGRAPAGGGIGRAMHRIOTOSSEPPLEQWELDSLE NGSYDMGRAPAGGGIGRAMHRIOTOSSEPPLEQWELDSLEY PAEARTCLLISPEESGRIKKLEENKOPLCLIPPUNGCNTTPEE LKQAEKUNFLEWRGOLVELEESGKLILTFPERNLDFWRQLMTPE LKQAEKUNFLEWRGOLVELEESGKLILTFPERNLDFWRQLMFV PAEARTCLLISPEESGRIKKLEENKOPLCLIPPUNGCNTTPEE LKQAEKUNFLEWRGOLVELEESGKLILTFPERNLDFWRQLMFV PAEARTCLLISPEESGRIKKLEENKOPLCLIPPUNGCNTTPEE LKQAEKUNFLEWRGOLVELSKSSIGHVATSLATKGAL PIHMAAAALRADIVISPLOPVENSHEENLARSASN DDLLMAGVAISDSDEEDLVSYGTGLEPLEEGERPKKPTPLODOTVAD PHEVTVMYTVI PIKSKYVLVKPUTOVPSVELEKHLENSASN DDLLMAGVAISDSDEEDLVSYGTGLEPLEEGERPKKPTPLODOTVAD EKGRYKRFRGAFSGFSAGYFNTVGSKRGHTPSTFVSSRONDAD KSVLGEDPINGEBLISBEGILFPLAVALTVOTTSCHEIPELEGG EKGRYKRFHGAFSGFSAGYFNTVGSKRGHTPSTFVSSRONDAD KSVLGEDPINGEBLISBEGILFPLAVALTVOTTSCHEIPELEGGG RVKRRPRRGKDEBLISBEGILFPLAVALTVOTTSCHEIPELEGG RVKRRPRRGKDEPGVKIYGGLIPPCSGESGREGGVGUALERGLEGGVG RVKRRPRRGKDEPGVKIYGGLIPPCSGESGREGGVGUALERGEGGGG GERAGLIBE LGLANKGRLGIFSGGAFCVGALEFENSHLLQV LSESAGKATPDPGTHISKGLNASKEABLLGEPPTGGSBFTULEG SLASKELSKKIYPPLENDERDVRYPHYFERTVASSENHLLQV LSESAGKATPDPGTHISKGLNASKEABLLGEPPTGGSBFTULEG LSGOKERIKKRKGATDLKANGVSPNPLLIPPSGSHTLESR LSGOKERIKKRKGATDLKANGVSPNPLLIPPSGSBFTULEGR GGKNABERGLOBPMTHERGERBEDEPRAALILGEPTGGSBFTULEG LSGOKERIKKRKGATDLKANGVSPNPLLIPPSGSBFTULEGR FPOSKDLLKOLUERVSRCKNSVSPNPLLIPPSGSBFTULEGR FPOSKDLLKOLUERVSRCKNSVSPNPLLIPPSGSBFTULEGR FPOSKDLKGULGUERVSRCNSVSPNPLLIPPSGSBFTULGSGR FPOSKDLKGUERVSRCSPNTSKHEKKEDSISEFTLARGKBPPK GGSPLUNKEEBERBERBERBARGHSGANGVANGKANGHANGHCHISTERNHLLQVTKNS THAKEEDDSDQVSVPRDGENDVGNGGANVENKHOULTTVTGSBF FPOSKDLKGUERVSRCSPNTSKHEKKEDSISEFTLARGKSRDEKR FPOSKDLKGUERVSRCSPNTSKHEKKEDSISEFTLARGKSRDEKR FPOSKDLKGUERVSRCSPNTSKHEKKEDSISEFTLARGKBPPK FPOSKDLKGUERVSRCSPNTSKHEKKEDSISEFTLARGKSRDEKR FPOSKDLKGUERVSRCSPNTSKHEKERDSISEFTLARGKTSPNK LUURUNGKTSGLLGUERVSRCSPNTSTARGECENNY CHARLOPPUERVSRCSSPNTSTARGEERNAN LUURUNGKTSGLLGUERVS	1		sequence	Codon, /=possible nucleotide deletion
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TO42  7  345  PIHMAAALRADI\SPEPHIGGYILLISASIG\ATSLITKGAL PLETVITYVIYDYDYDA  7043  2  2170  ARGMAARDSDSEPLIVUKUKPDTOYPYSENLDEFKRLAENSASN DDLLMARVAISDYGRULFIELEGERPKKFI FLODOTVRD EKGRYKRFHGAPSGGFSAGYFNYUGSKEGNTPSTFVSSRQNRAD KSVLGPBEDDMEDENISSERGIAPKATURITRGAL KSVLGPBEDDMEDENISSERGIAPKATURITRGAK GULAAATAPIPGATLLIDLITPALLVTTDDFASKTORITRGKAG RVKRPBERGKPDFDWERDISSERGIAPKATURITRGKEGOVGP RVKRPBERGKPDFDWERDISSERGIAPKATURITRGKKEGOVGP RVKRPBERGKPDFDWERDISSERGIAPKATURITRGKKEGOVGP RVKRPBERGKPDFDWERDISSERGIAPKATURITRGKKEGOVGP RVKRPBERGKPDFDWERLSERGIAFVCHFASKTORITRGKKEGOVGP RVKRPBERGKPDFTRENVIGLAYKULPHGALFGTSGEHRINLESGG SERAGLIGSIGLINKGRKIGISGGAFGVGALEEEDDDIYATETLIS KYDTVLUGBERDDGLIVGNTAFRQYINGSEKSLLKETVKLLOGF SLASKELSSKKIYPPFELPRDVRPVHYFTRWAATEENSHLLOGY LSESAGKAFTPDGTTHSKHGNATSELAGETPIGSASTSVLEF LSOKOKERITKSKRKGATDLKAAGLKARSIAQNAGSSRAQPSPAAA AGHCSINNALGGGTTALTKASNFKFPSHEKKERUSTSVLEF LSOKOKERITKSRRYDDGTVENFORDINDUNGSCASKINKHFCKLITEDTER HADRILFORDSOVGVENFORDINDUNGSCANKMHFCKLITEDTER HADRILFORDSOVGVENFORDINDUNGSCANKMHFCKLITEDTER HADRILFORDSOVGVENFORDSOVGNOKMHSTEKLITEDTER HADRILFORDSOVGVENFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGVENFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGVENFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGVENFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER HADRILFORDSOVGNOKHMSTEKLITEDTER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGGTESOFORNICHER FORSONAN AGG		1		PAEARTGLLSFEESORIKKLHEENKOFLCIDER DNEWONTTDER
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PIEMAAALRADI\[15PLPFHIGSTLLISASHG\NTSLHTKGAL PIETTYHYTTIPKSYLSUKPDTQYPYSENLDEFKRLABNSASN DDLLMABVA15DYGDKLTLEIREKY  ARGMARADSDSEBULVSYGTGLEPLEEGERPKKETPLODOTVRD EKGRYKRFHGAFSGGFSAGYPNTVGSKEGWTPSTTVSSRQNRAD KSVLGPBDFMDEBDLSGFGIAPKAIVTIDDFSKTKDRIREKAR QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMKKEGGCVGF RVKRRPRROKPDGVKIYGCALPPGSSEGSEGEDDDVLPDNVTF APKDVTPVDFTREDWHCLAYKGLOALPGSSEGHINLFSGG SERAGDLGEIGINKGRKLGIGGQAFGVGALEEEDDDIYAFTTLS KYDTVUDTFTROWNGSEKDLRYVGKTLDGF SIASKHLSKKTYPPELPRDYRRVHYFRPMVAATSENSHLLQV LSEASGATPDPGTISKKKQLANASKSEKDLRYVGKILDGF SIASKHLSKKTYPPELPRDYRRVHYFRPMVAATSENSHLLQV LSEASGATPDPGTISKKKQLANASKSEKDLRYVGKILDGF GSATSVLEF LSOKDKERIKERMQADTLKAAOLKARSLAQNAQSSRAQPSPAAA AGHCSMMALGGGTATLKASNFKPFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDELGEFTPIGSATSVLEF LSOKDKERIKERMQAATLKASNFKPFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGRERDFFAKDPEKKRYDEFLVHKKGATERTTOWN FAKTOR GOKDALERCLDPSMTEWERGRERDFFAKDPKKRYDEFLVHKASSKAPPK QOKSAPLVNKEEHAPBELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNI FBRIYLLITVGVVYVKS FFOSKOLLKALVEWERGVHENGEFLKNYLLOCTENILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQCHSRDREKR ERROCHRITUKLSQV EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQCHSRDREKR ERROCHRITUKLSQV EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQCHSRDREKR ERROCHRIPTUKLSQV LEFTDILPDSCATTSTADLTGQVALYTFCP KANQWEKTDISGTLFFVYRRSASFYHGFTIVKRLMMINLVEPVNK DLEFQLHEPFLLYKNASLSIYSHIYFDKNDCHRIAKMADVVEE ETRRSQQA/RSGQTESOPGQULQRPQAHRHPGDAEGGG KANGWENGHERBELTGLAQAVYEE ETRRSQQA/RSGQTESOPGQULQRPQAHRHPGDAEGGG KANGWENGHERBELTGLAQAVYEE ETRRSQQA/RSGQTESOPGGNLQRROCHRIPTTALKLMADVVEE ETRRSQQA/RSGQTESOPGGNLQRROCHRIPTTALKLMADVVEE ETRRSQQA/RSGQTESOPGGNLQRROCHRIPTTALKLMADVVEE ETRRSQQA/RSGQTESOPGGNLQRROCHRIPTTALKLMADVVEE ETRRSQQA/RSGQTESOPGGNLQRROCHRI	7042			IERSDIVVQIVDA
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EGGYYKEHGAFSGGYSAGYFNTVGSKEGWTPSTTVSSRQNRAD  KSVLGPEDFMDEBLESFGILAVITTDDFASKYKDRITRKAR QLAAATAPI PGATILIDDLITPAKLSVGFELIRKMGWKEGGVGP RVKREPRRQKEDPOVKIYGCALPPGSSEGSEDDDVLPDNVTT APKDVTPVDFTPKDNVHGLAYKILDPHQALFGTSGEHFNLFSGG SERAGDLGBIGLKGRKLGISGQAFGVGALEEEDDDIYATETLS KYDTVLKDEEPGGDLIGWTAFPGYKNQKESKENLEYVGKTLDGF SLASKPLSSKKIYPPELPRDVRPVHYRPWAATSENSHLLQV LSESAGKATPDFGTHSKHQLNASKRAELLGETPIQGSATSVLEF LSOKDKER I KEMKOATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSWNMALGGGTATLKASNFKPFAKDPEKOKYDEFLUHMKO GQKNALERCLDPSMTTWERGGRERDEFRAALLVASSHSTLSSHF THAKEEDDSDQVEVPRDGENDVGDKGSAVMKHFGKLTRDTFEW HPDKLLFQ/RLUCHPVKRDKYSVFTLTLETASLPTTOASSE KVSCHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QSSPLVNKEEFHAPLSAN  7044 276 734 EVYLTDEFAXGRKVADLYELVQYAGNIIPRLYLLITVGVVVVKS FPOSRKULLKDLVEMCRGVGHFLRGLFLRBYLLQCTRNILPDEG EPTDEETTGDISDSDFVLLARFENKIMVWRQHCGHSRDREKR FOSRKULLKDLVEMCRGVGHFLRGLFLRBYLLQCTRNILPDEG EPTDEETTGDISDSDFVLLARFENKIMVWRQHCGHSRDREKR ERROGELRILVGTNLVRLSQV  LGFKMEALSRAGGWSLAALKOHDPYTTSIADLTGQVALYFFCP KANGWEKTDIEGTLFVYRRASSPYHGFTIVNRIMMINLVEPVNK DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESOPGOULORPQAHRHEDBAEGSGG KANGWEKTDIEGTLFVYRRASSPYHGFTIVNRIMMINLVEPVNK DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESOPGOULORPQAHRHEDBAEGSGG KANGWEKTDIEGTLFVYRRASSPYHGFTIVNRIMMINLVEPVNK DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESOPGOULORPQAHRHEDBAEGSGG FORGENSLAALKOHDPYTTSIADLTGGVALYFFCP KANGWEKTDIEGTLFVYRRASSPYHGFTIVNRIMMINLVEPVNK DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESOPGOULORPQAHRHEDBAEGSGG FORGENSLAALKOHDPYTTSIADLTGGVALYFFCP KANGWEKTDIEGTLFVYRRASSPYHGFTIVNRILNINKN DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESOPGOULORPQAHRHEDBAEGSGG FORGENSLAALKOHDPYTSIADLTGGVALYFFCP KANGWEKTDIEGTIFVYRRASSPYHGFTIVNRILNINKN DLEFQLHEPFLLYRRASLSIYSIMFYDKNDCHRIAKLHANDKYEE FORGENSAMGRAGGASVAGACSVGKIPARCYEEBEANY WKDLAMTYKQRAENTQEELREFQGGSREVARALETQLQQISTRN ROLLSENNRIMBELETIKEFCYNCHSEGYRQISALEDLLAGTKA IKQLQKYIRRLEGANDDLERAKRATDHGLSKTFF\QRINCHKHRAKGAVREL NYEIRBASSYGGPFGLGGARXASVAGRCSSVGKIPARRCYED	1 /043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLODOTYPD
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RVKRPBRQKPDEGVKITGCALPPGSSEGSEGEDDDYLPDNVTF APKDVTPVDFTPKONVIGLAYKGLDPGALPGTGGEHFINFSGG SERAGDLGEIGLNKGRKLGISGQAFGVGALEEDDDIYATETLS KYDTVLKDEEPGDGLYGMTAPRGYKKQKESEKDLRYVGKLLDGF SLASKPLSSKKIYPPPELPBYRPVHYFRPWAATSENSHLLQV LSESAGKATPDPGTHSKHQLNASKRABLLGETPIGGSATSVLEF LSOXDKERIKEMKQATDLKAAQLKARSLAQNAGSSRQPSPAAA AGHCSWMNALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ GOKDALERCLDPSMTEWERGERDEFARALLLYASSHSTLSSRF THAKEEDDSDQVEVPRDQEMDVODKOGAVGMKMFGKLITDFTEW HPDKLLFG/LLVGLPRVKRDKYSVFMFLTIPETASLPTTQASSE KVSGHROPDKSRYBSRMDTSKHEKKEDSISEFLRLARSKAEPPK QSSPLVMKEEEHAPELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPOSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDETTTGDISDSMDFVLLNFAEMMKLWVRMQHCGHSRDREKR FPOSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDETTGDISDSMDFVLLNFAEMMKLWVRMQHCGHSRDREKR FRERGELRILVGNILVRLSQV KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSISISIFITVORLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSISISIFITVORDCHRIKKLMADVVEE ETTRSQQA/RSGGTESOPGOWLQRPQAHRHPGDASDSGG  7047 103 486 OMSIEKGGSGESUGSMLGRPQAHRHPGDASDSGG FTRRSQQA/RSGGTESOPGOWLQRPQAHRHPGDASDSGG  7047 103 486 OMSIEKGGSGESUGSMLGRPQAHRHPGDASDSGG FTRRSQQA/RSGQTTSSPGGWLQRPQAHRHPGDASDSGG  7048 92 627 FFCLTLLSSWDYRHHATRRVISSPYTYHEDSKKFEKKNLLNSKN NEVLPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER RDLLSEMNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA RDLLSEMNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA RDLLSEMNRLRMELETIKEKFEVGHSEGYRQISALEDDLAQTKA RDLLSEMNRLRMELETIKEKFEVGHSEGSVGKIPARRCYEDEL EKKW  7049 393 938 KRTGSASYGGPPGLGGPATXASVAGRSSVGKIPARRCYEDEL NNYEIRPGLLGVCSVDNCRLPTGGIPKMKKREELEETAKVT EGVLDVLVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAMX ASSLWG	1	1 1		QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGOGVGD
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SERAGDIGEIGLINGERIJGGGAFUGALEEEDDDIYATETIS KYDTUKURGEPODGIJYGHTAPROYINQKSEKDLRAYUKILDGF SLASKPLSSKKIYPPELPRDYRPVHYFRPMVAATSENSHLLQV LSESAGKATPDPGTHSKRQLINASKAELLGETPIGGSATSVLEF LSOKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSWMNALGGGTATLKASNFKPFAKDPEKOKRYDEFLVHHKQ GQKDALERCLDPSMTMERGREDFPFARALLYASSHSTLSSRF THAKEEDDSDQVEVPRQGENDVGDKQSAVKKMKFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLEETASLPTTQASSE KVSQHROPDKSRKESRMDTSKHEKKEDSISFELRLARSKAEPPK QGSSPLVNKEEEHAPELSAN  7044 276 734 EVYLTDEPÄKGRKVADLYSELVQYAGNIIFRLYLLITVGVVYVKS FPQSRKOILKDLVEMCRGVQHPLRGLETRNYLLQCTRNILDDEG EPTDEETTGDISDSDMDFVLLMFAEMNKLWVRMQHQGHSRDREKR FPQSRKOILKDLVEMCRGVQHPLRGLETRNYLLQCTRNILDDEG EPTDEETTGDISDSDMDFVLLMFAEMNKLWVRMQHQGHSRDREKR FRERQELRILVGTNLVSLQV  1045 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMHHLVEFVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGGTESQPGGWLQRPQAHRHBGDAEGSG  7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMHHLVEFVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGGTESQPGGWLQRPQAHRHBGDAEGSG  7047 103 486 QMXIEKGGMSEGLTSIYGNCHDFYTAISHDLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMHHLVEFVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGGTESQPGGWLQRPQAHRHBGDAEGSG  7047 103 486 QMXIEKGGMSEGLTSIYGNCHDFYTAISHDLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMHHLVEFVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGGTESQPGGWLQRPQAHRHBGDAEGSG  7047 103 486 QMXIEKGGMSEGLTSIYGNCHDFYTAISHDUTYELKNLLNSKN INLIDVRSIWELLEYQKIPESINVPLDEVGGALQMNPROPKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTILSSWDYRHHATRRVISSPVFMBEGSKTFSSEEEEANY WKDLLMTYKQRAENTOGELEPGGSPEYBELEDGLQQIETRN RDLLSSNNELRRELETIKERFEVQHSEGYRQISALEDDLAQTKA RDLLSSNNELRRELETIKERFEVGASRCSSVGKIPARRCCEDEL RKKW PVEVBAVGRIYSLARMDPGGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCSVDNCRLFIGGIPKMKREELLEEIAKVT EGVLDVIVYASAADKMNRGLRLRGVREPPRGCHWLGRKLIAMX ASSLWG	1	1 1		APKDVTPVDFTPKDNVHGLAYKGLDPHOALFGTSGEHFNLFSGG
RYDIVLKDEERGOLIGHTARROYNOKESEKDLRYVGKILDOF SLASKFLSSKKIYPPPELDPRDYRPWIPFPRPWAATSENSHLLQV LSESAGKATPDPGTHSKHQLNASKRAELLGETPIGSATSVLEF LSOKDKER IKEMKOATDLKAAQLLKARSLAQNAQSSRAQPSPAAA AGHCSWMALAGGTATLKASNFKPPAKDPEKOKRYDEFLVHMKO GQKDALERCLDPSMTEWERGRERDEFARRALLYASSHSTLSSRF THAREEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTTEW HPDKLLFQ/RLVGLPRVKRDKYSVPNFLTLETASLFTTQASSE KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSS KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QSSPLVNKEEHAPELSS KVSQHROPDKSRKRESRWDTSKHEKKEDSISEFLRLARSKAEPPK QSSPLVNKEEHAPELSS KVSQHROPDKSRRKWDTSKHEKKEDSISEFLRLARSKAEPPK QSSPLVNKEEHAPELSSAURTUNGTVALLTUNGVVYVKS FPQSRUDILARDAWN FROM THE STANDARSKAEPK ERPROGLISIONDEWCHAPALANDAWN FROM THE STANDARSKAEPK ERPROGLISIONDEWCHAPALANDAWN FROM THE STANDARSKAEPK RANQWEKTDIEGTLFVYRRSASPYHGFTIVARLAMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQOA/RSQTESQPGQWLQRPQAHRHPGDAEQSOG  7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLINSKN INLIDVRSIWEIKELTEVQKIPSINVPLDEVGEALQMNDPRKEKY NEVKPSKSDS/IVFSILAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFIMEDSGKTAELETQLQOIETRN RDLLSSMNPLRHELETIKEKFEVQHSEGYRQISAFEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFSSEEEEANY WKDLAMTYKQRAENTQEELEREFQEGSREYBAELETQLQOIETRN RDLLSSMNRLRHELETIKEKFEVQHSEGYRQISAFEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFSSEEEEANY WKDLAMTYKQRAENTQEELEFTLGGIFPKMKREEILEEIAKVT EKKW  7049 393 938 KRTGSASYGGPPGLGGPATXASVAGRCSSVGKIPARCYEDEL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREELLEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAMX ASSLWG	1	(		SERAGDLGEIGLNKGRKLGISGOAFGVGALEEEDDDIVATETLE
SLASK(ISSKKTYPPPELRBTYPPVHYPRYMVARISENSHLLQY LSSESGKATPDPOTHS KHQLINAS KRABLLGETP I (GSATSVLEF LSSKJKKER I KEMKQATDLKAAQLKARSLAGETP I (GSATSVLEF LSSKJKKER I KEMKQATDLKAAQLKARSLAGETP I (GSATSVLEF LSSKJKKER I KEMKQATDLKAAQLKARSLAGETP I (GSATSVLEF LSSKJKKER I KEMKQATDLKAAQLKARSLAGETP I (GSATSVLEF AGHCSWNNALGGGTATLKASNFFFFARDPERQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEFFARALLLYASHSTESRF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHROPDKSRKPSRWDTSKHEKKEDS ISEFLRLARSKAEPPK QGSSPLVNKEEEHAPELSAN  PO444 276 734 EVYLTDEFAKGRKVADLYELVQYAGNII PRLYLLITVGVVYVKS FPQSRKDI LKDLVENCRGVQHPLRGLFLRNYLLQCTRNILDPOG EPTDETTGDISDSMDFVLLNFFALMKLWVRMQHQGHSRDREKR FPGSRKDI LKDLVENCRGVQHPLRGLFLRNYLLQCTRNILDPOG EPTDETTGDISDSMDFVLLNFFALMKLWVRMQHQGHSRDREKR ERERQELR ILVGTNLVLSLQOV  ANAQMEKTILGOV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANQMEKTILGGV KANGMEKTILGGV HCSWNMALGGGTATLKASNFKPFAKDPEKQKKYDEFLVHMKQ GQKDALERCLDPSMTEWERGREBDEFARAALLYASSHSTLSERF THAKEEDDSDQVEVPROPRODVODKOGSAVKMKMFGKLTRDTFEW HPDKLLFQ/RLUGLPRVKRDKYSYFNFLTLPETASLPTTQASSE KVSQHGRDPKSKKPSWDTSKHEKKEDSISEFJRLARSKAEPPK QQSSPLVNKEEHAPELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELUQYAGNIIPRLYLLITVGVVVVKS FPOSKIDILKDLVEMCRGQOHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMOHQGISRDREKR EPROGELRILVGTKHVRLSQV ANAQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHINLVEFVNK DLEFQLHEPPLLYRNASISIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSGC  7046 3 513 LGFKMEALSRAGGEMSLALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHINLVEFVNK DLEFQLHEPPLLYRNASISIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSGC  7047 103 486 OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVRRIWEILEFQKIPESINVPLDEVGGALQWNPEPFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSSMDYRHAPTRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNELRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRIN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFBAVGRIYBLELKHMDPGGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLPIGGIPKMKGRESILEEIARKVT EGYULVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1			SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSFNSHLLOV
AGHCSWIMALGGTATILKASQUEKPEKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEFARALLLYASSHISTLSSRF THAKEEDDSDQVEVPRDQEBDUGDKQSAVMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVPNFTLTDFTASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNITPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLINFAEMNKLWVRMQHQCHSRDREKR FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPETDEETTGDISDSMDFVLLINFAEMNKLWVRMQHQCHSRDREKR FPQSRKDILKUTUVRLSQV  1045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLINMINILVEPVNK DLEFGLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHPGDAEQSQG  KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLINMINILVEPVNK DLEFGLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLINMINILVEPVNK DLEFGLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  WKIEKGWSEGLTSIKGNCHNPYTALSKDTYKELKNLLINSKN INLIDVREIMFILEFOKIPSITNYRLDEWGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTALSIGFHSYVER  7047 103 486 QMKIEKGWSEGLTSIKGNCHNPYTALSKDTYKELKNLLINSKN INLIDVREIMFILEFOKIPSEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFFQRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYEIRPGRLLGVCCSVDNCRLPIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG ASSLWG				LSESAGKATPDPGTHSKHOLNASKRAELLGETPTOGSATSVILER
AGHCSWNALGGTATLKASHFKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCLDPSMYERGKERDEFARAALLYASSHSTLSSRF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKHFGKLTRDTFEW HPDKLLFQ/RLUGLPRVKRDKYSVFNFLTLPETASLEPTOASSE KVSQHRGPDKSRKPSMDTSKHEKKEDSISEPLRLARSKAEPPK QQSSPLVNKEEHAPELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELUQYAGNIIFRLYLLITVGVYVVKS FPOSRKILKDLVENCGRYQHPLRGLFFLRYYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFABMNKLWVRMQHQCHSRDREKK ERERQELRILVGTNLVRLSQV  105 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMINLVSPVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEDDAEQSQG  7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMINLVSPVNK DLEFQLHEPFLLYRNASLSIYSIMFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHEDAEQSQG  7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN INLIDVREIMEILEFUQKIPESINVPIDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGPHSYYER  7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENDRLRMELETIKKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFF\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYEIRPGRLLGVCCSVDNCRLPIGGIPKMKKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG ASSLWG	1	1		LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSDAQDSDAAA
THAKEEDDSQUEVERDQENDVGDKQSAVKMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLITLEETASLPTTQASSE KVSQHRGPDKSRKPSRMPISKHEKKEDSISEFLRLARSKAEPPK QCSSPLVMKEEBLAELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHELRGLFLRNYLLQTRNILPDEG EPTDEETTGDISDRDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV  7045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQGTESQPGGWLQRPQAHRHPGDAEDSQQ  7046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQGTESQPGWLQRPQAHRHPGDAEDSQQ  7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKOVTYKELKNILNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPROFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYQISALEDLAQTKA RDLLSENNRLRMELETIKEKFEVGHSEGYGGFBFGCHWLGRKLIAWX RDLASSAMA	1	i i		AGHCSWNMALGGGTATLKASNFKPFAKDPEKOKPYDFFLJUMWO
THAKEEDSSQVEVPROGENDVCDKQSAVKMMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVMKEEHAPELSAN  7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLLITVGVVYVKS FPQSRKDILKDLVMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR FPQSRKDILKDLVMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR FRQELRILVGTNLVRLSQV  1045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHPGDAEQSQG  7046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHPGDAEQSQG  7047 103 486 QMKIEKGGWSGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKERY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYVER  7048 92 627 FFCLTLLSSMDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELERFQEGSREVEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRIMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRILGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVVASAADKMNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	J			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSCDF
HPDKLLFQ/RLVGLPRVKRDKYSVPNFLTLPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEEHAPELSAN  EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPIRGLFIRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV  7045  3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLPVYRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETTRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  7046  3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETTRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  7047  103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMISPEDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048  92 627 FFCLTLLSSWDYRHHATRRVISSPVFIMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQELREFQEGSREYEAELTQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGYLDVIVYASAAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLMG	1 1	ſ		THAKEEDDSDQVEVPRDOENDVGDKOSAVKMKMFGKI.TPDTPPW
TO44 276 734 EVYLTDEFAKGRKVADLYELVQYAGNITPRLYLLITVGVYVVKS FPQSRKDILKDLVEMCRGVQHPLRGLFIRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR EPERQELRILVGTNLVRLSQV  TO45 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEDDAEQSQG  TO46 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEDDAEQSQG  TO47 103 486 QKKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVRSIWELFGVKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKALDTAISLGFHSYYER  TO48 92 627 FFCLTLLSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQGESREVEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  TO49 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKKAVREL MNYEIRPGRILGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPFRGCHWLGRKLIAWX ASSLWG	1	İ		HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV RERERQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGGTSQPGQWLQARQAHRHEDDAEQSQG  7046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEDDAEQSQG  7047 103 486 QMKIEKCGWSEGLTSIKGRCHNFYTAISKDVTYKELKNLLNSKN IMLIDVRSIWEILEYQKIPESINVPLDEVGEALQMMPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSWDYRHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETOLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1	]		KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQTRINILPDEG FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQTTRINILPDEG EPTDEETTGGISDSMDFVILNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV  LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLPVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEIPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQQTESQPGQMLQRPQAHRHPGDAEQSQG  7046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEIPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQQTESQPGQMLQRPQAHRHPGDAEQSQG  7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEFQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTWEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVLDVIVVASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLMG	7044	276		QQSSPLVNKEEEHAPELSAN
TO45  3  513  LGFKMEALSRAGGEMSLAALKOHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEGDAEQSQG  KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEGDAEQSQG  KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048  92  627  FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFF\QRLN\QAI EKKW  7049  393  938  KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		2,0	/34	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
TO45  3  513  LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  1046  3  513  LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG  TO47  103  486  QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNILNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  TO48  92  627  FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049  393  938  KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGVAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1			FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLOCTRNTLPDFG
S13	) ;			EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMOHOCHSDDDEVD
RANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG CANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG CANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKIMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSSWDYRHHATRRVISSFVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLMELETIKEKFEVQHSEGYRQISALEDDLAQTKA KRDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7045			ERERQELRILVGTNLVRLSQV
RANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADDVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG ETRRSQQA/RSGGTESQPGQWLQRPQAHRHPGDAEQSQG KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKGRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRILLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		, i	213	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
TO46  3  513  LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQQTESQPGQWLQRPQAHRHPGDAEQSQG  7047  103  486  QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNILINSKN IMLIDVREIWBILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048  92  627  FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTF5SEEEEANY WKDLAMTYKQRAENTQEBLREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049  393  938  KRTGSASYCGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKRREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1	j		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRINMHNIJERUNY
GFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	l í	i		DEFQUHEPFULYRNASLSIYSIWFYDKNDCHRIAKIMADUNGE (
TO49  313  GFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049  393  938  KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYJELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7046	3	633	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
TO47  103  486  QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER  7048  92  627  FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKGRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049  393  938  KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRILGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1		213	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
7047 103 486 ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNILINSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER PFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRRMELETIKEKFFVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYCGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVCRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKRREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1	,		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
7048 92 627 FFCLTLLSSWDYRHATRVISSPVFTMEDSGKTFSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1	į.		DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
7048 92 627 FFCLTLLSSWDYRHATRRÜSEDTSKALDTAISKDVTYKELKNLLNSKN NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7047	103	406	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7048 92 627 FFCLTLLSSWDYRHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQIETRN RDLLSENNRLMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1	205	400	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
7048 92 627 FFCLTLLSSWDYRHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQIETRN RDLLSENNRLMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1	i		IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY
FFCLTLLSSWDYRHHATRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	704B	92		NEVRESKSDS/IVESYLAGVRSKKALDTAISLGFHSYVER
WKDLAMTYKORAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYCGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVCRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKRREEILEEIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	''	32	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEFFFANV
RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	i i	[	1	WKDLAMTYKQRAENTQEELREFOEGSREYEAELETOLOOJETPN
TKDQLQKYTRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW  7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		[		RDLLSENNRLRMELETIKEKFEVOHSEGYROISALEDDIAOTKA
7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		1	1	IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\ORLN\OAT
WRIGSASYGGPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7049			EKKW
VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRILGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	,549	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDFI.
NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	l l	i		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVDEI.
EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1	1	1	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEETAKUT
ASSLWG	]			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKT BADDOVEDBT	7050			ASSLWG
	,,,,,	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEO	Predicted	Dwo di ata	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
1			NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREBILEEIAKVT
			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
Ĺ	<u> </u>		ASSLWG
7051	119	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
1	1		VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDFPV
1			SCQDEPFRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR
ł			SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
1			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
<u></u>			KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAAROGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTI
7054			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAAROGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
ł	]		RRCRWDAMEYDEKLARFRQAHLNPFNKOSGPROHEOGPGEEVPD
1	1		VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1			VQQLRQAIEECKQVILELPEOSEKOKDAVVRITHLRIKLOFI,KD
1	<b>f</b> 1		PNEDEPNIRVLLEHRFYKEKSKSVKOTCDKCNTITWGLTOTWYT
			CTGCYYRCHSKCLNLISKPCVSSKVSHOAEYELNICPETGLDSO
1	1 1		DYRCAECRAPI/CS/DGVVPSEAROCDYTGOYYCSHCHWNDIAU
7055	2	500	IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
1	1	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
j	1		EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
1			SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
	1 1		FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
			EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
	]		SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
			M W TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
7057	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
			SGEVPSQASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL
[ ]			SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSQKGQPRAPM
ļ l			AQKLPTCRECGKTFYRNSQLIFHQRTHTGETYFOCTICKKAPLR
l i			SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
į l		•	YKCPICEKSFIQRSNFNRHORVHTGEKPYKCSHCGKSFSWSSSt.
1 1			DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR
7058			GYPC
,,,,,,	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
}			PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVDFO
1 1			NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
7059	1	1377	ARN*SCTQLLQHPQLCTLPFLILA
'	* 1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
	ł		APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
[ ]	ı		CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
			VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
	ł		FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
[	j		GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
]	j	j	RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
	1		QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
7060	90	1670	TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
		2070	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
			YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

CEC	I p 32 - 2 - 3		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
,	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	Doquence	\=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
į	Į.		QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
i	1	{	LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
1	}		RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
1	1		VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
1	l		TAEEICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
Ī	ľ		SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
ļ.			QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
1	ı	ł	SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
1 .		ł	PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
			ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
I.	1	1	RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
Į.			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
1	1	}	QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
1			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
f	[		YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
			TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
			FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
7063	2		менн
/ /003	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
1			FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
1			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS HKGFLLRLDM
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
ŀ		001	SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
{	i i		SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
1			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
1	1		PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG
			RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
1	·		FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI
l	·		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
			RAGPFDEFQ
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
	ļ		YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
2002			VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ
			QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ
!	.		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
			TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
[			NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
			FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
7068	222	916	HSPFCWAPF
	666	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV
		•	VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
7069	1147	1765	AELRIHENKVKKIQKDTPKKK FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKO
		-,05	TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
	J		TLLQSNVPVLQPPLPLEMPPPPPPPPPESPPPPPPPPPPPAPKMPPP

Deginning   nucleotide   location   corresponding   contion   corresponding   cofirst   amino acid   amino acid   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   seq	SEQ	Predicted	Predicted end	I Amino poid
NO:   nucleotide		1		Amino acid segment containing signal peptide
corresponding to first amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	,			Glutamic Acid F-Dhonylelening C Classics
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SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE KQRYLDBADRDKERYMKELEQYQKTEAYKVPSRKTQDRQKGKSH RQDAARQATHDHEKETEVKERSVFDIPJIFTEEFLNHSKAREAEL RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM  1119 SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQPPLGPSSS  7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLPAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	7076	279	1049	
KQRYLDEADRDKERYMKELEQYQKTEAYKVPSRKTQDRQKGKSH RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLINHSKAREAEL RQLRKSDMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM  7077 3 1119 SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVAROR ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGFSSS  7078 483 767 FQQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL RQLRKSNMEFEERNAALQKHVESMRTAVEKLEUDVIQERSRNTV LQQHLETLRQVLTSSFASMPLPEKGETPTVDTIDSYM  3 1119 SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKKILDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGFSSS  7078 483 767 FQQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	l			
RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQOHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM  3 1119 SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNMDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS  7078 483 767 FQQGMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	Ī	]		
TOTO TOTO TOTO TOTO TOTO TOTO TOTO TOT		[		RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
3 1119 SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR ELKWILDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAHHEERRRQQPPLGPSSS  7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQBLAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				LOOHLETLROVLTSSFASMPLPEXGETPTVDTIDSYM
ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVAROR
SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA RGGHGQQDLYRILKATTIYRPDEGYCQAQAPVAAVILMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGFSSS  7078 483 767 FQQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGBLIELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ		[		
RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS 7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYYFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVILRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS 7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS  7078 483 767 FQQGMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQBLAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ		[	•	
IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF LVHEVTNIPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGPSSS  7078 483 767 FQGQMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQBLAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ			•	
TOT9  LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQQPPLGFSSS  767 FQGRMAGEQKPSSNLLEGFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
RAIHEERRRQQPPLGPSSS  7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY  7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	7078	483	767	
7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
7079 2 376 SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ				
	7079	2	376	SVVEPKRPKEPSGSDGESDGPIDVGOEGOLSOMARPLSTPSSSO

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	i	\=possible nucleotide insertion)
			AEVLOMTVDHLKMLHATGGTGTHALLFQASFIQQIF
7080	200	595	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPQDGIPY
ł			LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
			CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
7081	213	506	AVTEEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
			VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRTCEREQN
			RVVFQMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL
			CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
			SSLENLRLPTLREESSPRELEDSSGDOGRCGPTHOGSEDPSMLS
1			QAQSATEVEERHVSPSCSTSRERPFQAGELILAETGEGETKFKK
ı			LFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKOYMLRRP
i			ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG
			GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
1 .			VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
7083	115	541	YPHLKHGGVCPVYVVNITQVIELLD
		341	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP
			SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
1		•	PFPLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
			VKNKAPAEVQITAEQLLREAKERELELLPPPPQQKITDEEELND
•			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
			RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
			AELVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
			YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
1			DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR
			AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
1			DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSO
1 1			KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
1	į.		NLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL
1			KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
7086	256	525	SHQHQKLVVSKQNPFPPLSTGC
	-55	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP
l i			SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
1 1		. = •	NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
1	i		VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS
1 1			ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
I			HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
1 1			MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
1	į.		KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVQRRGS
, ,		. 1	PNPFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
<u> </u>			AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
j Í	1		HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
	* [		SPIHTSVQFQASYLPKPGAQLYQFRYVNROGOVCGOSPPFOFRE
]	j		PRPMDELVTLEEADGGSDILLVVPKATVLONQLDESOOERNDLM
	į		QLKLQLEGQVTELRSRVQELERALATARQEHTELMEOYKGISRS
	1	j	HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
1	1		RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELOVAOOENHHL
		<u> </u>	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
(	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1	l	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
}	}	1	LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1	Į.		LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
]	]	}	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
1	ļ.	l	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
ļ	1		EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETO
1	ł	<b>}</b>	ASLLIGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
1	Ì		HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
i	!	ŀ	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
1	i	1	PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
			QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
1		ţ	
[		ĺ	HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
	1	1	RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
1	1	ľ	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
1	1		LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1	•		LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
	1		LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
	i		TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
1			EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
			ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
	1		EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
1		1	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
	i		SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
ł	1	1	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
	1	i	HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
1	Į.	l	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRLGEGCEPISKRQMKKLIKQKQWEEQRELR
1	1		KQKRKEKRKKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
1			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACOLVLGLLMTSLTESSIONS
	1	1 055	ECPQLCVCEIRPWFTPQSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
'''	"	308	
	1	ľ	DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
1	1		LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
7095	<del> </del>	<del> </del>	ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
'095	1	411	IASSLPKMASILQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1	l	Į.	SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
1	1	}	TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
		<b></b>	KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC
1			SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
	j		APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
1	1	1	QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
1	1	1	EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
1	<b>!</b>	1	LYAYRCVLGPHODPPEEAELLLONLOSKGPRDCVVLMAAAGHFA
	1	1	GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
		1	LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
1		l	FGGKGAPLORGDPRLWDIPLATRRPTFOELORVLHKLTTLHVYE
1	1		EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ
1		l	NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
I		]	RKRNKKEKSRDQEAGAHRTLLOOTQEEEPSTQSSQAVAAPLGPL
i .	1	1	_ ~~ -
1		l	LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
7097	256	7222	LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
1	]	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
L	L	L	FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ctox
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSTPGSHDTMTVC
			LNKKSPISHEESRLLQLLNKALPCITRPVVIKWSVTOALDVTFO
i			LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTAI.VEDTI.TETCR
			WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
•			EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
7098	82	956	TEALIRYLETMKSCGR
ſ		236	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT
			EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
1			LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
1	]		LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
1			AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCPF
			LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLAROGYHOIWAFPFLPSGATATWPAASPSPSLA
			ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPGAD
			GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
]			ROSCOMNNLPHLOVVGLTWGHISWDLLALPPODIILASDVFFFD
			EDFEDILATIYFLMHKNPKVOLWSTYOVRSADWSLEALLVKWDM
7100	205		KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSI.
/200	203	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1 1			FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV
			DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN
7101	2	503	SSVPVAFSHFRFDVERGDEVLYW
	ļ		WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEBPPEEVPPRAEEITIPADVTP
1 1	1		ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1 1	į		VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTD
1			ERVPTHIVDYSEAEQSDEQLHQEISOANVICIVYAVNNKHSTDK
7103	119		VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
1,203	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSSES
1 1			LSDKGSELKKSFDAVVFDVLKVTPEEYAGQITLMDVPVFKAIQP
7104	1670	795	DELSSCGWNKKEKYSSAP
	-0.0	795	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDILINNAGV
1	1		MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
1 1			GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA
1 1	1		HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS
1	[		KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAED
		1	EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
j		)	LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST
		1	SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
( l		j	MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFOAGOHFKPR
7106	34		FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
1.100	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLORAFDSIVNKDHKRMFGT
			YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGOCF
		ļ	GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
			TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
	1		PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
	1	j	AKMLQMVLQGSVGATVNQGPLEVAQVPLAEIPADPKLYRHHNKL
	į	i	RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
7107	1145	591	RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS *I*WLQTGKKK
			* "INTANTA

SEQ	Predicted	nand:	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	l .	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
]	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
7108	1	942	\=possible nucleotide insertion)
1 /100	1 *	342	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
1	į		FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
1		}	QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
ŀ			QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
1			RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
i	•	1	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
1		1	DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
7109	964		WHVLAW
/109	704	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
1	1		TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
1			SEKLATOTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
1		1	VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
1			SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
1	1		QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
7110	96		KAYGWCSELIRHRRVHARKEPSH
1	[ ~	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
1			SPSTKRRGQMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
	1		KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
İ			LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE
7111	2	414	YKKIKAKLRLLEVLISKQDSSKSI
/	-	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
<b>\</b>			LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
Į.			MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD GAVLW
7112	103	495	
	1 203	4,23	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
ſ	Į.		FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
7113	<del>                                     </del>	824	KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
	1 -	024	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1			LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
i	<u> </u>		ALGLPHLPSFKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
ļ			QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEOKKTMADRNL
1			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
1			SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRKI
	[		IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGONRSYVRKKDDG
1			CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
1			QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
1	ļ		SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
1	]		KPFVCDKCPKAPKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYO
	(		RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
I			FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
!			EKPYECRRCGKAFGEKSTLIVHORMHTGEKPYKCNECGKAFSEK
1			SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
1			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
J	]		KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
1			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
l			HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
{			SNPGVDFGDVSERLALRORLKCRSFKWYLENVYPEMRVYNNTLT
}			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
			LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
			FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
			WIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
ļ			PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
	<u> </u>		

Amino acid segment containing signal peptide containing beginning contained beginning to first amino acid amino acid amino acid amino acid amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid sequence   Amino acid se	550	10-32-5-3	T =	
Mo: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Costion   Corresponding   Coffice   Corresponding   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Co			:	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1		1	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid areide of samino acid amino acid amino acid amino acid sequence  8 equence  equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 equence  1 e				hanistidine, Talsoleucine, Kalysine,
amino acid residue of amino acid sequence solvente sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen				D-Broline, M-methionine, N-Asparagine,
residue of amino acid sequence    Martyprophan, Natyrosine, Xaunknown, **Stop Code sequence   Natyrosine   Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyrosine, Natyros	1			S-Sering Turbus - in William ine,
Codon, /-possible nucleotide deletion, /-possible nucleotide insertion	ı	residue of		W=Truntonhan V=Truncing V H-1
ASNINVELSINGSTEARNSIKLITASPESYITITSLAHELMIKVP LPPKNITAPSRYPPGLITGOKPPLSTKOMSPERIGGGMONDARY TPGSSMGESSSGRITMINULVIKUNITPOIDGSTEATLCMOMEPLIT FILMIPHGRALVMYSSKEEVVKAQKSLHISDLFILLT  1117 695 1261 LLISTEGGGMPPSSTEETYTGAMGRALPAPEAGPALPGGA FVSQAARAIPLLQPSQAAQAGGLSQPARACCALCSLPMPLRING SPIRLBEGGLARPTPINORKTRYRAMGALPAPEAGPALPGGA FVSQAARAIPLLQPSQAAQAGGLSQPARACCALCSLPMPLRING SPIRLBEGGLARPTPINORKTRYRAMACWARACHLOPLAPEAGAL GKVCLRHPPTOVKGGGGAAGRQGOMGTRRGTFTSGARDFGGL RVKIRCOPTGHLP  1863 PHICEPMPGAGAMVILMVLFEHAVGYALLAREVEETSLLQPQVE ESVAMLSKHPTSUVLVAACPPSSSQVALENANUSGVVHEDLAV LLLETHLPSKKKVLLGVSDPKIGAALGEELGYNCOTGGV TAET LEGVRLHFRINVKSLTDLSACKAQGLGLEHSVACVFFWNRUV NNITQSISLLDQLDKDINTPSMEVREWGYHPPELVXIIINDKAT VCRLAGPIGNREENBOKLERLEELIMDGAKACHPSNIKKU NNITQSISLLDQLDKDINTPSMEVREWGYHPPELVXIIINDKAT VCRLAGPIGNREENBOKLERLEELIMDGAKACHPSNIKKU RONTPKYGLIFHSTFIGRAARNIKGRISVLANKCSIASRIDGF SEVPTSVFGELHEROVEERLEFFFTEGETPRAKAKIPPALKT RONTPKYGLIFHSTFIGRAARNIKGRISVLANKCSIASRIDGF SEVPTSVFGELHEROVEERLEFFTGETEPRAKKESTLAESEL MSSDLEETAGSTSIPKKKSTPKEETVUNDPEERAGRSGSKKKRK RONTPKYGLIFHSFTIGRAARNIKGRISVLANKSCSTASRIDGF SEVENINGKRISVLANACTOPASGVALEMANSCRUVHEDLE LLLETHLPSKKKKVLLGVGDPKIGAALGELGYNCOTGGVTAET LRGGYRHFRILVKGLIDLSACKAGLGLGHISTSGVVFFWENDF NNITQSISLLDQLDKDINTPSMEVERWYGYHPPELVXIINDNAT VCRLAGPTGORRELBEDLEKELEELITMGGAKAKALLDASRSSMS WEISADLINTESFSSRVVSLSEYRGSLHTTLRSSMSQVAPSLS ALIGEAVGARLINKGGILHARGSTINTAKAYFSVVVGUNEAMVQAS WEISADLINTESFSSRVVSLSEYRGSLHTTLRSSMSQVAPSLS ALIGEAVGARLINKGGILHARGSTSTINAKYFSTVVOUNEAMVGAS WEISADLINTESFSSRVVSLSEYRGSHTTLRSSMSQVAPSLS ALIGEAVGARLINKGGILHARGSTSTINGKVTONDEREMONDR SERVENKKKOKORPOPVORGMEDPSISFSPKKKKFFKSETDECE MSSEKKKKKOKORPOPVORGMEDPSISFSPKKKKSFFSEELE MSSDLEETAGSTSIPKRKSTPREETVONDEERACHLSSSKKKR HKTVYLGTUTTARSTANGOVTONDR SERVENKKKOKORPOPVORGMEDPSISFSPKKKKSFFSEELE MSSDLEETAGSTSIPKRYFTFFTETTONDREMALERINGFTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHANGTONDR TONDRACHTHAN	ł	amino acid		Codon /-nossible pushoptide deletion
ASNINIVELSTRAGSTSARSISSKLITUSSEGSVITITSLAHELINVP LEPRNITATAS REPREJITOROPELSTRADSELRIGGGGMENDARY TPGSSWGESSGRITIMIL/URINITPOLIOSTILRILCMOHPLIT FILINIPHIGALALVINSKEEVUKAQKSLIISISERIGGGGMENDARY TPGSSWGESSGRITIMIL/URINITPOLIOGSTILRILCMOHPLIT FILINIPHIGALALVINSKEEVUKAQKSLIISISERIGGGGA FILINIPHIGALALVINSKEEVUKAQKSLIISISERIGGGA SPILINIPGGGAPPESSTEFTYTGAWGGALFAPRHPCAPGALFGA FYLINIPGGGAPPESSTEFTYTGAWGGALFAPRHPCAPGALFGA FYLINIPGGARTPTINDEKTRITESAMACMARAQWDTLGPLICHER GKVCLRIPPPTVONGOGGAAGAGGGGGGGTTRAGATTGARDGGG FYLINIPGGARTPTINDEKTRITESAMACMARAQWDTLGPLICHER GKVCLRIPPPTVONGOGGAAGAGGGGGGGTTRAGATTGARDGGGG FYLINIPGGARTVALIVITYPETRAGAGAGGAGGGAAGAGAGGAGGGGGGAAGAGGAGGAGGA		sequence		\=possible nucleotide insertion\
LPPKNITAPSRPPGUTGCKPPLSTYDDSPLRIGGGGGNDDARY TPGSSMGESS SCRITHMULNULNIDTOIDGSTUCKTOMHOPLIT				ASNYNVPLSSTAOSTSARNSDSKI.TWSPGSVTNTSI AURI WICID
7117 695 1261 LLISTEGGCHPPSSIEFTTGAMGKALDFLITL FINLDLPIGGALVEYSSKEEVVKAGKSLIDFLITL FINLDLPGGLAVEYSSKEEVVKAGKSLIDFLITL LLISTEGGCHPPSSIEFTTGAMGKALDAFBHEVGAGLEGGLEGGALFGGA FVSQAARJ FLLUPGGAAGAGCAGCAGLAGHVEURING SPILKLPGGLRTPTNDRKTETRSAMACMARAGMOTLEDPLKLSHR GKVCLRHPPPTOVRGG FGAAGAGGGGTRRRFTFGGARDPGGL RVKHRCOPTGHLP PHICEPPSGAGAWVLLHVLFEHAVGYALLALKEVZETSLLOPVE BSVLMLGKFISIVRLVAFCPFASSQVALENNAMVSEGVVHEDLR LLSTHLPSKKKVLLAGVOPPKIGAATGGENYOTGGVIAE LEGVUGLHFRNLVKGLTDLSACKAGLGIGISYSPAKVKPFIVNRVD NNITIGSISLDOLDKOIT INFSKRVEBVELGVROOTGGVIAEI LEGVUGLHFRNLVKGLTDLSACKAGLGIGISYSPAKVKPFIVNRVD NNITIGSISLDOLDKOIT INFSKRVEBVELGVROOTGGVIAEI LEGVUGLHFRNLVKGLTDLSACKAGLGIGISYSPAKVKPFIVNRVD NNITIGSISLDOLDKOIT INFSKRVEBVELGVROOTGGVIAEI LEGVUGLHFRNLVKGLTDLSACKAGLGIGISYSPAKVKPFIVNRVD NNITIGSISLDOLDKOIT INFSKRVEBVELAVROCTABORTAL VCRLAQPIGNREHENDEKLEKLELTHDGAKAKAILDAGESSMA MDISAIDLINIESSSSAVYLSLEVTHGAKMANITIGSIAEIL SEVPTSVFGEKLRROVEERLSFYSTGGIPROILDWRAMVOABLA EARABITIKLKENGKKKLKKKKKOKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKKAGKPOEVPORNOMBOPSISTEKEKKKAGKPOEVPORNOMBOPSISTEKEKKKAGKAGAGATALAGSSTANTAKAGSTSTATAKAGSTATAKAGSTSTATAKAGSTSTATAKAGSTSTATAKAGSTATAKAGSTATAKAGAGATAAAAAAAAAA	j	}	I	LPPKNITAPSRPPPGLTGOKPPLSTWDNSPLRTGGGWCNSDADY
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FYSOARATIFLIQPSQAAQAGEGLSQPARAGCALCSLPHILMING SPILLRIPGGIRTPTINDRIKTRISAMACAMPONTLOPILLSHR GRVCLRIPPTOVRGGFGAAGRQGMGTRRGTFTSGARDPGGL RVKHRCOPTGHLP  7118 49 1863 PHICEPNSGAGAWLLHVILPSHAVOYALLALKEVERTSLLOPPOVE ESVINLIGKERIS LVRILANGPCPASSQVALLALKEVERTSLLOPPOVE LLLSTHIPSKKKVLLGVGDPKIGAATQEELGYNCOTGGV TAET LLGVELHFINLVKSLTDLSACKAGLGLGISPRAKVERVIVNEVD NNIT JGSISLLDGLUNDINTTSKRVBBYYGYHPPELVKI INDNAT YCRLAQPIGNREELINELKELEELIMDGAKAALLDAGRSSMG MDISAIDLINIESPSSRVVSLGEVROSIHTRIKHSGVORPSLG ALIGGAVGALLAHAGSLIVILAKTPASTYQTIGAGRAALPALKT RCNTPKYGLI PHSTFJIGRAAANNKGI ISRJANCSIASRIDGC SEVPTSVFGEKLERQVERLERSTYTGTIFRRHLDSVMKSMYOAPSLS ALIGGAVGARLIAHAGSLIVILAKKPASTYQTIGAGRAALPALKT RCNTPKYGLI PHSTFJIGRAAANNKGI ISRJANCSIASRIDGCF SEVPTSVFGEKLERQVERLERSTYTGTIFRRHLDSVMKSMYOAPSLS ALIGGAVGARLIAHAGSLIVILAKKPASTYQTIGAGRAALPALKT PSKEEVSSGFERAAGKSSKKKKKFRKASQED PHCEPPNEGAGRAVLLAVILEHINGVERLERSVERSTEECE EMSSKYRKKKKGKQRQEVPGENOMEDPSISTSKPKKKKKRSTSKEEL LLGTHLPSKKKKVLLGVORPFGAAGTSTYRKKKYNTHNOTYD NMITQSISLDQLKDINTPSHRVERWYGYHPPELVKI INNDAT YCRLAQPIGNREELINDLKEKKKLLIAKTERSWGVYHEDLR LLGTHLPSKKKKVLLGVORPFGAATGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALDOCA
SPILLELPGGLETTHDERKTETESAMACWARAGWITLGPLKLSHER GKVCLRHERPTGYMEGFGAAGROGGGGTREGTTSGARDFGGL RVKHRCOPTOHLP  PICEPROAGAMVLLHVLFEHAVCYALLALKEVEETSLLOPPVE ESVLMLCKFHSTURLVAFCPPASSQVALENAMAVSGVVHEDLE ESVLMLCKFHSTURLVAFCPPASSQVALENAMAVSGVVHEDLE LLLETHLPSKKKKULGGDRIGGADELGYNCOTCOV LAEI LEGVELHFRHLVKGUTDLSACKAQLGLGHSYSRAKVKRIVKRVD NNITOSTSLIDDQLDHOTINTFSMRVRENYCHTHDGARAGATLDAGSSMA WD15AIDLINTESFSRVVSLSSTRQSHTYLKSKNSOVAPSLS ALIGEAVGRAFLAHAGSSTINLAKYPASTVQTLGAEKARPFALKT RGNTPKYGLIFHSTFIGRAARKKGKRGSVALAMKCSLASRIDGF SEVPTSVFGCKLRGVVGERLISFYETGETPRRULDVHKRAMVQAE EAAAEITRKLEKQEKKRLKKGKKRGSRYLAMAKCSLASRIDGF SEVPTSVFGCKLRGVVGERLISFYETGETPRRULDVHKRAMVQAE EAAAEITRKLEKQEKKRLKKGKRGSTANLAKARVGSASSKKKKK SSKEPVSSGPEAAGKSSSKKKKKFRASGED  7119  49 1863 PHCPPNFGGGAMVLHVUFFEHAGVALLALKEVEETSLLOPVE EAMSENFRKKKKGKRQPVGENGMEDPSISFKFKKGSFREEL MSSDLETAGSTSIPKRKSTPKETTVADPEERGHRSGSKKKR FSKEPVSSGPPEAAGKSSSKKKKKFHASGED  7119 A9 1863 PHCPPNFGGGAMVLHVUFFEHAGVALLALKEVEETSLLOPVE ESVLNLKKKKGKRQPVGENGMEDPSISFKFKKHSPSKEEL MSSDLETAGSTSIPKRKSTPKETTVADPEERGHRSGSKKKR CRUBPFORGRAMVLHVUFFEHAGVALLALKEVEETSLLOPVE ESVLNLKKHSIVKULAVFFFASGVALLALKEVEETSLLOPVE LLLETHLPSKKKKULJUGDPKIGAAIQEELGYNCOTGGVIABI LLGGRALFHRILVKGLIDLSACKAQLGLGHSVSRAVKVENWBVD NNIIQSISLLDQLDKDINTFSMRVEWYGVHPEUVKIINDNAT VCRLAPPIGNREELMERKLEKGEKRIAANASGSTVATSRSSM MD1SAIDLINIESPSSRVVSLBEYRQSHTYIRSKNGVAPSIG ALIGEAVGRAFLIAHAGSLASTSHNSTRSSMAV MD1SAIDLINIESPSSRVVSLBEYRQSHTYIRSKNGVAPSIG ALIGEAVGRAFLAHAGSLITHLAXYPASTVQILGARALFRALKT RGNTPXYGLIFHSTFICRAAAKNKGIISRVLANKGSIASTPECC EMSEKPKKKKKOKPQEVPQENMEDPSISFSKKKKFFPECC EMSEKPKKKKKOKPQEVPQENMEDPSISFSKKKKFFPECC EMSEKPKKKKKOKPQEVPQENMEDPSISFSKKKKFPILGT  GOTTPKTTTTPLFFFGTDAAANNAGGIASTPECC EMSEKPKKKKKOKPQEVPQENMEDPSISFSKKKKFPILGTIILOPK RGSDLETAGRGSVTINAMOPPLVTNIEGFFFFFFTDAALALKSTSS LGEBPLINGFFONCHLAPSMADLERLIEHINDBVH RDFRCINNIEDFYNGFONCHLAPSMADLERLIEHINDBVH RDFRCINNIEDFYNGFONCHLAPSMADLERLIEHINDBVH RDFRCINNIEDFYNGFONCHLAPSMADLERLIEHINDBVH RDFRLINLENGFFONCHLAPSMADLERKFGFDJENITENVI LSYNISLEPHANKAGOLGACHTON LLEVERS MTYLUQSVIENNELQVITQTIQDLLKALKGIVIDTISTISTERVIVI AUEIPT	ľ	1	1	FVSQAARAIPLLOPSOAAOAEGLSOPARACGALCSI, PWPI, PNWG
7118 49 1863 PHICEPNEAGAWULHVILFEHAVEYALLALREVEETSLLOPOVE ESVINILGKFISTURILVAFCPPASSQVALEARMAYSEGVVHEDLR LLLETHLPSKKKKVLLGVEDPKIGAAIQEELGYNCQTCGVTAEI LLGVELLHFRILVKGLTDLSACKAQLGLLGHSYSRAKVKFWVNRVD NNIIQSISLLDQLDDCINTFSMRVRSWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA YCRLAQFIGNRERLMEDELFROMWGYHFPELVKIINNAA ROMPKKGLIFHSTIGRAAANKGISKHAKUKCSIARSILDSRSSMG REAABLITRKLEKQEKKRIKKKKKHALALASSEMSSTPECE EMSSKPKKKKKOKPQEVPQENGHEDPSISFSKPKKKKSFPECEL MSSDLEETAGSTSIPKKKKKKKKKKKKKKKKKKKKKKKFPAANCCIARSTPECE EMSSKPKKKKKOKPQEVPQENGHEDPSISFSKPKKKKSFPECEL MSSDLEETAGSTSIPKKKSTPKEETULALEVEETSLLQPQVE ESVINICKFHSIVRLVARCOPASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKVLLGVEOPHIGAAIQELEGVKVNGVO NMIIQSISLLDQLDKDINTFSMRVERWYGHPPELVKIINNAA YCRLAQPIGNRERLMERVLEKEELTHMGAKAKAILDASSSMG MDISAIDLINIESFSSRVVSLESTROGSKAKKKNWRVD NMIIQSISLLDQLDKDINTFSMRVERWYGHPPELVKIINNAA YCRLAQPIGNRERLMERVLEKEELTHMGAKAKAILDASSSMG MDISAIDLINIESFSSRVVSLESTROGSEPPROMUDHKERMWQAR EAAAEITRKLEKQEKKELKEEKITHMGAKAKAILDASSENSSTPECE EMSSKPPKKKKKOKPQEVPOENGMEDPSISFSKPKKKSPSKEEL MSSDLEETAGSTSIPKKKSTPEETVNDEERGRIKGSKKKK RGNTPKYGGIFHSTFICRAANKKGISRIANKKGISRICHG SEVPTSVFGEKLRGUVERLSFYFEGEIPPROMUDHKERMWQAR EAAAEITRKLEKQEKKELKEEKIRALALALSSENSSTPECE EMSSKPPKKKKKKOKPQEVPOENGMEDPSISFSKPKKKSISIGGGOOP NSTYPLIFULSPGIDPAADIKTRAEKKFSKLESISIGGGOOP RAZAMMRSSISRGKWVFFONCHLAPSMPALERULEHTHDKVH RDFRLWITTSLESNFFVYSILQUSKSSIKKKKRR FSKEPVSSGPEAAGRSSSKKKKRTHAALALASSENSSTPECC EMSSKPFKKKKKKOKPQEVFONCHAPSKRYDAMALLKSYSS LGEDFLINSCHKWMFFKSSSSKKKKRTHALALASSENSSTPECC EMSSKPFKKKKKKOKPQEVFONCHAPSKRYDAMALLKSYSS LGEDFLINSCHKWMFFKSSSSKKKKRTHALALASSENSSTPECC SEVTSTVFGEKKKKKKKKOKPQEVFONCHAPSKRYDIVAMALLESTSS LGEDFLINSCHKKKKKKKKKKKKIKITAALASSENSSTPECC SEVTSTVFGEKKKKKKKKKKKKKKIKAKSIASIGGGOOP NSTTPLIFVLSPGIDPAADIKTRAEGRIFGKELTHENDKVH RDFRCHINTHAAAAAAIAASCERULFTHMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1	}		SPILRLPGGLRTPTNDRKTRTRSAMACWARAOWDTLGPLKLSHR
7118 49 1863 PRICEPREAGAMULINULFERAVGYALLALKEVEETSLLOPQVE ESVINICKFRISTURIVAPCPPASSQVALENANAVSGVUHEDLR LLIETHIPSKKKKULIGVEDKIGAAIQEELGYNCOTGGVITAEI LLIETHIPSKKKKULIGVEDKIGAAIQEELGYNCOTGGVITAEI LEGVELHFRBLUKGITDLSACKAQUGLCHSYSRAKVKPNVRRVD NNIIQSISLIDLOBIDINTTSRBVREWGYHFPELVKIINNAAT VCRLAGPIGMREKIBEDKIEKEELITHOGAKAKAILDASRSMM MDISAIDLINISFSSRVUSLISTRGSLHTILKSKSGVAPSLLS ALIGEAVGARLIAHAGSLTNIAAYPASTVQILGAEKALFPALKT RGNTPKYGLIFHSTFIGRAAAKKGRISRYIANKCSIASRIDCF SEVPTSVFOGEKLREQVEERISFFTCFSFENKINGVAPSLS EANABITRKLEKGEKKRIKKEKRIAAIAALASSENSSSTPEGCE EMSKEPKKKKKKORDEVERISFFTCFSFENKKKSFSKEEL MSSDLEETAGSTSIPKKKSTPREETVADPEEAGHRSGSKKKK FSKEEPVSSGPEAAGKSSSKKKKRFRKASGED  7119 49 1863 PHCEPNFGRGAWULHVLFEHAVGYALLALKEVEETSLLOPQVE ESVINICKFHSIVRIVAGITDLSACKAQUGLGHSYSRAKVKRIVANVAVD NMIQSISLDQLORDINTSSMRVEWHYPELWKIINNAT YCKLAGPIGNREENBENKLEKLEELTMGGAKAKAILDASRSSMM MDISAIDLINIESPSSRVVSLESPKGELGYMCOTGOVIAEI LRGWRLHFINILVKGLTDLSACKAQUGLGHSYSRAKVKRIVANVAVD NMIQSISLDQLORDINTSSMRVEWHYPELWKIINNAT YCKLAGPIGNREENBENKLEKLEELTMGGAKAKAILDASRSSMM MDISAIDLINIESPSSRVVSLESPKGHEYSPKETGEIPRKNLDWKESAMVARSL ALIGEAVGARLIAHAGSLTHLAKYPASTVOILGAEKALFRALKT RGNTPKYGLIHSTFICRAAAKNGRISRYLANKCSIASRIDCF SEVTSVFGEKLREQVEERLSFYETGEIPRKNLDWKERAWQAE EAAAEITRKLEKGEKKELKEKKRRAALALASSENSSTFEECE MSSERVKKKKKOKPOPOGNOMEDEISSPKKKKKTARSICE SEVETSVFGEKRKKKOKPOPOGNOMEDEISSPKKKKKTARSICE SEVETSVFGEKRKKKOKPOPOGNOMEDEISSPKKKKKTARSICEGGGOP RAEAMMRSSIERGKWVFONCHAPSMWPALERLIEHINDEKVH RDFFLHITALSPNKFPVSILQNGSKMITEPRGVGRANLLKSYSS LGEDFLNSCHKWMEFKSLLLSLCLFHONALERKRGGIRGGSKKKKK SSAGSGGGEIVEDVTYDLIEPFREDGTANLSVVFKDS MNTYLUGSVIRYMRLQVTTOTLODLLKALKGITTOLOPK SSAGSGGGEIVEDVTYDLIEPFREDGTANLSVVFKDS MNTYLVQSVIRYMRLQVTTOTLODLLKALKGITVINSSOLEMM ASIYNNTUPELMSAKAYPSILKLESSWOLICARDISTHOPPTYTUHGY LSYKKSLEINDMPSICKIALHIGGROFOTD DMRRCINNILEDFYNPEDILJERGHTANLJORMAKFYVIJTHEN AVIWLLPTPRKAQDQDFYLCTIVKTIRAGTISTTCHSTNYVI AVEIPTHOPQWGVITIGLELEGARNDPEAFQLAESOPKELYTEM AVIWLLPTPRKAQDQDFYLCPIVKTIRAGTISTTCHSTNYVI AVEIPTHOPQWGVITIGLERGROFOSLOTMMELIPFFREDGTANSTVYTI AVEIPTHOPGWGVTIRLERGERGSLOOPAAALEEGERGY		}	{	GKVCLRHPRPTGVRGGPGAAGROGGMGTRRRGTFTSGARDPGGI.
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LLLETHLPSKKKKULIGVGDVIGANIGESIGNCOTGGVIAET LEGVELHPHILVKELTDLSACKGLGLENSYSRAVKENVARVU NMI IGSISLIDGLDKI INTESMRVEBWYGYHPPELVKI INDNAT YCRLAGPIGWRRELNEKLEELITMGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLESTYRGSLHTYLRSKMSGVAPSLS ALIGEAWGARLIAHAGSLITNLAKYPASTVUJIGAEKALFRALKT RONTPKVGLIFHSTFIGRAAAKMRGISRVLANKGSISRIDGF SEVPTSVFGEKLEQUEERLSFYSTGSIPPKILDVMKEAMVOAE EAAAEITRKLEKGEKKRIKKEKKHKALALALASSENSSTPEGEE EMSERFKKKKKOKPOEVPGENOMEDPSISTSKPKKKKSFSKEEL MSSLEETAGSTSIPPKKSTSPEKTUNDPEEAGHRSGKKKKK FSKEEPVSSGPEEAAGKSSKKKKKFHKASQED PHCEPNFGRGAWVLLHVLFEHAVGYALLALKEVESISLLÖPGUE ESVINLACKFHSI VINLAVECPPASSAULENAMAVSEGGVHEDLR LLLETHLPSKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIAEI LLGETHHILVKGLIGHSVARAVKFNANVO NNIIQSISLLDQLDKDINTFSMRVERWYGYHPPELVKI INDNAT YCRLAGPIGMRRELAEDELKELLEIGLGISTSKRAKVKFNVNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGYHPPELVKI INDNAT YCRLAGPIGMRRELAEDELKELLEIGLGISTSKRAKVKFNVNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGYHPPELVKI INDNAT YCRLAGPIGMRELAEDELKELLEIGLGISTSKRAKVKFNVNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGHTPELVKI INDNAT YCRLAGPIGMRELAEDELKELLEIGLGISTSKRAKVFNNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGHTPELVKI INDNAT YCRLAGPIGMRELAEDELKELLEIGLSTSYRAKVFNNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGHTPELVKI INDNAT YCRLAGPIGMRELEDELLEILEIGLSTSKRAKVFNNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGHTPELVKI INDNAT YCRLAGPIGMREKEKKKVKFNREDELGHSSKKKKFNNRVO NNIIQSISLLDQLDKDINTFSMRVERWYGHTPELVKI INDNAT YCRLAGPIGMREKEKKKKVFNREDELGHSSKKKKKNNAVAPASTVOLIGAEKALFRALKT RGNTTPKKKE (FSKRESTPEGEDKLEKLERSTALALASSENSSTEECE EMSEKPKKKKKOKPOEVPGENGMEDSISFSKKKKKSPEKEEL MSSLEETAGSTSIFKKKETPERFORMALLAASSENSSTEECE EMSEKPKKKKKOKPOEVPGENGMEDSISFSKKKKKFRKKESKELE MSSLEETAGSTSIFKKKETPERFORMALLAASSENSSTEECE EMSEKPKKKKKOKPOEVPGENGMEDSISFSKKKKKFRKKE FSKEEPVSSGPEBAAGKSSKKKKKHHAOQUE  GARACHMANSSIERGKWVFFONCHLAPSWMPALERILEHINDDKVH RSCHULTSLESNKKFVFONCHLAPSWMPALERILESKYKKE LEGDFLINSCHKWMFFSKILLSLCLFFIGNALERKFGGLGFRIPY DÜNDRCINNILEDFYNDDVJ.SPEHSVSAGGIYHQIPPTYDLHGY LSYIKSLPLNDMPETFGLHDNANITFAQRGVTD DÜNDRCINNILEDFYNDDVJ.SPEHSVSAGGIYHQIPPTYDLHGY LSYIKSLPLNDMPETFGLHDLANDVAKKYVPLYEES NNTTVJUGEVIENNALQGVITOTLOPLKALGELVANSO				ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
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YCRLAQFIGNRELNENKLEKLEELIMDGAKKAILDARSRSMM MDISAIDLINIESFSSRWUSLBYROSLHTYLRSKMSOVAPSLS ALIGEAVGARILAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAAKNKERISRYLANKCSIASRIDGF SEVPTSVEGEKLREQVEERLSFYETGETERKINDVMKEAWOAB EAAABITRKLEKGPKKRLKKEKKRIAALALASSENSSSTPECCE EMSSRPKKKKKGPGVPOPENDENDPSITSFSRFKKKKSFSREEL MSSDLEETAGSTSIPRKKSTPKETVJDDEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKFKHASQED  7119 49 1863 PHCEPNPGRGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLKKFHSIVALVAFCPFASSQVALEALRAVEVEEISLLQPQVE ESVLNLKKFHSIVALVAFCPFASSQVALEANNAVSEGVUVEDLR LLLETHLPSKKKKVLLGVCOPPKIGAALGERGYNOOTGGVIBLE LRGVRLHFHNLVKGLTDLSACKAQUGLGHSYSRAVVKFNVNRVD MNIIGSISLLDGLDKNINTFSRAVERWGYHPPELVKIINDNAT YCRLAQPIGRRELINBOKLEKLEELTMDGAKAKAILDASRSMG MDISAIDLINIESFSSRVVSLSEYRSHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKFGISTALANKSSIASRIDGF SEVPTSVFGEKLREQVEERLSPYEGEPRINLDVMKEAMVQAE EAAAEITRKLEKGEKGRLKEKKRLALALASSSNSSSTBEECE EMSSRPKKKKKORQDSVPQENDEDDEDSISFSKPKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGEKKKK KKSPKEVENSGPEEAAGKSSSKKKKFHRAGSGD  7120 1991 64 OLGTRRCLGGDKVTNAMQDFJVTNLPERFIEPGTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMFFSKKLSAISLGGGGGP RAEAMMESSIERGKWVFFONLDHSVKKKSPSKKLSGINGGGVTD DWDRRCLMRILEDFYNDPULSPEHSYSASGIYHQIPPTVDLHGY LSYIKSLEPLNDMEPFIGHDVANLFKREENTPGPLGFNIPY DWDRRCLMRILEDFYNDPULSPEHSYSASGIYHQIPPTVDLHGY LSYIKSLEPLNDMEPFIGHDVANLFRANFGPLGFNIPY DWDRRCLMRILEDFYNDPULSPEHSYSASGIYHQIPPTVDLHGY LSYIKSLEPLNDMEPFIGHDVANLFRANFGPLGFNIPY DWDRRCLMRILEDFYNDPULSPEHSYSASGIYHQIPPTVDLHGY LSYIKSLEPLNDMEPFIGHDVANLFRANFGPLGFNIPY DWDRRCLMRILEDFYNDPULSPEHSYSASGIYHQIPPTVDLHGY SSAGGGGREIVEDVTONILLKVPEPINLOWMAKYPVLYEES MYTVLVQEVIRYNRLLQVITQDLLKKRIG.VVWSSGLEMA ASLYNNTVPEUMSARAYPSLKPLSSWWDLLQRLDFLQAWIQG IPAVFWISSFFFPQAFLIGTLQNDRAFRYVSIDTISFDFKWFE APSELTJORPOVGVIHGLPLEGARNDPEAPGLAEGOPKSLTYEM AVULLPTBYRRAQDOPFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTPROPRINIERKGROPGSLDTTMRRLIPPFREASAK LTILVDADAERFRAQDGETRAVKRERGRERGPGLEGRRAV LTILVDADAERFRAGLEGRERGVEGGGGLERRAV SUPLITAETVASLURPALGLEGRANGERGREGGGELRAW	1			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
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RONTPKYGLIFHSTEIGRAARNINGERISPYLANKCSIASRIDGE SEVPTSVEGERIKREQVEREISPYETGEIPRKILDVMKEAMVOAE EAAABITRKLEKQEKKRLKKEKKRALALALASSENSSSTEECE EMSEKPKKKKQKPQEVPQERGMENDEPSISTSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKKSTPKEETVINDPEBAGHRGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASOED  PHCENPFGGARMVLLHVLFHAVGYALLALKEVEEISLLQPQUE ESVLNLGKFHSIVRLVAFCPFASSQVALEMANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAAQELGYNCQTGGVIABI LRGVRLHFHNLVKGLTDLSACKAQLGIGHSYSKRAKVKFNVRVD NMIQSISLLDQLDKDINTFSMRVREWGYHPPELWKIIMDNAT YCRLAQPIGMREELMEDKLEKLEELTMDGAKAKAILDASRSSMS MDISAIDLINIESFSSRVVSLSEYRQSLHTYLEKSMSQVAPSLS ALIGEAVGARLIAHAGSLITHLAXYPASTVQILGAERALFPALKT RGNTPKYGLIFHSTFIGRAARNINGRISRYLANKCSIASRIDGF SEVPTSVFGEKLREQVERELSPYETGEIPRKNLDVMKEAMVQAE EAAABITRKLEKÇEKKRLKKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGREDPSISFSKFKKKKFSKEEL MSSDLEETAGSTSIPKKKKTPKRETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPERAAGKSSKKKKKFHKASQED  7120  1991  64  QLGTRGCLRGDKVTNANQDPILVTNLEPFIFEPOTABLSVVFKDS NSTTPLIFVLSPGDPAADLYKFAEEMKFSKKLSILGQGGGP RAEAMMRSSIERGKWPFFONCHLAPSWMPALEELLEHINPDKVH RDFRLWITSLPSNKFFVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKWEFFKOHLEFHINALERKFGPLGFNIPY EFTOGDLRICISQLKWPLDFRYSASGIYHQIPFYTÜHLGY DDDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPFYTÜHGY SSSAGSGGREIVEDVTQNILLKVPBSPINQWMAKYPVLYSES MNTVLQEVIRVRRLQVTTOTLODLLKALKGIVWNSGLEIMA ASLYNNTVPPELMSAKAYPSLKPLSSWWMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLITGTLQNFAKKFVISIDTISFPFKWMFE APSELTQRPQVGGYINGLFLEGARNDPEAFQLGSVMSCHIMA ASLYNNTVPPELMSAKAYPSLKPLSSWWMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLITGTLQNFAKKFVISIDTISFPFKWMFE APSELTQRPQVGGYINGLFLEGARNDPEAFQLGSVTNAWIP AVIKLLPTRNKAQDQDFYLCPIYKTLRAGTLSTTGHSTNYVI AVEIPPHOPQDRIMIKGVALCLDY  7121  2 546 RPLRFWVLSLGSMVGLMTYGRROFGSLDTTMRRLIPPFREASAK LTTLUDADAEAFTAYLEAMRLEKNTPEEKDRRTAALQGELRRAV SUPLITAETVAALBWALQELAGRALGRENDPEAFQLOVAAKALEMGVF				MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
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PARABITRKLEKQEKKRLKEKKRIAALALASSENSSTPEECE EMSERPKKKKKOKOROPOROMEDPSISFSKPKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK PSKEEPVSSGPEEAAGKSSSKKKKRHKASQED  PHCEPNFGAGAWULHVLFEHAUGYALLALKEVEETSLLOPQUE ESVLNIGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDIR LLLETHLPSKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIABI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFWNRVD NMIIQSISLLDQLDKDINTFSMRVEWYGYHPPELVKIINDNAT YCRLAQPTIGNRELMEDKLEKLEELTMGGAKKAAILASRSSNS MDISAIDLINIESFSSRVVSLSEYRQSLHTYLKSKMSQVAPSLS ALIGEAVGARILAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVETSVFGERLREQVEERLSFYEGEIPRKHLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALASSENSSSTPEECE EMSERPKKKKKOKDQEVPQENOMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKKK FSKEEPVSSGFEEAAGKSSKKKKFHRASQED  7120  1991  64  QLGTRRCLRGGKVTNAMQDFLVTNLEPRFIEDGTANLSVVFKDS NSTTPLIFVLSPGTDPAAKKFAEMMFSKKLSAISLOGGGGP RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNNFPVSILQNGSKMTIEPPRGVEANLLKSYSS LGEDFLNSCRKWFFKSLLSLCLFHGBALERKKFGLFMIPY EFTDGDLRICISQLKMFLDEYDDIFKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNDPVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIOLQPK SSSAGSGGREIVEDVTONILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVITYNELLQUTTLQLDLLKALKGLVWNSKSLEIMA ASLYNNTVPELWSTRYLTGTLQDLLKALKGLVWNSKSLEIMA ASLYNNTVPELWSKAKAYPSLKPLESGWMDLLQRLDFLQAWIQDG IPAVFWISGPFFPQAFLTGTLQDLKALKGULVMSKYELFEN AVIWLLPTPNRKAQDQFYLCPIYKTLTRAGTLTSTGHSTNYVI AVIBLIPTROPQOGCTIHCLIPLEGARMDPEAFGLAESQFKELTEM AVIWLLPTPNRKAQDQFYLCPIYKTLTRAGTLTSTGHSTNYVI AVEIPTHOPQORMHIKKGVALICALDY  7121 2 546  RPLRPWVLSIGSWGLMTYGRRGFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTALLEGALLPKARPEEKORFTAALGGGLRRAV SVPLTLAETVASLWANLEGKLUFMASLEMAV		•		RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
### BMSEKPKKKKKOKPOEVPOEMSMEDFISISSEKKKKSFSKEEL ### MSSDLEETAGGTSIPISKKKSTFREETVNDPEEAGHRSGSKKKR ### FSKEEPVSSGPEEAAGKSSKKKKFHKASQED  ### 1863 PHCEPNFGAGAMVLHVLFEHAVGYALLALKEVEETSLLQPQVE  ### ESVLNLGKFHSIVRLVAFCPASQVALLALKEVEETSLLQPQVE  ### ESVLNLGKFHSIVRLVAFCPASQVALLALKEVEETSLLQPQVE  ### ESVLNLGKFHSIVRLVAFCPASQVALLALKEVEETSLLQPQVE  ### ESVLNLGKFHSIVRLVAFCPASQVALLALKEVEETSLLQPQVE  ### ESVLNLGKFHSIVRLVAFCJGLGEHSYSRAKVKFWVNAVD  ### INTIQSISLLDQLDKDINTFSMRVVEWYGYHPPELVKIINDNAT  *## YCRLAQPIGNRRELMEDKLEKLEETTMCGAKAKAILDASRSSMG  ### MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS  ### ALIGEAVGARLIAHAGSLTNLAKYPASTVQLIGABKALFRALKT  ### RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF  ### SEVETSVYGERLREQVEERLSFYETGEIFRKNLDWKEAMVQABE  ### EAAABITRKLEKQEKKRLKKEKKRLALALASSENSSSTPEECE  ### EMSEKPKKKKKQKQEVPQENGMEDPSISFSKPKKKSFSKEEL  ### MSSDLEETAGSTSIPKRKKSTFKEETVNDPEEAGRRSGKKKRK  ### FSKEEPVSGGFEAAGKSSSKKKKKFHKASQED  ### OLGTRCLARGBVTNAMQOFLVTNLEPRFIEPQTANLSVVFKDS  ### ALIGENVSTAMAODPLYTNLEPRFIEPQTANLSVVFKDS  ### ALIGENVSTAMAODPLYTNLEPRFIEPQTANLSVVFKDS  ### ALIGENVSTAMAODPLYTNLEPRFIEPQTANLLKSYSS  ### LIGHTMADALERKFFONCHLAPSWMPALERLIEHINPDKVH  ### RDRFRLWITSILENSKFFONCHLAPSWMPALERLIEHINPDKVH  ### RDRFRLWITSILENSKFFONCHLAPSWMPALERLIEHINPDKVH  ### ALIGENVSTAMADALKFFAEMVFSKKLSAISLGQGGGP  ### RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH  ### ADEDLRICISQLKMFLDEVDDIPKVLKYTAGEINYGGRVTD  ### DMDRRCIMNILEDFYNPDVLSPEHSYSASGITYHOIPPTYDLHGY  ### LISTINDAMPEIFGLHOMANITFAQNETFALLGTIQDKK  ### ALIGENVSTAMADALARLARLARLARLARLARLARLARLARLARLARLARLAR	1	<b>]</b>		SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKBAMVQAE
MSSDLEETAGSTSIPKRKKSTPKEETVADPEEAGRKSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED  7119 49 1863 PHCEPNPGAGANVLHVLFEHAVGYALLALKEVEETSILLQPQVE ESVLNLGKFHSIVRLVAFCPFASGVALLENANAVSEGVVHEDLR LLLETHLPSKKKKVLJGPPKIGAAIQEELGYNCOTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQPTGNRELINEDKLEKLEELTHDGARKAKALDARSSSM MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGAAAKNKGRISTRYLLANKCSIASRIDCF SEVPTSVFGEKLREQVWERLSPVETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKKKKRLAALALSSENSSTPECCE EMSKRPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLETTAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEAAGKSSKKKKKFHKASQED  7120 1991 64 QLGTRCLRGDKVTNAMQDPLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLIYKFAEMKFSKKLSAISLGQGGGP RAEAMMSSIERGKMVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKNTIEPPRGYRANLLKSYSS LGEDFLNSCHKVMEFKSLLISLCLFHCNALBERKFGPLGFNIPY EFFTOGDLRICISQLKMFPONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKNTIEPPRGYRANLLKSYSS LGEDFLNSCHKVMEFKSLLISLCLFHCNALBERKFGPLGFNIPY EFFTOGDLRICITSQLKMFDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSGOREEIVEDVIDDLLKVDEPINLQWWMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKELSSWVMDLLGRLDFLQAMIQDG IPAVFWISGFFFPQAFLTSTLONFARKFVISIDTISFDFKWMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCFIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY AVEIPTHQPQRHWIKRGVALICALDY AVEIPTHQPQRHWIKRGVALICALDY SVPLTLAETGASNVGLMTYGRRQFGSLDTTMRRLIPPFREASAK LTTLUDADAEAFTAYLEAMRLIPKNTPEEKURRRTAALGEGRRAV SVPLTLAETVASLWPALGELARCGNLACKSDLQVAKALEMGVF	j			EAAAEITKKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
7119 49 1863 PHCEPNFGGAMVLHVLFEHAVGYALLALKEVEISILQPQVE ESVLNIGKFHSIVRIVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGPPKIGAATQEELGYNCOTGGVIAEI LRGVRHHFHNIVKGIDSACKAQLGIGHSVSRAAVKFNVNRVD NMI IQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNREELNEDKLEKLELITHDGAAKAAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSHTYLRSKEMSQVAPELS ALIGEAVGARLIAHAGSLTHLAXYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRINCF SEVPTSVFGEKLREQVEKRIKKEKKRLAALALASSNSSSTPEECE EMSREPKKKKKKKDEPOENGMEDPSISPSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKK FSKEEPVSSGPEEAAGKSSKKKKKHKAGSCDD  7120 1991 64 QLGTRCCIRGDKVTNAMOPFLVTNLEPFIFPGTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKLSAISLGQGGP RAEAMMRSIERSKKWKFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWITSLESNKFPVSILQNGSKWTIEPPRGYRANLLKSYSS LGEDFLNSCHKWMEFKSLLISLCIFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDBYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNDPVLSPEHSYSASGIYKGIPPTYDLHGY LSYIKSIPLNDMPEIFGLHDNANITRAQNETFALLGTIIQLQPK SSSAGSGOREEIVEDFUNLLKVPEPINLQWUMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTIQDLLKALKGLVWMSKQLEIMA ASLYNNTVPELWSAKAYPSIKPLSSWMDLLQRIDFLQAWIQDG IPAVFWISGFFPOADTILLKVPEPINLQWUMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTIQDLLKALKGLVWMSCQLEIMA ASLYNNTVPELWSAKAYPSIKPLSSWMDLLQRIDFLQAWIQDG IPAVFWISGFFPOADTILLKVPEPINLGWUMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTIQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSIKPLSSWMDLLQRIDFLQARIQDG IPAVFWISGFFPOADTILLKVPEPINLTSPPKWMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWILPTPRNKAQDQDFYLCPIYKTLTRAGTISTTGHSTNYVI AVEIPTHQPQRHWIKGAULGALDY  7121 2 546 RPLRPWULSIGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLUDADABAFTAYLEAMGLIKANTPEEKDRRTAALQEGRRAV SVPLTLAETVASLWPAULGLALDY	İ	<u> </u>		MSCDI FETACOTCI DED VEGTE VEDE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE STORE
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LLLETHLPSKKKKVLLGVGDPKIGAAIGEELGYNCOTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQIGLGHSYSRAKVKFNVMRVD NMIIGSISLDQLDKDINTFSMRVREWGYHFPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSRRVVSLSETRGSHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRLKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVETSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAABITRKLEKGEKKRLKEKKRKAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEBTVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED  7120 1991 64 QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGGGP RAEAMMRSSIERGKWVFPONCHLAPSWMPALERLIEHINDDKVH RDFRLWLTSLPSNKFPVSILQNSKMTIEPPFGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDGYDDIPYXVLKYTAGBINYGGRVTD DWDRRCINNILEDFYNDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSGGREIVEDVTQNILLKVPSPINLQWVMAKYPULYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELMSAKAYPSLKPLSSWMDLLGRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLPLEGARNDPEAFCLAESQPKELYTEM AVIULLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVISLGSWGEMTYGRRGFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALGELRRAV SVPLITLAETVASLWPALGELARRGNLACRSDLQVAAKALEMGVF	1	] ]		ESVINIGKENSTVELVA ECDEASSOVAL EXAMANGE CURRENT D
LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMI IQSISLLDQLDKD INTFSMRVREWYGYHPPELVKI INDNAT YCRLAQFIGMRRELMEDKLEKLEELIMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSPYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSERPKKKKKQKPQEVPQENGMEDPSISFSKPKKKESSEELE MSSDLBETAGSTSIPKRKKSTPKEBTVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFIKASQED  7120 1991 64 QLGTRCLRGDKVTNAMQOPLVTNLEPPFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGGGQGP RAEAMMRSSIERGKWVFFONCHLAPSMWPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVWEFKSLLLSLCLFHENALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYXVLKYTAGBINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIOLOPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELMSAKAYPSLKPLSSWYMLLQRLDFLQAWIQDG IPAVFWISGFPFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARNDPEAFGLABSQPKELYTEM AVIWLLPPPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLGTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLITLAETVASLWPALQELARRCGNLACRSDLQVAAKALEMGUF		}		LLLETHLPSKKKKVLLGVGDPKIGAAIOFFIGVNCOTCCUTAFT
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### VCRLAGPIGNRRELNEUKLERLTMOGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLINLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSPYETGEIPRKINLDVMKEAMVQAE EAAABITRKLEKQEKKRLKKEKKRLAALALASSENSSSTBECEE EMSERPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLBETAGSTSIPRKKKSTPKEBTVUDPBEAGHRSGSKKKRK FSKEEPVSSGPEBAAGKSSSKKKKKFHKASQED  7120 1991 64 QLGTRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKPSKKLSAISLGGGGGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFFLWLTSLPSNKFFVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMMILEDFYNDPUSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREIVEDVTQNILLKVPEPINLQWWMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWWDLLQRLOFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGGTIHGLPLEGARMPPEAFGLAESQPKELYTEM AVIWLLPTHNRKAQDDGFYLCPIYKTLTRAGTLSTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWUSLGSWWGLMTYGGROFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	j	1		NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
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7120 1991 64 QLGTRRCLRGDKVTNAMQDPLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1	·		PSSULEETAGSTS I PKRKKSTPKEETVNDPEEAGHRSGSKKKRK
NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLUDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGUF	7120	1991	64	
RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQMGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKKFGPLGFNIPY EFTOGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1		U*1	NOTTELLEU CECTERA DE VERRENCE CO
RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVPWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLUDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF		1		PARAMMPSSIEDGYWURDONGUI ARGUMDAI ERI ININININININININININININININININININI
LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTOGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			RDFRI.WI.TSI.DSNKEDUSTI.ONCGUMUTERDROGEDANT
DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSOGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MMTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	1			LGEDFLNSCHKVMEFKSLLIGIGT PUCNAL PROVEDED CONTENT
DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQMETFALLGTIIQLQPK SSSAGSQGREBIVEDVTQNILLKVPBPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF				EFTDGDLRICISOLKMFLDEYDDTDVKWLKVTAGETNVCGDVMD
LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKAKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFYISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	Į į			DWDRRCIMNILEDFYNPDVI,SPEHSYSASGIYHOIDDTYDT HOU
SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES  MITVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDE IPAVPWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGUF				LSYIKSLPLNDMPEIFGLHDNANTTFAONETFALLGTITOLORY
MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	<b>}</b>	J		SSSAGSQGREEIVEDVTONILLKVPRPINTOWVMAKYDUT.VFFC
ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFITGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF		Ì		MNTVLVQEVIRYNRLLQVITQTLODLLKALKGLVVMSSOLRIMA
IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	l i			ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLORLDFLOAWIODG
APSELTQRPQVGCY1HGLPLEGARWDPEAFQLAESQPKELYTEM AVIWLLPTPNRKAQDQDFYLCP1YKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKGVALICALDY  7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	<u> </u>			IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY 7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	j ĺ	ĺ	Í	APSELTQRPQVGCYIHGLFLEGARWDPEAFOLAESOPKET.YTEM
7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	j j	1		AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
7121 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	<u> </u>			
LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	/121	2	546	
SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF	. '	i	-	LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALOEGLRRAV
GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL	j 1			
				SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF

SEQ	Predicted	Predicted end	l Amino and a second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1	1		LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
]		İ	SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
į	1		GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
	i		ETROE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
1	1		AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE
			VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTEQOKIMO
1	,		HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
			EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV
			MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
			VGBETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV
1	· ·		KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM
1	Į.	ľ	LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDQSPCWHPGPALSPGTLGPLSWAM
1 :			ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS
1	1		KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
			FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
<b>j</b>			LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSEKH
1 1			AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
	]		RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
			RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
1			ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
1			ACVYVSRGWNOLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
			SHSQAREPORPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
			OVATGRRAVOVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
j i			PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
1			WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
L			PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
]			AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
] ]			RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC
		•	ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
1			*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
, 1			CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
			PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRFL
1 7736			LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP
1 1			SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE
			DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
]			LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPT
1 1			WETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSD
			LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
j 1			GMDIESLHKCALDDRRELHQFAQDGLICQDMDCLMLTFGDIPHH
į ĺ			APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQ
1			SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA
			CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
1 1			RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
			RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
	:	•	TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
	Į.		
			DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA

SEO	Predicted	1 5	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS
ł		}	LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG
1		ļ	QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEOALSOHGAH
			GNNLIAVLAKYIYHKHDPALPRLAIOLLKRLATVAPMSVVACLG
•		•	NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETOP
	ļ.		GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSOO
1			QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENIT
	1		SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDOP
1			LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM
ļ.	ŀ		LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
İ	}		PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
ŀ	1		VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV
			CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ
	1		RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
1			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
1			LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG
	1		FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML
			QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE
1	{		ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
			EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
1			EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISOAMRYLRD
1			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
7129	1		SPQGKSTSLSKASPESQEPLIQLVQAFVRHMOR
/125	1	1054	FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
1			WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
	ĺ		PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
1			TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL
	1		GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
1	- 1		NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA
L	j		TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL
7130	2	780	HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG
i i	ł		ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS
			RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN
1 [			AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
1 1	ł		DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP
7131			YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA
1 '131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVOFNHLEVV
7132	1420		KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
'-3"	1420	1087	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
1 1	ŀ		IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI
7133	2	3648	RLIHKELSCPGSATGDQVPFKEQ
[	- 1	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
ļ			EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ
]	1	(	RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL
] .			RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
			MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS SEEVKOVESGTLPFOESI GSEEU DA DEED WOOD DOOR DOOR DOOR DOOR DOOR DOOR DOO
1	1		SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
J.			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS
	1	[	IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
		ļ	EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
			RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS
		l	SGALTHILVPVSRDGTFDAGSPGFOLRYMVGPGFLKPGERRCFA
			RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE

Deginning	SEO	Predicted	Predicted end	
No: nucleotide corresponding to first baino acid residue of amino acid residue of amino acid sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Seq		1		Amino acid segment containing signal peptide
Cocation   Corresponding   Cofirst   Station   Corresponding   Cofirst   Station   Cofirst   Station   Cofirst   Station   Cofirst   Station   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   C				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque	Í		•	Halistidine Talcolougine V Institute
amino acid residue of amino acid	i	corresponding		L=Leucine M=Methionine N=Acapragine
residue of amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequ	1	to first	amino acid	P=Proline. O=Glutamine R=Arginine
maino acid sequence  whityptophan, Y=Typtoshae, X=Ukdeleton, Y=possible nucleotide deletion (codon, /=possible nucleotide deletion) (v=possible nucleotide insertion)  LEVWATEYEQDNWYSGMLAGSKYRIGVUSVYKGRIHUTLAN VGHECGKVRGCSTLPPSRSRVISNUSASPSGSGLITTGSSRS RENVOAOKLADVSSLAAMLITHAGGKSEPQDVSRSSSAATRIRK RENVOAOKLADVSSLAAMLITHAGGKSEPQDVSRSSSAATRIRK LERMSVSLOBAGGGLGRRGTSVLAQOSUSTQUILBDLQVIANG RETARSISALISLALIATISHITHATUGAKEFPETYLKRPHNYOH TYTVEIDHPELSVIUDGGRRDFKGAAGLHTVVEEDHMYHNGSI APQUILRHETARSHYPHTYSFSGAAGLHTVVEEDHMYHNGSIDNY ICETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY ICETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPSTPINGENGERPEDIFLKANSGGSREINVICLITVELQPHVVDCUSPY UCETORNOGERPSTPINGENGERSUNGSSERNENPESEDERC ULDALELALECSILLRIGGTCKANGGGEPGTSPDASPSSLCQUSP SATUMPDQLIFFHAMSSLENDARSSERNENPESEDERC ULDALELALECSILLRIGGTCKANGGGEPGTSPDASPSSLCQUSP SATUMPDQLIFFHAMSSLENDARSSERNENPESEDERC ULDALEKALANGSSLINLANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSERNENPESEDERCONSTRUME UCETORNOGERPADIFLKANGSERN			residue of	S=Serine, T=Threonine, V=Valine
sequence    Codon, /-possible nucleotide deletion, /-possible nucleotide dissertion			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
LEVVATEXED/DEFORMATION	1		sequence	Codon, /=possible nucleotide deletion
LEVVATEXEONMUNSGOMLGFGRVERTGYHSVYKGRLHHTLAN   VGMPCECKYKGCSTLPPSSERVISIONGASHSGOLHTGSSER   KHVVQACKLADVDSELAAMLLTHARGGGFODVSRESDATRRIK   LERMSVHLGGRGGDLGKRESVLAGOGSVTGHDQVTAAYR   ERTKABSIASILSIATTEHTLHATLGVAFFFEFFLKRIPHINTOH   TUTVEIDMPELSVILVDSGOMBYGLAGOLHTCHDQVTAAYR   ERTKABSIASILSIALTTEHTLHATLGVAFFFEFFLKRIPHINTOH   TUTVEIDMPELSVILVDSGOMBYGLAGGLHTCHDGVATAYR   ERTKABSIASILSIALTTEHTLHATLGVAFFFEFFLKRIPHINTOH   TUTVEIDMPELSVILVDSGOMBYGLAGGLHTCHDHVUQOFF   FYRPELSFLKKARRLPPHTFCGAPVGMLGEDPPHTWCCSDDNV   LCETCONVEGGEPERDTI-LKVARGSSERIMDFUHVUGUTH   CHOLVASHLVCLCCROPILSKARGTHAVCHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVCHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVCHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVCHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSKARGTHAVACHARVARD   CHOLVASHLVCLCCROPILSK		sequence		\=possible nucleotide insertion)
WORDCEGKYRGCSTLEPSGRRYISNDGASFSGGGSLATTISSER  KHWYQAGKLADVDSELAMILITHARGGGGDOVSREDATRERU  LERNESVELGEAGGDLGRGFTSVLAQGGVETOHLRDLQVIAAYR  ERTKASEJASLIGLATTEHTHATIGVABFFEFVLKNPHNYOH  TUTVETDNPELSVIVDSGENDEKGAAGLHTPVEEDMFHIRGSL  APGUTURPHETAHVPRKOSFSAGQLAMVQSAGSHEGKEKMDAV  SPMKSSAVPTHAKULFRASGGFTAVLCLTVELQPHVVQOFR  FYRHELSFIKKARTLPPHHTFGAPVGMLGGDISHEKGMDAV  SPMKSSAVPTHAKULFRASGGFTAVLCLTVELQPHVVQOFR  FYRHELSFIKKARTLPPHHTFGAPVGMLGGDIVAGVGGFTAVLGAT  ICETQWGGGFPROIFLKVASGSFDEILDFVIITSDRMLATPT  OTMQVILHSLQLCRGPLISKARSFSVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMAGSKSFTVILLMIDVD  CHQLVASHLVCLCCRQPLISKASFEMIRATSGFTX  FYSKRTPHHHEDHPELLFFREGSFTVILGOFT  GEEGLIIVINDHEDKREBAFCVVITY  GEEGLIIVINDHEDKREBAFCVVITY  GEEGLIIVINDHEDKREBAFCVVITY  GEEGLIIVINDHEDKREBAFCVVITY  CHULTANG  GEGGFSYPPHOGISLGTFLODDHITVLLAGKSTRMLTDV  CHULTANG  GEGGFSYPPHOGISLGTFLODDHITVLLAGKSTRMLTDV  GEGLIIVINDHEDKREBAFCVVITY  GEGGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGELILIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVKITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVVITY  GEGLIIVINDHEDKREBAFCVKGSTVITKORABMT  GEGLIIVINDHEDKREBAFCVKGSTVRVITHAR  GEGLIIVINDHEDKREBAFCVKGSTVITKORABMT  GEGLIIVINDHEDKREBAFT  GETACCHPHOLOCALLINGHILL  GEGLIIVINDHEDKREBAFCVKGSTVITHAR  GEGRIIVINDHEDKREBAFCVKGSTVITHAR  GERGRAFT  GETACCHPHOLOCALLINGHILL  GEGLIIVINDHEDKREBAFT  GETACCHPHOLOCALLINGHILL  GEGLIIVINDHEDKREBAFT  GETACCHPHOLOCALLINGHILL  GEGLIIVINDHEDKREBAFT  GETACCHPHOLOCALLINGHILL  GEGLIIVINDHEDKREBAFT  GETACCHPHOLOCALLINGHILL  GE	1			LEVVATEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN
HINVOACKLADVDSELAAMLITHARGCKGPQDVSRESDATRERK     LERMSSURLDGEAGGLORGTSVLAQOSVCHIREDGOVLAAYE     ERTKASSIASILISLATTEHTLHATLGVAEFFEFVLKNIPHNYOM     TUTVEIDNELSVIVDSGEMPDFKAAGLATVELEQPHVVDOVFE     FRIERSFLASILISLATTEHTLHATLGVAEFFEFVLKNIPHNYOM     TUTVEIDNELSVIVDSGEMPDFKAAGLATVELTQPHVVDOVFE     FYREELSFLKKAIRLPPHHTFFCAPVGMLGEDPPUVHCSDPNV     CETONVEGEPROIFLKKASGEREIDLANGSEPPHILAUTCSDPNV     CETONVEGEPROIFLKKASGEREIDLANGSEPPHILAUTCSDPNV     CETONVEGEPROIFLKKASGEREIDLANGSEPPHILAUTCSDPNV     CHOLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTNP     YPERRIPHHIBSHBELLERFERDSFOVGGASFPHILAUDVD     CHQLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTNP     YPERRIPHHIBSHBELLERFERDSFOVGGASFPHILAUDVD     CHQLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTNP     YPERRIPHHIBSHBELLERFERDSFOVGASFPHILAUDVD     CHQLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTNP     YPERRIPHHIBSHBELLERFERDSFOVGASFPHILAUDVD     CHQLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTNP     YPERRIPHHIBSHBELLERFERDSFOVGASFPHILAUDVD     CHQLVASMIVCLCCROPLISKAFSIMLAAGEGKEVANRITTYTINGPASSERICTIONSG     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVIVO     GEEESLIJYINDHEDKNERAFCVKVVIVO     GEEESLIJYINDHEDKNERAFCVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEEESLIJYINDHEDKNERAFCKVKVVIVO     GEE	1			VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSSRR
LERNSVHLOGAGGOLGARGTSVLAQGSVETQHLEQUIADANA  RETTASSIALISLATITETHHATICULAPTEVALNIPHNTOH  TUTUG INNDELSYLVDSQEMEDEGGAGGAGGHTPVEEDVLANIPHNTOH  TUTUG INNDELSYLVDSQEMEDEGGAGGAGGHTPVEEDVLANIPHNTOH  TUTUG INNDELSYLVDSQEMEDEGGAGGAGGAGGHTPVEEDVLANICAGGAS  APQUILARE HERTHALPPK PERGYSPAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	{	1		KHVVQAQKLADVDSELAAMLLTHARQGKGPQDVSRESDATRRRK
APOLITER PERTAHPER PER SPESSAGARGANG LATRIVEED HILLIAGE APOLITER PERTAHPER PER SPESSAGARGANG SELANE KOMDAV SPMKSSAVPT KHAKVUFRAS GERFLAVLCLITVELOP HILLIAGE FYRPELS FLKKAR ILLIP PHAT FER APVEMENT FER SPESSAGE LANGLANG AND		1		LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHLRDLQVIAAYR
APOLYLRPHETAHUPFKYOSFSAGOLAWQASPSLENBEKGNDAY SPMKSSAVPTKHAKULPRASGERPI TAULCITURELOPHUVDOUFR FYRRELSFLKKAIRLPPMHTFFGAPVGMLGEDPPUTVRCSDPNV ICETONVGGEPRDIFKKANGGSPEN IFFVANGGSPEN IFFVITYSTRANGTATPT OTWOYLHSLORUDGSCPROIFFUNGSCREVHLANGTSCHNALAPT OTWOYLHSLORUDGSCPROIFFUNGSCREVHLANGTSCHNALAPT OTWOYLHSLORUDGSCPROUDGHUGGERGSREVHLANDVD CHOLNASMLVCLCCROPLISKAFEIMLANGGGKOVNKRITYTNP YPSERTPHHISDHPPELLERPEDSPOQUGGGERGAGSGREVNKRITYTNP YPSERTPHHISDHPPELLERPEDSPOQUGGGERGAGGSREVNKRITYTNP GEBEILLYINDHEDKNEAPCVKYTYQ  TO GEGFSYPFWGISLGTFLDPHYVLLEWHYDNPTYEEGLIDNSC GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVKYTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCXYTYP  ACHONAPCXTYQ  GEBEILLYINDHEDKNEAPCVXTYQ  GEBEILLYINDHEDKNEAPCXYTYP  ACHONAPCXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GEGYATYPERGESTILLYINDHEMCHAAPCXXTYQ  GEBEILLYINDHEMCHAAPCXXTYQ  GE				ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH
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POCEKTDPKGVFVLPPGRGVQDLHWGVRPLRASSRFVHLNLUDVD CHGUNSMULUCLOCRPLISKAR PASSRV GESEILTYINDHEDURASGEKGWINKITTYND YPSRRTFHLHISDHPBLLRPREDSFQVGGGETYTIGLQFAPSQRV GESEILTYINDHEDUREAFCVWLY THE GEGETYPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG LRLPYTMDIRKYDAGVIEAGLWVSLFHITTPGMPFFQSEGRCTI. ECLEEALEABKPSGTHVPAULLHAHLAGRGILKURFHRGKEMK. LAYDDDFDRNFQSFGYLKEEGTILPGDNLITECRYNTKDRAEMY WGGLSTRISENCLSYLLYYPRINITRCASIPDIMEGLQFIGWEIT YRPYTWPFIIKSPKQYKNLSFMDAMMKFKWTKKEGLSFNKUJ. SLPVNVRCSKTDNAEWSIGGMTAJPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLISCTLSTKSI.  7135 2 2072 FVRVTTPRSISIQGFKGESVGSTTQPLPSSYLIFRAASESDGRC WLDALEALARCSSLLRLGTCCPGGRGCEPGTSPDASPSSLCGLPA SATVHPDQDLPPLNGSSLENDAPSDKSERENPESDTTTQDHSR KTESGSDQSTTGAPVRRGTTYVQCESIGELGERSQVETVSE ENKSLWHTLIKQLRFGMDLGRVULPTFVLEPRSPLNKLSDYYTH ADLISRAAVEEDAYSMKILVTRYVGCESIGELGERSQVETVSE ENKSLWHTLIKQLRFGMDLGRVULPTFVLEPRSPLNKLSDYYTH ADLISRAAVEEDAYSMKILVTRYVALGEFYKKPKGIKKPYNPILG GSITAKSRFYGNSLSALLDGKATLTTEINRAEDYTLTMPYAHCKG ILVGTWTLELGGKVTIECAKNNQAGLEFKLKPFFGGSTSINGI SGKITSGGEVLASLSGHWDRVFIKEGSGSSALFWTPSGGVRVR QRRGGTTVPLEEQTELSERLIMGWTAISKGDQHRATQEKFAL EEAQRQRABERGESLMPWKPQLFHLDPTTQBWHRYLEDHSPWDP LKDIAQFEQDGILBRITAQGAVARATTGSKGDQHRATQEKFAL EEAQRGRABERGESLMPWKPQLFHLDPTTQBWHRYLEDHSPWDP LKDIAQFEQDGILBRITAQGAVARATTGSKFDQHRATQEKFAL EEAQRGRABERGESLMPWKPQLFHLDPTTQBWHRYLEDHSPWDP LKDIAQFEQDGILBRITAGAGNATTGSKFDQHRATQEKFAL EEAQRGRABERGESLMPWKPQLFHLDPTTQSBPHRHERSGFDQRL RKASDQPSGHSQATESGSTFESCPPLSDEGDGDFVPGGESPC PRCKKERRIQALHEAILSIREAGDGRLHRHHILDDMLK SQORKWORDECLORNSAVIOSKDATIGSLEKKITHLDDMLK SQORKWORDECLORNSAVIOSKDATIGSLEKKITHLDDMLK SQORKWORDECLORNSAVIOSKDATIGSLEKKITHLDDMLK GSFKVATOERNPQRAQMRLRRQKKGVVPFLGEFTELQRLDSAI PDDLLCONTNKSKSKEVVLOEMQLLQVAAMNYRRPLEKFVTYTF RMSQLSDKESVALSCQLEPENP  7137 2 466 WASGMSTVPGGSRISLGIQVGGWGVTGGEEESLTVFVADTWQA GSFKVATOERNPQRAQMRLRRQKKGVVPFLOEFTTELQRLDSAI PDDLLCONTNKSKSKEVRLOEMQLLQVAAMNYRRRPLEKFVTYTFT RMSQLSDKESVALSCQLEPENP  7138 2 466 WASGMSTVPGGGRHSLGIQVGWGWGTGEEESLTVFVADTWQA GSFKVATOERNPQRAQMRLRRQKKGVVPFLOEFTTETQRLDSAI PDDLLCONTNKSKSKEVRLOEMQLLQVAAMNYRRPLEKFVTYTFT RMSQLSDKESVALSCQLEPENP	1	[		OTWOVYI, HST. OPVOVSCVA COLUMN OF THE POMORE TO THE
CHQLVASMLVCLCCRQPLISKAFFIMLAGEGKGYNRRITTIND YPSRRTPHLHSDHPELLKPREDSPOVGGGETTIGLQFAPSQRV GEEELLIYINDHEDKNERAFCVKVIYQ GEEELLYTHDHEDVILEVHYDNPTYEEGLIDNSG LRLPYTMDIRKYDAGVIEAGLWVSLPHITPPGMPEFQSEGHCTI ECLEEALEAEKPSGTHVPAVLLEVHYDNPTYEEGLIDNSG LRLPYTMDIRKYDAGVIEAGLWVSLPHITPPGMPEFQSEGHCTI ECLEEALEAEKPSGTHVPAVLLHAHLAGKSIRLRHFRKGKEMKL LAYDDDPDRNFQEFGYLKEEGTILPGONLITECRYNTKDRAEWI WGGLSTTSENCLSYLLYYPRINLTRCASIPDHEQLQFIGWEI YRPVTWPFIIKSPYKAPPLVCGTSSS SJEHNPSTINLLVCLLLLSCTLSTHQAMNKFWYKKEGLSFNKLVL SLPVNVRCSKTDNABWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRPSTSINLLVCLLLLSCTLSTHQBEGTSPDASPSSLCGLPA WLDALELALRCSSLLBLATCXGPRGDEPGTSPDASPSSLCGLPA SATVHPDQDLPPLNGSSLENDAFSGSPGTSPDASPSSLCGLPA KTESGSDQSEJFGAPVRNGTTTYVEQVQEBLGGLGEASQVETVSE ENKSLWHTLLKQLRFQMDLSRVVLTVLEFRSFINKLSDYYTH ADLLSRAAVEEDAYSRMKIVLRWLSGFYKKFGIKKFYNPILG ETRRCCWFHPQTDSSTFYIAEOVSHCSFFYSHESEKPEESDTTTGDHSR KTESGSDQSEJFGAPVRNGTTTYVEQVQEBLGGLGEASQVETVSE ENKSLWHTLLKQLRFQMDLSRVLTSULSTPYTHEPSSFINKLSDYYTH ADLLSRAAVEEDAYSRMKIVLRWLSGFYKKFGIKKFYNPILG ETRRCCWFHPQTDSSTFYIAEOVSHCSGSSSALFWTPSGSVRR QRLRQBTVLELEGGKTSTFYIAEOVSHATSKGOQHRATYGEKFAL ESTRACKPHPQTOSTFYIAEOVSHATSKGOQHRATYGEKFAL ESTRACKPHPQTOSTFYIAEOVSHATSKGOQHRATYGEKFAL EEAQRQRAARERQESLMPWKPQLFHLDPITQEWHTRYEDHSPWDR GSTAASRFYGSLSSSTFESCFPEISDERQDGDPVGGGESC PRCRKEARRICQAHEAILSIREAQQRLHRHLSAMLSSTARAAQA PTGGLLOSFSSWFILLCVFLACOLFINHILK RASDQPSGHSQATTESSSTFESCFPEISDERQDGDPVGGGESC PRCRKEARRICQAHEAILSIREAQQRLHRHLSAMLSSTARAAQA PTGGLLOSFSSWFILLCVFLACOLFINHILK SQRKKYGMIBELOKNIKAVIOSNOLGKEKTAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVUST  7136 2 466 WASGMSTVPGGSRISLGIOVRGWGVTGGEEESLTVPVADTWQA GSFKVATOERNPQRAQMRLRRQKKGVVPFLGDFITELQRLDSAI PDDLLOGNINKRSKSVRVLOGMQLUQVAMMYRLRPLEKFVTTYT RMBQLSDKESVKLSCQLEPENP  7137 3 357 SLENDSRISHARSARARGAAGAALRRSINGPVAFREFLEKFVTTYT RMBQLSDKESVKLSCQLEPENP  7138 2 466 WASGMSTVPGGSWRSLGIOPPSGEGESLTVFVADTWQA GSFKVATOERNPQRAQMRLRRQKKGVVPFLOGFTTELQRLDSAI PDDLLOGNINKRSKSVRVLOGMQLUQVAMMYRLRPLEKFVTTYT RMBQLSDKESVKLSCQLEPENP  7139 1 357 SLENDSRISHARGEKRARGSRARGAAGRATERSINGPVAFRETBWTAASSQ LKEHRAGGGWRTACILPPSKFOOTH				POELKTDPKGVFVI.PPRGVODI.DIGUDDI DAGGDEIRIT
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LRLFYTMDIRKYDAGUSLAGLMUSLPHITIPGMPEFGSEGHCTL ECLEPALEARERPSGIHPPAULIAHLAGGGIRLRHPRKGEMKL LAYDDDEPGREGETOYLKEEGTILPGDNLTTECRYNTKDRAEMT WGGLSTRSEMCLSYLLYYPRINTTRCASIPDIMEQLGFIGVKEI YRPVTTMPFILKSPKQYKNLSFMDAMMKFKKEGLSFMKLVL SLPVNVRCSKTDNAEMSIQGMTALPPDIERPYKAEPILVCGTSSS SSLHRPFSINLUCLLLISCTLSTKSL  7135 2 2072 FVPRVTFPSLSLGGPKGESUGSITOPLDESSYLIFRAASESDGRC WLDALELALRCSSLLRLGTCKYGRDGEPGTSPDASPSSLCGLPA KTESGSDOSETPGAPVRRGTTYVEQVOELGELGEASQVETVSE ENKSLMMTLLKUKLURSGWDLSEVVLPTFVLEPRSFILKKLSVYYH ADLLSRAAVEEDAYSRMKLVLRWLSGFYKKPRGIKKPYNPILG ETFRCCWFHPDTDSTFFILAGSVULFTVLEWSPHLWSPHYNKACFGIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILKGTMTLELGGGVTIECKANNPQAGLEFKLKFFFGGSTSINGI SKKITSGEVLASLSGHUNDAVFIKEGSGSSSLFMTPSGEVRR QRLRGHTVVLEEGTELESBERLMOHVTRAISKGDGHRATGEKFAL ERAGQRGARERGESLMPMKOLFFTLSSERLMOHVTRAISKGDGHRATGEKFAL ERAGQRGARERGESLMPMKOLFTLDITTGWHIYNZEDHSPMDP LKDIAGPEGDGILRTLQGRAVARGTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPLELDBITGDGBTVPGGESPC RCRKRARRLQALHEAILSTREAQGSLHHHLSAMISSTARAAQA PTFGLLQSPRSWFLLCUFLACQLFINHILK  7136 2 418 DFVPSFRPSGNTSGTVUKLEAATLEKEVAGLREKIHHLDDMK SQGKKVQMIEQLQNSKAVIQSKDATIGELKEKIAYLEABNLEM HDRMEHLIEKQISHGNTSGTARAATLEKEVAGLREKIHHLDDMK SQGKKVAGMTEGLQNSKAVIQSKDATIGELKEKIAYLEABNLEM HDRMEHLIEKQISHGNTGGWGVTGGEESSLTVPVADTWQA GSFKVATGERNPGRAGMRIKRGKKGVVPFLGFFITELQRLDSAI PDDLDGNTNKRSKEVRULQEMQLLQVAAMNYRLRPLEKFVTYFT RMGCLSDKSSYKLSCQLEPENP  7139 1 357 SLENSARGLKMAASAARGAAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCLIPPSKEOPHTGLGWVGFSSEEGLRNALQ QENHILDGWKQVVHTREPELFOTSDEKKDF  7140 1401 1957 RASSIGNATURGELFFSTSOOHTGOVAFEREFLIKKLSC	7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG
ECLEBALBABENGSI HVAULLHAHLAGRGIRIRHFRIKGEMKIL LAYDDDEDFINGEPGYVIKBOTL PLOGINLITE CRYNTKDRAEMT WGGLSTRSEMCLSYLLYYPRINTRCASIPDIMEQUOFIGVKEI YRPVTWPFIIKSPKQVKNLSFMDAMMYKWTKKEGLSFMKLVI. SLPVNWCSKTUDNAEWSI QOMTALPPDIERPYKAEPIVCTSSS SSLHRDFSINLLVCLLLISCTLSTKSL  7135  2 2072 FVPRVTPFSISLQGPKGESVGSI TOPDIPSSYLIFRAASESDGRC WLDALELALRCSSLLRIGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERENPESSTETCHDHSR KTESGSDQSSTPCAPVRRGTTYVEQVQEELGEASQVETVSE ENKSLMMTLLKQLRFCHDLSRVULPTFVLSPRSFLIKLSDYYH ADLLSRAAVEEDAYSMKLVHYPVLSPFSFLIKLSDYYH ADLLSRAAVEEDAYSMKLVHYPVLSPFSFLIKLSDYYH ADLLSRAVEEDAYSMKLVHYPVLSPFSFLIKLSDYYH ADLLSRAVEEDAYSMKLVHYPVLSPFSFLIKLSDYYH ADLLSRAVEEDAYSMKLVHYPVLSPFSFLIKLSDYYH ADLLSRAVEEDAYSMKLVHYPVLSPFSFSFLIKLSDYYH ADLLSRAVEEDAYSMKLVHYPVLSPFSFSFLIKLSDYYH ADLTSRAVEEDAYSMKLVHYPVLSPFSFSFLIKLSDYYH ADLTSRAVEEDAYSMKLVHYPVLSPFSSFLIKLSDYYH ADLTSRAVEHOPLORGEVTITVEQUOPELGIGGASQVETVSE ENKSLMMTLLKQLRFCHDLSRVLLPTLENREDYTLTMPYAHCKG GSITAKSRFYGNSLSALLDGKATLTFINREDYTLTMPYAHCKG GSITAKSRFYGNSLSALLDGKATLTFINREDYTLTMPYAHCKG GSITAKSRFYGNSLSALLDGKATLTFINREDYTLTMPYAHCKG GSGKTTSGEEVILASLSGHWDDVFIKEGGSSSALFMTPSGEVRR QRLRGHTVPLEEDGTELESRHUGHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPTTCBHHYRYEDHSPMDP LKDIAGFEGGTILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESGSSTPESCPELISDEGGDGDPVPGGESGSC PRCRKERRIQALHEAILSTREAQGIRHRILSAMLSSTARAAQA PTFGLLQSPRSWFLLCUFLACOLFINHILK  7136 2 418 DFVPSFRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNKAVIQSIGDATIGLKEKIAYLEAENLEM HDRMEHLIEKGISHGMFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET  7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESLTVPVADTWQA GSFKVATOENNPQRAQMRLRRCKKGVVPPLGDFLTELQRLDSAI PDDLDGNTTKRRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP  7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESLTVPVADTWQA GSFKVATOENNPQRAQMRLRRCKKGVVPPLGDFLTELQRLDSAI PDDLDGNTTKRRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP  7139 1 357 SLENSRAGLKMAARSAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFPKERGULFGYBUGGWFGSFECLRNALQ QENHILDGVKQVHTRRPLLFOTSDDEKKDF	1			LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFOSEGHCTI.
LAYDDDFDFNFQEFQYLKPEGTLIPGDNLTTECRYNTKDRAEMT  WGGLSTRSEMCLSYLLTYPRINLTRCASIPDIMEQLQFIGVKEI YRPVTTWPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL SLEVNNYKCSKTDNAEWSIQCMTALPPDIERPYKAEPILVCGTSSS SSLEMPESINLLVCLLLISCTLSTKSL  FVPRVTFPSLSLGGPKGESVGSITOPLPSSYLIFFRASESDGRC WLDALELALRCSSLLRLGTCKYRGPDGEPGTSPDASPSLCGLPA KTESGSDQSETPGAPVURGTTYVEQVQELGELGEASQVBTVSE ENKSLMMTLLKGLRFCMDLGRVVLPTFVLEBFSPLMKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSMKKDGFCLS GSITAXSRYFGMSLSALLGGKATLTFLNRREDDTLTMPYYHACKG ILVGTWTLELGGKVTLTECAKNNFQAGLEFKLKPFFGGSTSINGI SGKITSGEVLASLSGHUNDFYKEEGSGSSALFWTPSCEVVRR QRLRQHTVPLEEQTELESERLWGHVTRAISKGDQHAATGEKFAL EEAQRGRAAERQSSLMPWKPQLFHLDPTTQEMHYRYEDHSPMDP LKDIAQFEQDGILRTLQGEAVARQTTFLGSPGGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILSIREAQGEHRHLSAMISSTARAAQA PTPGLLQSPRSWFLLCVFLACOLFINHILK SQORKVRQMTEGLCNSKAVIGCKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHHLDDMLK SQORKVRQMTEGLCNSKAVIGKNATIGEKEKHTHLEREN TRIME  7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATOGENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYNKLRPLEKKVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWGA GSFKVATOGENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYNKLRPLEKKVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLENSARGLKMAAASAARGAAALERSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEECLRNALQ QENHIIDGWKQVHTRRPKLEPGTSDDEKKDF  7140 1401 1957 RASSIQVLKAWGGLIPSSFOOOHTGOVALEELFPDLKVYDCFCSF	1			ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKL
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SEO	Predicted	Predicted end	
ID NO:	beginning nucleotide location corresponding to first amino acid	nucleotide location corresponding to first amino acid residue of	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of amino acid sequence	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7141	124	1073	QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG
	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLOPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMINGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG RDRKIYCTDLRNPDIRVLICE

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#### WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

International application No.

PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER  IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00  US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350			
	International Patent Classification (IPC) or to both nat DS SEARCHED	ional classification and IPC	
	cumentation searched (classification system followed b 36/23.1; 435/320.1, 455, 468, 530/300, 350	y classification symbols)	
Documentation	on searched other than minimum documentation to the	extent that such documents are included in the fields searched	
Electronic da MEDLINE, l	•	of data base and, where practicable, search terms used)	
	UMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where a	ppropriate, of the relevant passages Relevant to claim No.	
A	WAJIMA et al. The cDNA cloning and transient exp hydroxysteroid dehydrogenase of chickens. Gene. 19		
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially 1-11, 13-16, and 19-26	
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A.P	Database PubMed, ID No. 10919256, HENNEBOL generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.8	complementary deoxyribonucleic acid	
A	Database PubMed, ID No. 2760883, BEIL et al. Syr the baboon (Papio anubis). J. Reprod. Fertil. July 19 Abstract.		
A,P	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol.141	liates ovary-specific expression in	
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	documents are listed in the continuation of Box C.	See patent family annex.	
"A" document	pecial categories of cited documents:  defining the general state of the art which is not considered to be	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
-	lar relevance plication or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step	
	which may throw doubts on priority claim(s) or which is cited to the publication date of another citation or other special reason (as	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is	
•	combined with one or more other such documents, such combination		
"P" document published prior to the international filing date but later than the "&" document member of the same patent family priority date claimed		"&" document member of the same patent family	
	ctual completion of the international search	Date of mailing of the international search report  7 JUN 2001	
Corr Box		Authorized officer  All Marsh  Michael Woodward  Authorized of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the like of the	
Washington, D.C. 20231		Telephone No. (703) 308-0196	

Form PCT/ISA/210 (second sheet) (July 1998)

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)			
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:			
Claim Nos.:     because they relate to subject matter not required to be searched by this Authority, namely:			
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Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

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The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

### **CORRECTED VERSION**

## (19) World Intellectual Property Organization International Bureau





## (43) International Publication Date 26 July 2001 (26.07.2001)

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## (10) International Publication Number WO 01/53312 A1

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- (21) International Application Number: PCT/US00/34263
- (22) International Filing Date:

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	09/471,275	23 December 1999 (23.12.1999)	US
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	09/620,312	19 July 2000 (19.07.2000)	US
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	09/662,191	14 September 2000 (14.09.2000)	US
	09/693,036	19 October 2000 (19.10.2000)	US
	09/727,344	29 November 2000 (29.11.2000)	US

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US	09/488,725 (CIP)
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(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

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- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

#### Published:

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

01/533

(48) Date of publication of this corrected version:

1 November 2001

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(51) International Patent Classification?: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

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- (88) Date of publication of the revised international search report: 20 June 2002
- (15) Information about Corrections:
  see PCT Gazette No. 25/2002 of 20 June 2002, Section II
  Previous Correction:
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

# REVISED VERSION

### INTERNATIONAL SEARCH REPORT

International application No.

RSION		PCT/US00/34263		
A. CLASSIFICATION OF SUBJECT MATTER  IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00  US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350  According to International Patent Classification (IPC) or to both national classification and IPC				
B. FIELDS SEARCHED				
Minimum documentation searched (classification system followed by classification symbols) U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350				
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched				
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST				
C. DOCUMENTS CONSIDERED TO BE RELEVANT				
Category *	Citation of document, with indication, where ap		Relevant to claim No.	
A	WAJIMA et al. The cDNA cloning and transient exp hydroxysteroid dehydrogenase of chickens. Gene. 19		1-11, 13-16, and 19-26	
Α	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.		1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.		1-11, 13-16, and 19-26	
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of particular relevance  "E" earlier application or patent published on or after the international filing date			vance; the claimed invention cannot be be considered to involve an inventive step	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		"Y" document of particular relevance; the considered to involve an inventive ste combined with one or more other suc-		
"O" document referring to an oral disclosure, use, exhibition or other means		being obvious to a person skilled in the		
"P" document published prior to the international filing date but later than the priority date claimed		"&" document member of the same patent family		
Date of the actual completion of the international search		Date of mailing of the international search report		
		0.5 SEP 2001		
Name and mailing address of the ISA/US  Commissioner of Patents and Trademarks		Authorized officer  And Ward Woodward  Michael Woodward		
Box PCT Washington, D.C. 20231			· K.	
Facsimile No. (703)305-3230		Telephone No. (703)/308-0196	/ )	

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